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2018年甘肃省逆境生理生态重点实验室

科研工作总结

一、实验室基本信息

实验室名称：甘肃省寒区旱区逆境生理与生态重点实验室

学科（领域）：生物学(生态环境)

建立时间：2012年12月

建设依托单位：中国科学院寒区旱区环境与工程研究所

实验室主任：李新荣研究员

二、实验室建设目标、研究方向和主要研究内容

自从2012年12月立项建设以来，甘肃省寒区旱区逆境生理与生态重点实验室立足甘肃，面向西部，在基础和应用基础研究方面取得了系列重大进展和突破。在寒旱区沙害治理及其生态重建与恢复、干旱区生态水文学、人工植被稳定性及胁迫生理生态学、寒区旱区物种适应机制、西北百合产业发展等方面取得了重要进展，为退化生态系统的植被持续恢复提供了理论和技术支撑，实现了退化植被恢复与重建过程中有限水资源的高效利用，开发了适合当地立地条件的农业产业提升关键技术。使我国防沙治沙基础理论研究在现有基础上得到较大提升，推动了逆境生理生态学、自然地理学、水文学与沙漠科学的交叉、集成和创新，丰富了干旱区生态系统理论，提高了干旱区社会经济可持续发展的科技支撑能力。取得的成果在甘肃省及周边省份（宁夏、内蒙、西藏）广泛应用，产生了明显的生态、社会和经济效益。

实验室近3年承担的主要项目有：国家重点研发计划项目（973）1项，国家自然科学基金创新群体项目1项，国家自然科学基金优秀青年基金1项，国家自然科学基金重点项目2项，国家科技基础资源调查专项1项，国家基础研发计划项目1项和课题6项，中科院A类先导计划项目课题2项，中科院战略性先导科技专项3项，国家自然科学基金面上项目30余项，其他横向课题80余项。到位科研经费三年总计逾1.4亿元，发表高水平SCI论文180余篇，获得省部级以上

科技进步奖 6 项。

在此基础上，重点实验室进一步明确了研究方向、近期主要研究内容和研究目标。

2.1 实验室研究方向

针对甘肃省极端环境特征，以寒区旱区生态格局和过程的演化机理及调控为研究重点，注重基础研究与应用基础研究，形成了包括环境科学、生态学、生物学与地学等多学科交叉的优势和特点，其主要研究方向为：

2.1.1 生态格局与过程及脆弱生态系统恢复

从生态系统到景观尺度研究寒区旱区生态格局与过程的演变及其调控机制，探明脆弱生态系统恢复与重建的理论基础，研发退化生态系统可持续恢复的关键技术与模式。

2.1.2 生物对环境胁迫的生理应答、适应调控及生态分化

研究寒区旱区生物适应逆境的生理响应、信号调控、基因功能、个体发育及与环境互作的机理；通过不同生态种群的遗传多样性与群落的生物多样性，揭示物种与种群适应不同生态环境的机理，为极端环境生物多样性保育和生物资源可持续利用与生态健康提供理论支撑。

2.1.3 逆境农业生物技术研发

利用寒区旱区抗逆基因资源，选育和创建具有高抗逆性的生物品种，研发特色生物资源产品。

2.2 主要研究内容与方案

2.2.1 寒区旱区生态系统格局、过程和服务研究

寒区旱区的脆弱生态系统是陆地生态系统的重要组成部分，研究寒区旱区生态系统的结构和功能特征、服务价值及其稳定性维持机理，是该区资源优化配置、绿洲可持续发展和植被恢复与重建等实践工作的重要理论前提。具体研究内容与方案包括：

2.2.1.1 寒区旱区生态系统结构、功能和过程研究

围绕寒区旱区荒漠化防治、水土流失治理、植被恢复等重大理论和实践需求，基于对该区生态系统长期定位观测，开展脆弱生态系统结构、功能、过程和稳定性维持机理的研究。重点研究生态系统生物空间组成结构、营养结构及其功能，不同地理单元与要素的空间组成结构及其对生态系统的影响，以及生态系统能流、物流与信息流的循环过程与互馈机制，评价和预报寒区旱区生态系统各要素的发展动态和变化趋势，探索该区生态系统中人与自然耦合关系，维护生态脆弱区水土、生物资源的可持续利用，为甘肃省及我国西北地区生态环境保护、建设和决策管理提供科学依据。

2.2.1.2 寒区旱区生态系统功能评估与服务价值研究

针对长期以来人们对寒区旱区生态系统价值认识的局限性和片面性，对其改善环境等非商品性功能估计不足等问题，全面开展该区生态系统功能和价值的现状、发展趋势和影响因素等的研究。重点对祁连山及青藏高原高海拔区、腾格里沙漠和毛乌素沙地等生态系统进行长期定位观测，集成创新方法建立生态系统服务功能实物量评估指标和技术体系，构建脆弱生态系统服务功能综合评估模型，评估寒区旱区生态系统防风固沙、水文调控、土壤保育、碳氮固定、生物多样性保育、生物地球化学循环、文化游憩等服务功能，核算不同生态系统服务价值量，系统分析寒区旱区生态系统服务特点、空间格局及影响因素，为甘肃省及我国高寒和荒漠区资源可持续利用和社会经济健康发展提供决策和管理依据。

2.2.2 干旱半干旱区植被恢复和演替的理论模式与技术体系

水是干旱半干旱区诸多生态系统过程的驱动力和关键的非生物限制因子，任何生态系统格局和生态过程的变化都与水文过程相关联。水文过程和生态过程的时空耦合机制研究，可以客观、全面地诠释干旱区植被与土壤系统相互作用与反馈机理，可以为西部地区管理水资源和指导生态环境建设提供科学依据。同时，干旱半干旱区植被系统脆弱，易被破坏，恢复困难。实践证明受损植被依靠自然的恢复过程非常缓慢、甚至无法完成。因此，研究干旱半干旱区生态系统退化过程与恢复调控机制，集成生态恢复技术体系，通过人工促进植被恢复或植被重建，

是受损植被恢复的切实有效方法，也是干旱半干旱区生态文明建设和生态优先发展战略实施的重要保障。具体研究内容与方案包括：

2.2.2.1 植被 – 土壤系统生态水文过程及其调控机理

研究植被 – 土壤系统水动力学性质、不同类型植被的耗水量和对区域水量平衡的影响，探讨土壤水循环的植被调控机理和人工植被稳定性维持的生态水文学机理，明确水循环对土壤 – 植被系统演替的驱动作用，为干旱半干旱区生态保护与建设奠定理论基础。

2.2.2.2 生物土壤结皮形成机理、生态功能及在防沙治沙中的应用

研究荒漠地区生物土壤结皮的形成和演变对生态恢复的指示作用，明确生物土壤结皮对降水入渗、地表蒸发、凝结水捕获等水文过程的影响机制，量化生物土壤结皮不同组分对植被 – 土壤系统水循环和时空分布的调控作用，揭示生物土壤结皮在温带荒漠植被 – 土壤系统的“源 – 汇”关系，以及对植被格局和过程的驱动机制，研发人工结皮在防沙治沙中应用的关键技术。

2.2.2.3 生态系统退化过程与机理研究

研究退化生态系统的稳定性、多样性、抗逆性、生产力、恢复力与可持续性，先锋与顶级生态系统发生、发展机理与演替规律，不同干扰条件下生态系统的受损过程及其响应机制，生态系统退化的景观诊断及其评价指标体系，生态系统退化过程的动态监测、模拟、预警及预测，为退化生态系统的恢复和重建提供理论依据。

2.2.2.4 人工固沙植被稳定性维持机制研究

针对甘肃省及我国西北地区生态工程建设中的实践需求，对不同气候区、不同演替序列和不同配置的人工固沙植被进行长期定位观测，研究人工固沙植被结构、物种多样性、功能及演替规律，探讨固沙植被关键水文要素变异规律以及水文过程对固沙植被演替的驱动机制，研究种间竞争（物种组合）、环境压力（水分、养分、盐分等）和干扰三类因子对人工植被稳定性调控机制，为构建维持人工固沙植被稳定的管理范式提供依据和技术支撑。

2.2.2.5 退化生态系统恢复与重建的技术体系和应用研究

研发退化生态系统结构与功能优化配置及其调控技术、物种与生物多样性恢复与维持技术、生态工程设计与实施技术和环境规划与景观生态规划技术等。

2.2.3 极端环境生物互作与生态分化机理研究

应用分子生物学、生物信息学及各种组学技术，从不同尺度系统分析物种适应极端环境的基因特征、代谢特征以及遗传分化和进化特征，研究不同物种的内在调控机理及其环境驱动响应，探讨个体及种群的遗传分化和进化模式，阐明生态系统内不同要素相互作用的生态调控网络是农作物逆境栽培、濒危生物保护以及生物资源高效利用的理论前提和实践依据。具体研究内容与方案如下：

2.2.3.1 植物非生物胁迫应答机理

将植物生理生态学、分子生物学及遗传学相结合，利用转录组学、基因组学、蛋白组学、代谢组学等现代分子生物学手段，系统研究寒区旱区不同植物抗逆的物候、形态及细微解剖特征、生理响应过程、基因及代谢产物调控过程，探讨不同植物的耐受性维持机理及其遗传基础，阐明植物适应寒区旱区环境的生理生态机制及其基因调控机理。

2.2.3.2 植物—微生物相互作用的适应机理

针对寒区旱区长期演化形成的物种分布格局及特点，应用分子生物学最新技术对生物个体间和种群间相互作用的信号释放、传递、接收和响应的整个生物过程进行研究，阐明生物相互作用的内在分子机理。主要包括荒漠生态系统生物土壤结皮隐花植物与微生物群落结构的演替变化规律、隐花植物与微生物群落之间的相互作用、不同微生物群落（细菌、真菌、古菌）的互作及协同调控机理，并分析演替变化及相互作用过程中的非生物驱动机制；不同类型生态系统中植被、土壤微生物、土壤微小动物及其生物地化循环过程响应极端环境或环境变化的相互作用机制，通过不同类型生态系统中生物之间以及生物和非生物之间的相互作用，阐明生态系统稳定性维持的生物学依据，为寒区旱区绿色生态发展提供理论指导与技术支撑。

2.2.3.3 生态分化的生物学过程与遗传学基础

利用转录组、代谢组和简易基因组技术，对温带荒漠建群灌木红砂和先锋种一年生草本植物沙米（沙蓬）的遗传多样性和表型多样性进行了深入调查，阐明典型荒漠植物适应历史气候变化的分布区变迁、种群动态和基因组分化模式，解析不同地理种群的局域适应形成的分子调控、代谢和表型基础。

2.2.4 抗逆生物资源保育、开发与利用

针对寒区旱区特有抗逆生物资源，开展抗逆生物资源的收集、筛选、保育及评估，利用现代生物技术开发并有效利用该资源，为医学、农业、制药等领域的创新提供样本或工具，进而形成产业应用，提升我国在知识产权竞争格局中的优势。具体研究内容与方案如下：

2.2.4.1 寒区旱区珍稀濒危植物及特色药用食用植物研究

针对该区半日花、沙冬青、四合木和绵刺等珍稀濒危植物面临灭绝问题，研究其外在和内在濒危机制，如生境变化、生植物候、生殖时间、生殖力和生存力等，探明其濒危原因，为濒危物种的稳定繁衍与保护提供科学依据；针对寒区旱区虫草、锁阳、肉苁蓉、甘草和麻黄等特色药用植物资源，开展药用植物资源调查、生长发育特性与环境和其他物种关联性研究，为药用植物的保护和开发利用奠定理论基础；针对可作为食品、饮料、调味品和食用色素的野生食用植物资源为研究对象，重点对分布范围较广、储量丰富、具有保健价值的沙米和籽蒿等食用植物进行开发利用研究。开展资源收集、种子繁育及贮藏、田间农艺性状记录、评估及筛选；利用化学诱变方法创新种质资源，选择农艺性状良好的突变体；采用杂交育种方法聚集各种优良农艺性状，培育优良栽培品种，为沙区生态建设和粮食安全提供创新种质资源；研究流沙环境野外及室内物理与化学诱变方法，应用最新遗传修饰技术，增强沙漠植物遗传变异，应对流沙环境严酷的自然选择，加强其适应性，不断创新沙区生态建设急需的沙漠植物种质资源。

2.2.4.2 寒区旱区特色作物育种及栽培技术

利用沙漠植物创新种质资源，传统育种技术与最新生物技术相结合，培育沙区新作物（如沙米、花棒等）优良品种，研究相应栽培技术，良种改良法，为沙区粮食安全提供新模式；利用化学和物理诱变技术，对采集自各大沙漠区域的沙

米种质资源进行引种驯化，开展同质园实验对各类生态和农艺性状进行筛选，选育能够适应极端气候变化的新型高营养型作物。

2.2.4.3 草食动物抗性资源保育与开发

草食动物是生态脆弱区的重要物种，可以通过影响同化能量影响到整个生态系统能量流动，其种群结构、数量以及代谢效率对保证生态脆弱区的物种多样性以及动态平衡具有重要作用。我国的四大牧区（即内蒙、新疆、西藏和青海牧区）皆分布在寒区旱区生态脆弱区。目前我国生态脆弱区存在着严重滞后的草畜生产体系与生产效率给地区的生态系统恢复带来了极大压力，导致这些地区陷入生态环境退化，家畜陷入“夏饱、秋肥、冬瘦、春乏（死）”的恶性循环中。因此，结合传统动物营养学与现代分子生物学技术，全面解析北方土种反刍家畜抗逆营养代谢特征，发掘本土家畜优良遗传资源，建立抗寒基因检测体系，以期为发展寒区旱区特色畜牧业提供技术支撑。通过 3-5 年的积累，做出国内外有影响的寒区旱区牧区草畜高效转化模式，力图为北方寒旱地区放牧家畜全年营养均衡饲养、冷季科学补饲以及抗逆品种选育这三大核心问题提供解决方案，提高北方牧区畜牧业生产效率，增加牧民收入，实现草畜生态平衡。

2.2.4.4 甘肃省特色作物百合产业提升关键技术研发

针对我国西北地区百合生产中存在的主要问题，开发适合当地立地条件的产业提升关键技术，包括优质种源繁殖技术，为解决严重制约百合产业发展的种源退化问题提供重要的技术支撑；提质节本增效生产技术，开发百合种球优质低成本繁育技术，筛选能有效除去多年生恶性杂草的化学除草剂，研制碱性土壤百合补铁控释肥料，为解决西北地区普遍发生的百合黄化问题提供重要技术支持；病害综合防治技术，开发高效防治百合叶枯病技术，筛选针对百合根病的生防菌及能显著增强百合抗性的诱抗剂，制定百合主要病害的综合防治方案，通过优质种球推广、生物防治和化学防治的联合使用，使切花百合根病感染率和兰州百合叶枯病发病率大大降低，百合产量和品质得到大幅度提升；建立克服连作障碍关键技术，分析百合根系分泌物及自毒机制与微生物的相互作用，制定百合连作障碍克服方案，使百合产业得到全面提升。

2.2.4.5 甘肃省道地中药材广谱性生防菌剂研发与应用

通过分离鉴定解淀粉芽孢杆菌气态挥发物（VOC）有效成分，分析 VOC 诱导植物抗逆的信号机制，阐明解淀粉芽孢杆菌诱导植物抗逆性及抗病性的分子生物学机制；针对甘肃几种道地药材危害最为严重的土传微生物病害，主要为当归、党参、枸杞、黄芪的根腐病，当归和黄芪的麻口病等，研制兼备促进生长和生物防治功能的新型广谱性生防菌剂，促进中药材产业产量和质量的提升。

2.3 预期研究目标

通过对寒区旱区生态系统稳定性维持机理、脆弱生态系统恢复机理、生态系统内物种互作适应及分化机理，以及特有抗逆生物资源的研究，阐释寒区旱区极端环境生态系统功能及其理论与实践指导意义，为甘肃省抗逆育种、生物资源利用和退化生态系统恢复提供科学依据和科技支撑，为多学科交叉研究生态系统调控网络开辟途径，也为脆弱生态恢复的试验示范提供平台及技术支撑，推动生态学及相关学科的发展，引领国内干旱生态系统研究前沿。

2.4 预期发展目标

- (一)阐明寒旱区生物抗逆机理，揭示其特有逆境适应机制；
- (二)阐释脆弱生态系统各要素互作及其稳定性维持机理；
- (三)为寒旱区恢复生态学研究、试验示范提供平台及技术支撑；
- (四)为抗逆育种、生物资源利用和退化生态系统恢复提供理论和科技支撑；
- (五)成为国内外相关研究知名学术交流平台；
- (六)凝聚一支扎根于甘肃的优秀创新团队。

三、实验室学术委员会组成

3.1 实验室主任

李新荣，中科院西北生态环境资源研究院研究员，中科院特聘研究员核心骨干、国家杰出青年基金获得者、973 项目首席科学家、国家基金委创新研究群体负责人、“新世纪百千万人才工程”国家级人选、第七届全国优秀科技工作者奖获得者、甘肃省优秀专家、甘肃省领军人才、中国科学院 2018 年度“感动中国”科

技先锋人物。在 GCB、SBB、PNAS、FM、PS、《科学通报》、《中国科学-生命科学》和《中国科学-地球科学》等国内外 SCI 刊物上共发表论文 300 篇，其中 SCI 收录 120 篇，被 SCI 引用 3000 余次，出版专著 5 部。获授权发明专利 6 件。获得国家科技进步二等奖 2 项、省部级一等奖 4 项。

1987 年毕业西北林学院（现西北农林科技大学），1995 年在莫斯科大学生物系地植物专业获博士学位；1998 年中科院兰州沙漠所研究员、博士生导师；1999 年至今中科院西北生态环境资源研究院（原寒区旱区环境与工程研究所）研究员（2 级）、博士生导师、中科院沙坡头沙漠研究试验国家站站长、中科院沙漠与沙漠化重点实验室副主任、甘肃省寒区旱区逆境生理生态重点实验室主任；1999 - 2000 在澳大利亚联邦科工组织水土所进修；2003-2004 在美国宾夕法尼亚州立大学高访；2005-2006 在德国柏林工业大学高访；2009-2010 年应邀在德国 Alfried Krupp Kolleg 基金会做 Senior fellow。

3.2 实验室学术委员会组成

表一 实验室学术委员会组成

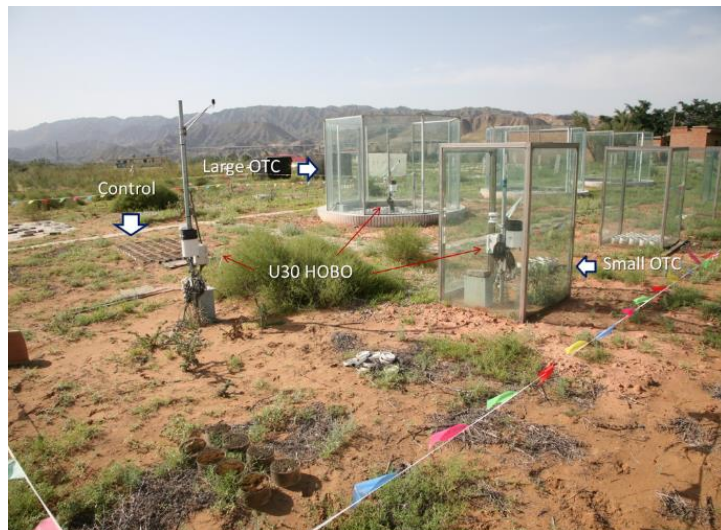
	姓 名	专 业	职 称	学委会职务	工作单位
1	魏江春	生物学	院士	主 任	中科院微生物所
2	安黎哲	植物生理学	教授	副主任	兰州大学
3	李新荣	生态学	研究员	副主任	中科院西北研究院
4	张敬仁	微生物学	教授	委员	清华大学
5	向成斌	分子生物学	教授	委员	中国科技大学
6	刘建全	分子生态学	教授	委员	四川大学
7	康振生	植物生理学	院士	委员	西北农林科技大学
8	王 刚	理论生态学	教授	委员	兰州大学
9	张文浩	生理生态学	研究员	委员	中科院植物所
10	毕玉蓉	逆境生理学	教授	委员	兰州大学
11	陈国雄	遗传发育学	研究员	委员	中科院西北研究院
12	王晓茹	进化生物学	研究员	委员	瑞典 Umea 大学
13	谢忠奎	农业生态学	研究员	委员	中科院西北研究院

14	赵学勇	恢复生态学	研究员	委员	中科院西北研究院
15	Jae-Seoun Hur	微生物学	教授	委员	韩国国立顺天大学
16	Eviatar Nevo	进化生物学	院士	委员	以色列海法大学

四、实验室科研创新点与新进展

1) 基于长期观测，我沙坡头站荒漠生物土壤结皮研究取得新进展

利用开顶式植物生长室 (OTC) 进行了 10 年的长期连续模拟研究，以入渗、凝结水和蒸发量变化作为生物土壤结皮水文功能的代用参数。研究发现，增温伴随降水的减少显著地改变藓类在生物土壤结皮群落中多度、盖度和生物量，相对而言，对蓝藻和地衣在结皮群落中地组成和结构影响不显著。由于结皮群落的种丰富度、多度、盖度和生物量在很大程度上由藓类决定，气候变化导致的结皮群落的这种变化直接降低了结皮对凝结水的捕获，增加了入渗，增大了地表蒸发，减少了表土层含水量，最终改变了原来的水量平衡，限制了草本植物的繁衍和定居，对生态恢复产生不利的影响。以上成果得到国家自然科学基金创新研究群体和重点项目资助，发表在 *Global Change Biology* (IF=8.997) 上。



2) 基于单次降水过程的连续观测灌木穿透雨时空格局研究取得新进展

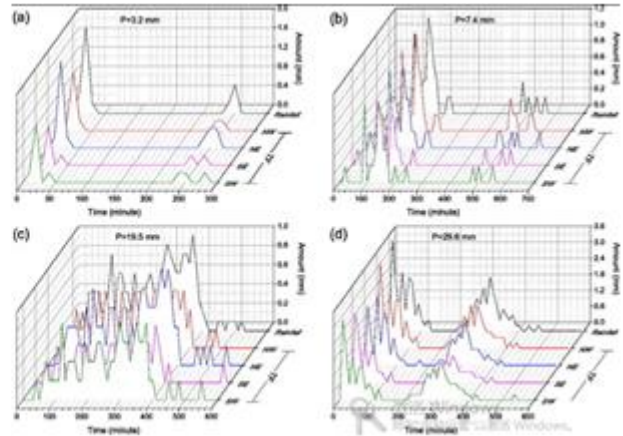
穿透雨是指降水发生后直接通过植物冠层空隙滴落或间接从树叶、树枝和主干滴落至地面的雨水。作为植物冠层对降水再分配的主要组分 (约占降水的四分之三)，穿透雨影响着土壤水分和养分的空间分布、土壤侵蚀、根系生长和分布、土壤微生物群落结构等一系列关键的生态、水文及生物地球化学过程。目前

关于穿透雨时空格局的研究主要基于单次或更长降水时间尺度（日、周、月）。然而，单次降水过程本身是一个随时间变化的不连续过程，导致穿透雨产量在降水过程中也呈现出不连续状态，这意味着穿透雨在非均一植物冠层下方不同方位上既表现出时间异质性又表现出空间异质性，因而对降水过程中更加精细时间尺度上穿透雨的观测研究有助于更好地认识穿透雨这一重要水文过程的发生、发展及其时间和空间异质性。

通过对腾格里沙漠东南缘固沙灌木柠条 (*Caragana korshinskii*) 穿透雨在降雨过程中的时间（间隔 10 min）和空间（冠层下方西北、东北、东南、西南 4 个方位）动态变化进行连续自动观测，量化了降雨过程中穿透雨在灌木冠层下方的时间和空间异质性，并基于主成分分析和多元线性方程模型分析了气象因子对其异质性的影响。

研究结果显示：在单次降雨过程中，降雨和穿透雨在其起止时间上存在着时间差，总体而言二者的时间异质性表现出很好的同步性；穿透雨在灌木冠层下方不同方位上表现出高度的空间异质性，该异质性与降雨过程中主风向紧密相关；对气象因子（降雨量、降雨强度、10 min 最大降雨强度、降雨历时、间雨期、风速、空气温度、空气湿度、蒸气压差）进行了主成分分析，显示 3 个主成分可以解释 84.2 % 的总变异；将 3 个主成分引入多元线性方程模型后发现，第 2 个主成分（在降雨量和 10 min 最大降雨强度两个参数上有较大载荷）是影响穿透雨产量及其空间异质性的主要成分。本研究强调了高分辨率降水和穿透雨观测数据对穿透雨时空格局研究的重要性，结果有助于改进降水再分配模型中干旱荒漠区灌木穿透雨的刻画及模拟。

以上成果得到国家重点研发计划和国家自然科学基金项目资助，发表在 *Science of the Total Environment* (IF=4.61) 上。

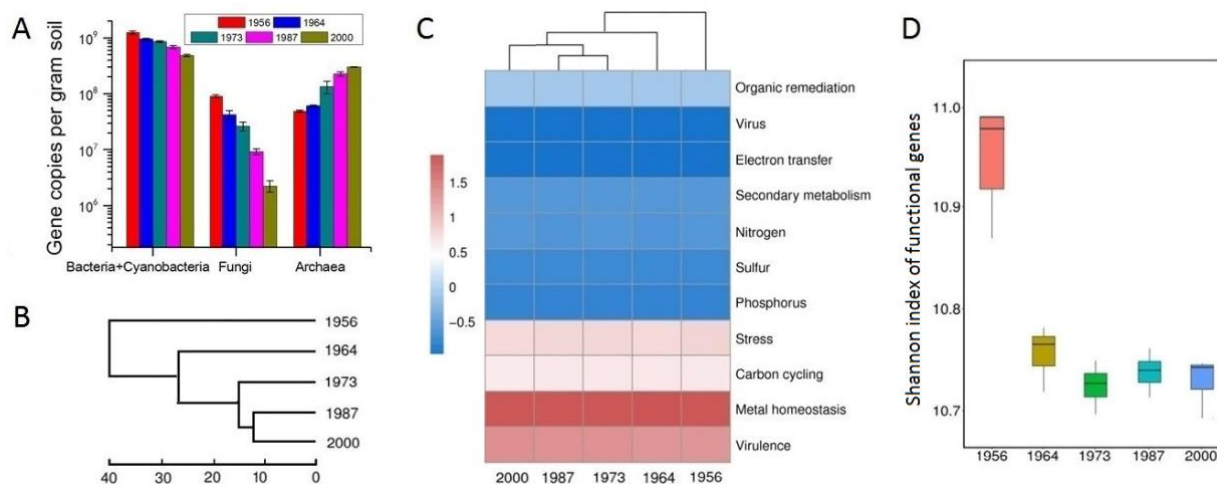


3) 固沙植被生物土壤结皮演替过程中微生物群落功能基因研究取得新进展

生物土壤结皮是由隐花植物如蓝藻、地衣、苔藓和其他微生物与土壤表层颗粒胶结而成的干旱区耐旱生物垫,是荒漠系统地表景观的重要组成部分之一。同时,生物土壤结皮也是退化植被恢复的先锋,通过其微生物群落的代谢活动而成为干旱地区的重要组织。此前,关于生物土壤结皮微生物仅限于群落组成结构特征的研究,而对参与生物地化循环过程的微生物代谢潜力缺少研究,因而难以准确评估生物土壤结皮演替过程对荒漠系统生物地化循环的贡献。

利用功能基因芯片技术回答以下问题:微生物群落功能基因结构随着生物土壤结皮的演替如何变化;参与碳氮循环过程的微生物功能基因如何变化,及其变化是否促进了演替过程中微生物的代谢潜力。分析了多年演替过程中沙坡头人工固沙植被生物土壤结皮微生物群落功能基因结构及其代谢潜力的变化特征。研究结果显示:生物结皮发育过程中,微生物功能基因丰度与微生物组分密切相关;发育年限长的结皮,其微生物功能基因丰度明显高于其他年限较短的;分析表明真菌和苔藓的丰度以及土壤理化性质是演替过程中功能基因结构变化的主要决定因子;参与碳氮循环过程的主要功能基因为碳降解和反硝化作用的基因,二者都与演替后期真菌丰度的增加有关;且发育年限长的结皮碳氮循环基因丰度的增加促进了微生物的代谢潜力。由此可见真菌是结皮发育后期碳氮循环的主要微生物调控者,微生物功能结构在一定程度上能够反应荒漠系统重建植被的稳定性。

以上成果得到国家重点研发计划和国家自然科学基金创新研究群体项目资助,发表在 *Soil Biology and Biochemistry* (IF=4.61)上。



4) 阐明了全球变化因素对草地凋落物和根系质量及其分解的影响

全球变化对草地生态系统的强烈影响正在改变着陆地生态系统的生物地球化学循环过程。通过开展模拟全球变化中 CO₂ 倍增、氮沉降和物种多样性变化对草地凋落物及根系质量及分解影响的研究，发现了 CO₂ 倍增、氮沉降和物种多样性变化均是单一因素影响凋落物和根系的质量。通过方差与协方差分析，CO₂ 倍增对凋落物和根系的分解没有直接影响，N 沉降促进了凋落物的分解，增加的物种多样性影响了凋落物和根系分解及其碳氮的释放，土壤碳氮、生物量和凋落物及根系质量作为协变量也影响着分解过程。然而，建立的结构方程模型表明，CO₂ 倍增间接地降低了凋落物分解过程中的 N 损失、增加了根系的 N 损失，N 沉降间接地增加了凋落物和根系的分解及其碳氮的释放，而增加的物种多样性直接地增加了凋落物的分解及其碳氮的释放、间接地降低了根系的分解及其碳氮的释放（图 1）。该研究揭示了全球变化因素能通过影响草地凋落物和根系质量来影响其分解的作用机制；阐明了 N 沉降能加速草地凋落物和根系的分解，从而缓解了 CO₂ 倍增对于草地土壤可利用性的限制作用；明确了草地凋落物和根系分解对 CO₂ 倍增和物种多样性变化的响应存在明显差异，为进一步深入认识全球变化背景下的草地碳氮循环提供了科学依据。相关研究成果 2018 年发表在美国生态学会主办的国际生态学杂志 *Ecosphere* 上。

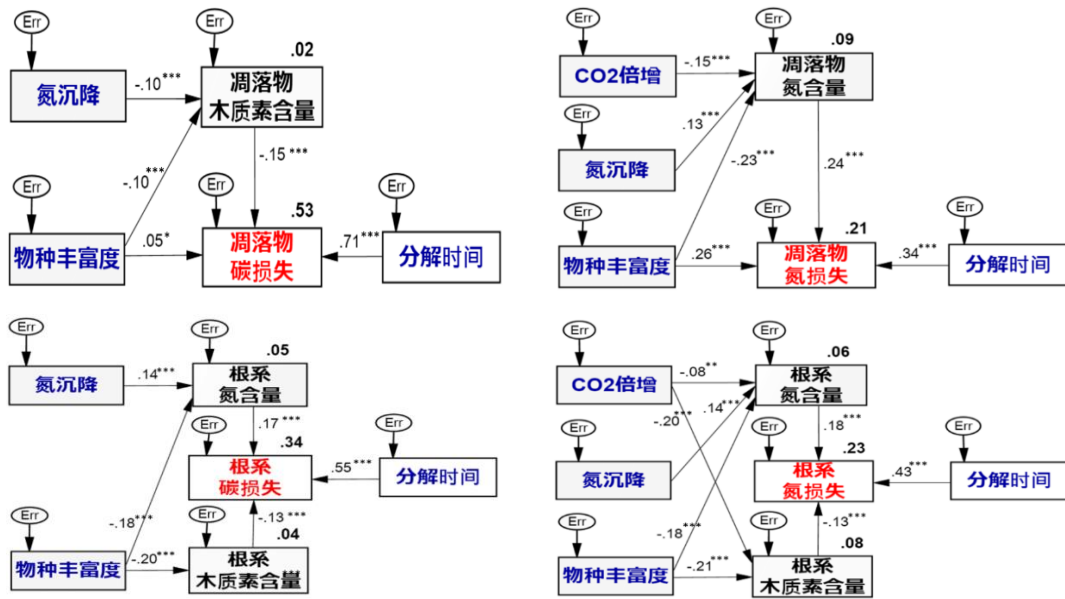


图 1. 全球变化因素对草地凋落物和根系分解影响的结构方程模型

5) 阐明自然干旱梯度和模拟干旱对草原冠层养分影响的差异性

在全球气候变化背景下，内蒙古草原干旱的强度和频度呈多发趋势，极端干旱事件势必对草原生态系统结构和功能产生重要影响。基于北方干旱荒漠草原到典型草原 3 个点的极端干旱处理实验，研究发现：在自然干旱梯度上，植物通过内稳态机制来提高氮、磷浓度，增强群落的抵抗能力，区域尺度上物种变化或者替代是群落养分增加的内在原因（图 2）。然而，模拟短期极端干旱条件下，草原植物群落氮浓度呈上升趋势，而磷浓度呈下降趋势，而种内竞争和物质周转共同影响该生态过程（图 3）。此外，不同区域群落养分响应程度具有明显差异。极度干旱的荒漠草原区，植物群落养分对极端干旱的敏感性较弱，抵御水分胁迫的能力较强。因此，未来研究不同草原或者陆地生态系统对干旱的响应，应该建立大型联网干旱实验平台，紧密结合控制实验和自然梯度实验，提高实验结果的准确性和有效性，为建立陆地生态系统自然评估体系提供科学依据。相关成果 2018 年合作发表于美国生态学会刊物 Ecology 上。

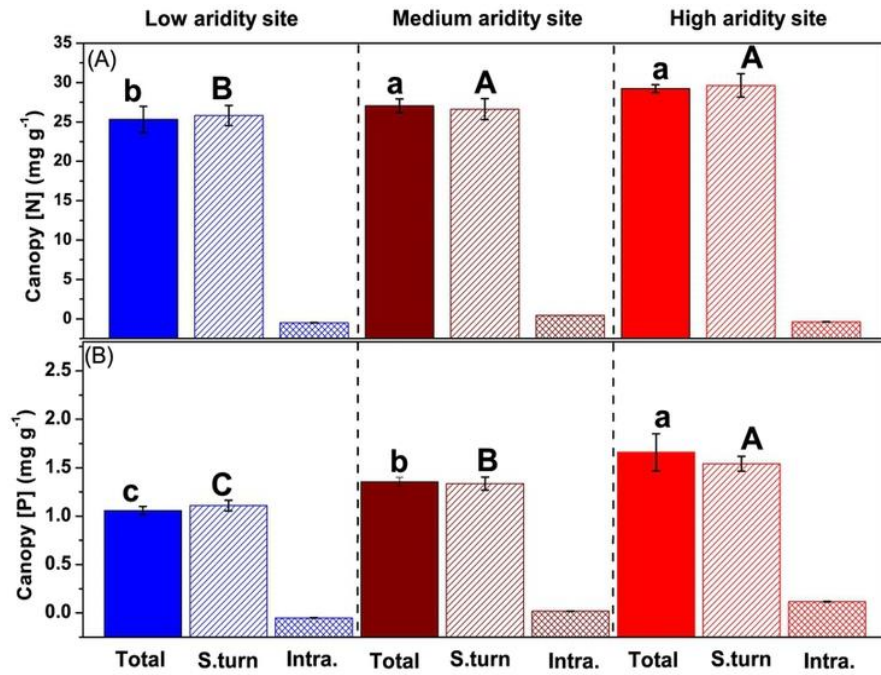


图 2. 自然干旱梯度上草原植物群落及其种间与种内的 N、P 含量变化

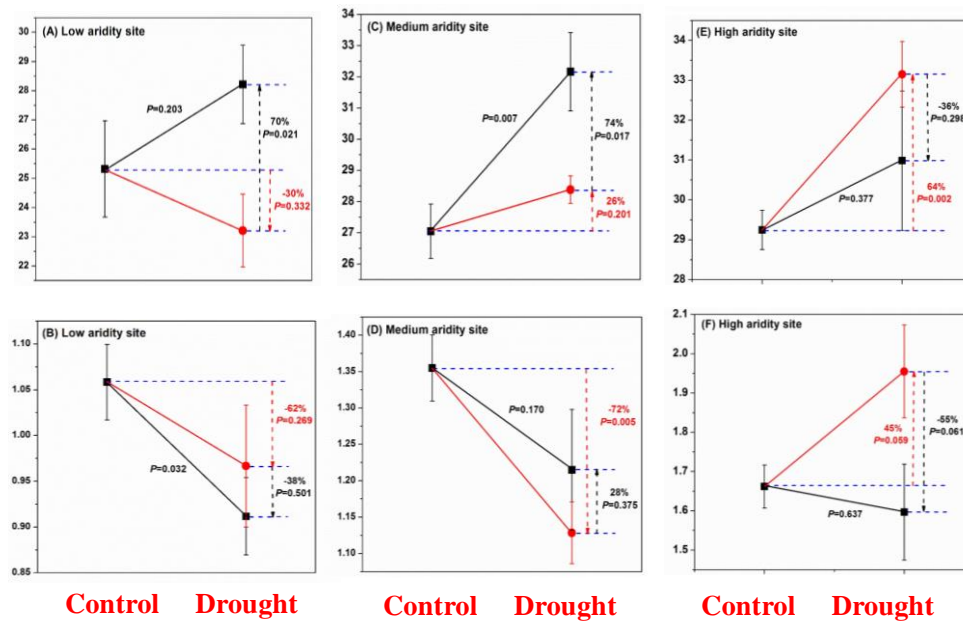


图 3. 模拟极端干旱下不同草原植物群落的 N、P 含量变化

6) 确定了放牧影响下草地植物功能多样性与生物量之间的关系

植物功能多样性极大地影响着生态系统的功能和过程，然而草地生态系统中长期放牧、土壤、植物功能多样性对群落组成和生物量的直接和间接影响关系仍然不是十分清楚。通过不同草地植物群落功能性状及其多样性对长期放牧的响应研究，明确了长期放牧降低了草地群落水平的植物高度和植物功能离散度

(FDIs)、降低了草地中植物比叶面积 (SLA)、增加了其叶干物质含量 (LDMC) (图 4)。应用结构方程模型 (SEM) 评价了长期放牧和土壤特性变化对植物功能多样性、群落组成和地上与地下生物量的直接与间接影响关系, 确定了放牧和土壤 N 含量对地上和地下生物量的直接影响, 阐明了放牧和土壤 N 含量也能通过影响植物高度和功能离散度来间接影响地上生物量, 阐明了土壤水分通过影响多年生草本丰富度来间接影响地上生物量。基于植物功能多样性的结构方程模型能够解释地上生物量变化的 84%, 极大地提高了放牧和土壤特性对地上生物量影响的解释关系 (图 5)。本研究支持了植物功能性状的“生物量假说”, 能很好的解释放牧和土壤变化对草地生态系统功能的影响, 阐明了植物功能多样性在长期放牧和土壤特性影响地上生物量中的调节作用, 为退化草地恢复及持续管理提供了依据。相关成果 2018 年发表于国际生态学杂志 Ecological indicator 上。

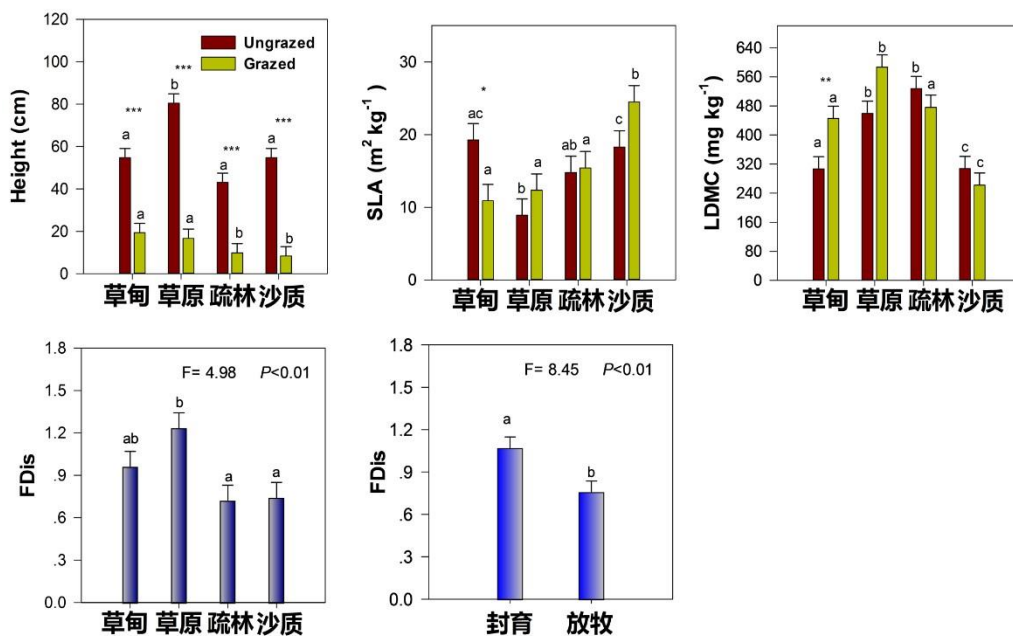
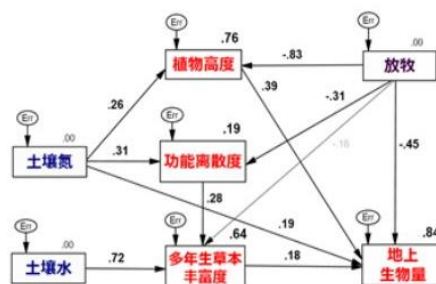


图 4. 长期放牧对北方草地植物功能性状及多样性的影响



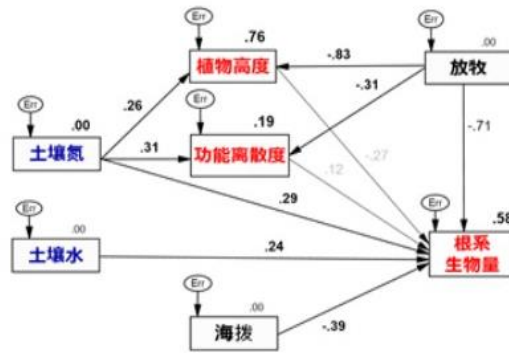


图 5. 北方草地植物功能多样性与放牧、土壤特性和生物量的关系

7) 阐明了荒漠区牧草-紫花苜蓿的生殖限制及传粉规律

花多果少是荒漠植物生殖的普遍现象，花粉限制和资源限制是植物生殖成功率低的主要原因，然而，授粉环境和可利用资源的变化会导致花粉限制与资源限制之间的转变。研究揭示了紫花苜蓿不同种群间开花和坐果比例的差异，阐明了虫媒传粉是影响紫花苜蓿坐果率的关键因素（图 6）。尤其在荒漠环境中，植物受环境、气候等因素影响，导致访花者不足，紫花苜蓿种群具有风媒的特性，从而提高了异花传粉机率。因此，虫媒和风媒传粉相结合是紫花苜蓿种群与荒漠环境相互选择的结果，也是苜蓿种群繁殖的保障机制。相关研究成果于 2018 年发表在国际生态学杂志 *Ecology and Evolution* 上。

研究结果揭示了花粉限制是影响紫花苜蓿传粉效率的关键因素（图 7），并且开花数目和昆虫访花频率具有显著相关性。阐明了异交是紫花苜蓿的主要繁殖方式。相关研究成果于 2018 年发表在国际生态学杂志 *BMC Ecology* 上。

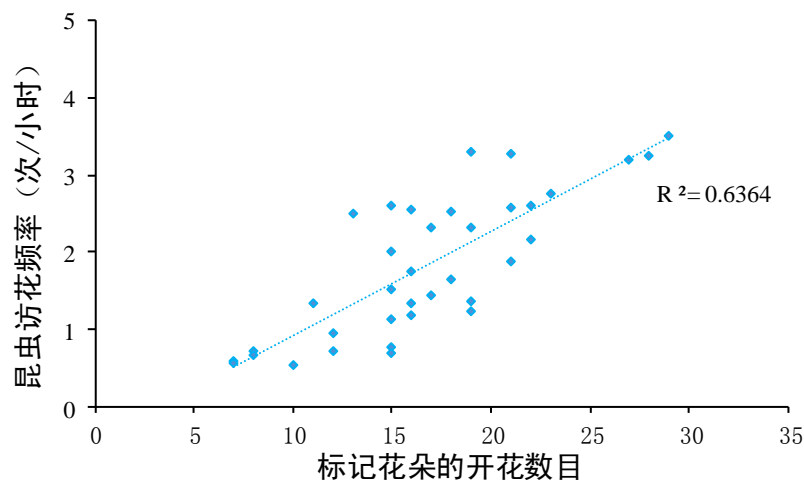


图 6. 苜蓿种群标记花朵开花数目和访花频率的关系

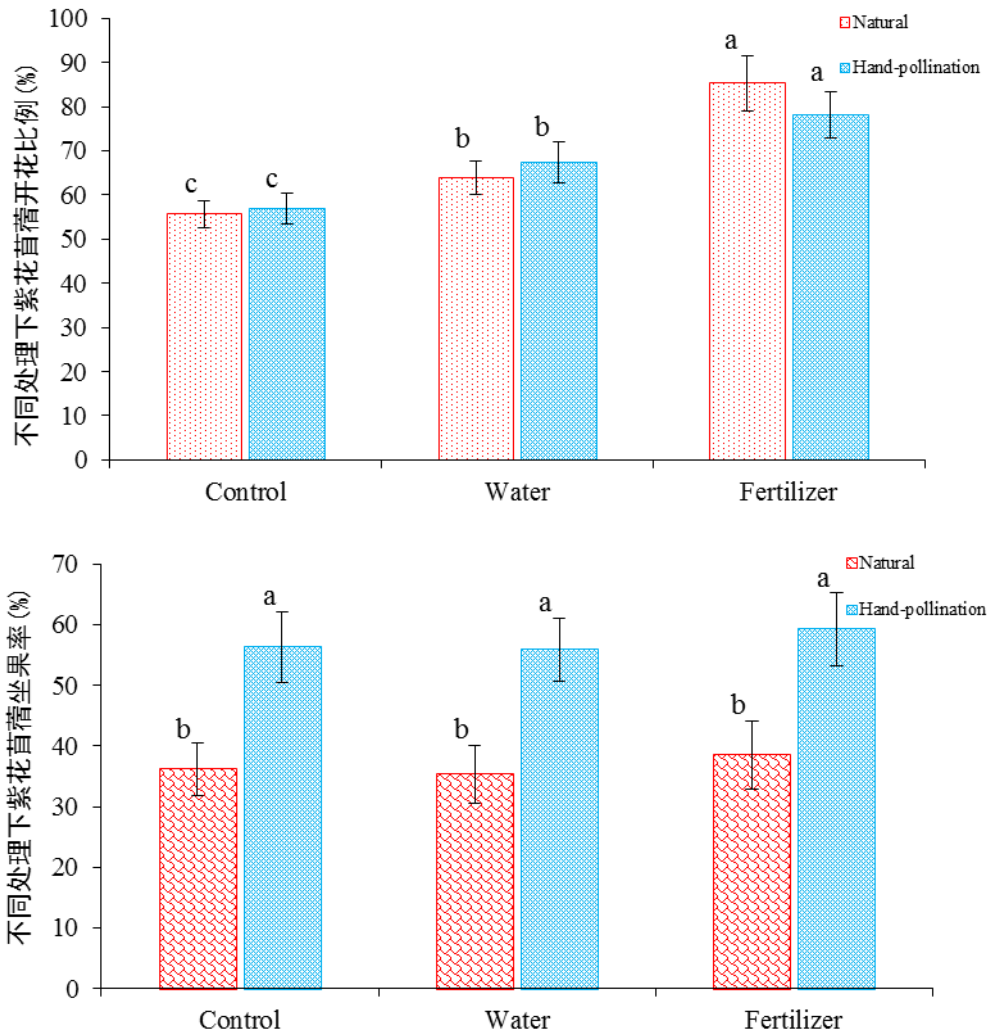


图 7. 不同处理下紫花苜蓿种群的坐果率

8) 解析了荒漠土壤呼吸对降水、温度和氮沉降多因素交互响应的特征

荒漠土壤每年的呼吸速率是 $1090.11 \pm 450.78 \text{ kg C ha}^{-1}$ ，非生长季呼吸量占全年的 20.65% (图 8)。增加氮沉降显著促进土壤呼吸，但是土壤呼吸速率在高氮沉降量下 ($1299.41 \pm 537 \text{ kg C ha}^{-1}$) 的响应低于低氮沉降量 ($1338.26 \pm 599.12 \text{ kg C ha}^{-1}$)；增加 30% 降水显著增加了土壤呼吸速率 33.03% ($1450.78 \pm 543.70 \text{ kg C ha}^{-1}$)；然而，增温 (OTCs) 减少土壤呼吸 10% ($981.19 \pm 371.34 \text{ kg C ha}^{-1}$)，这可能主要归因于土壤表层 0-5 cm 土壤湿度的。此外，增加降水和氮沉降的交互效应显著低于任何单因素效应，并且发现降水和高量氮沉降交互效应减少土壤呼吸速率为 4.25%。土壤可溶性有机碳含量(DOC)和 pH 与土壤呼吸显著正相关 (图 9)，但是与土壤微生物量碳、微生物量氮并没有显著的相关性，这可能主要归因

于土壤湿度的限制。土壤铵态氮含量对土壤呼吸具有重要的调控作用(图 10)，而结构方程模型结果表明土壤温度是影响土壤呼吸最重要的控制因素。此外，土壤呼吸的年际变化主要取决于春季短命植物的变化，并且土壤呼吸对增加降水、温度和沉降的响应十分敏感，但在增加降水、增温和大气氮沉降升高交互的作用下土壤呼吸明显低于任何单因素水平，甚至表现为负效应，这将对气候变化的反馈是一种正反馈，该研究成果于 2018 年发表在国际 SCI 杂志 Biogeoscience 上。

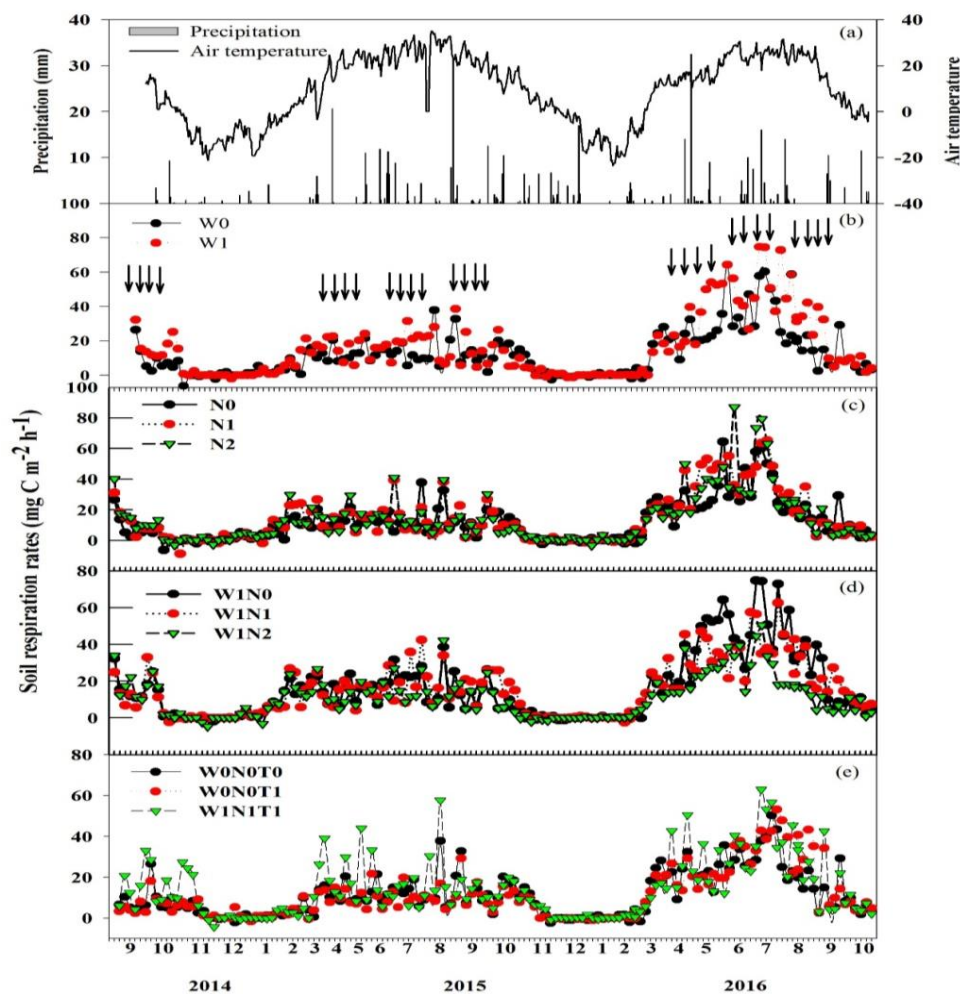


图 8. 自 2014 年 9 月至 2016 年 10 月自然降水和温度的变化特征(a)，以及荒漠土壤呼吸速率对增加降水(b)、氮沉降 (c)，降水和氮沉降交互 (d) 和增温、以及增温和降水、氮沉降交互的响应特征 (e)。

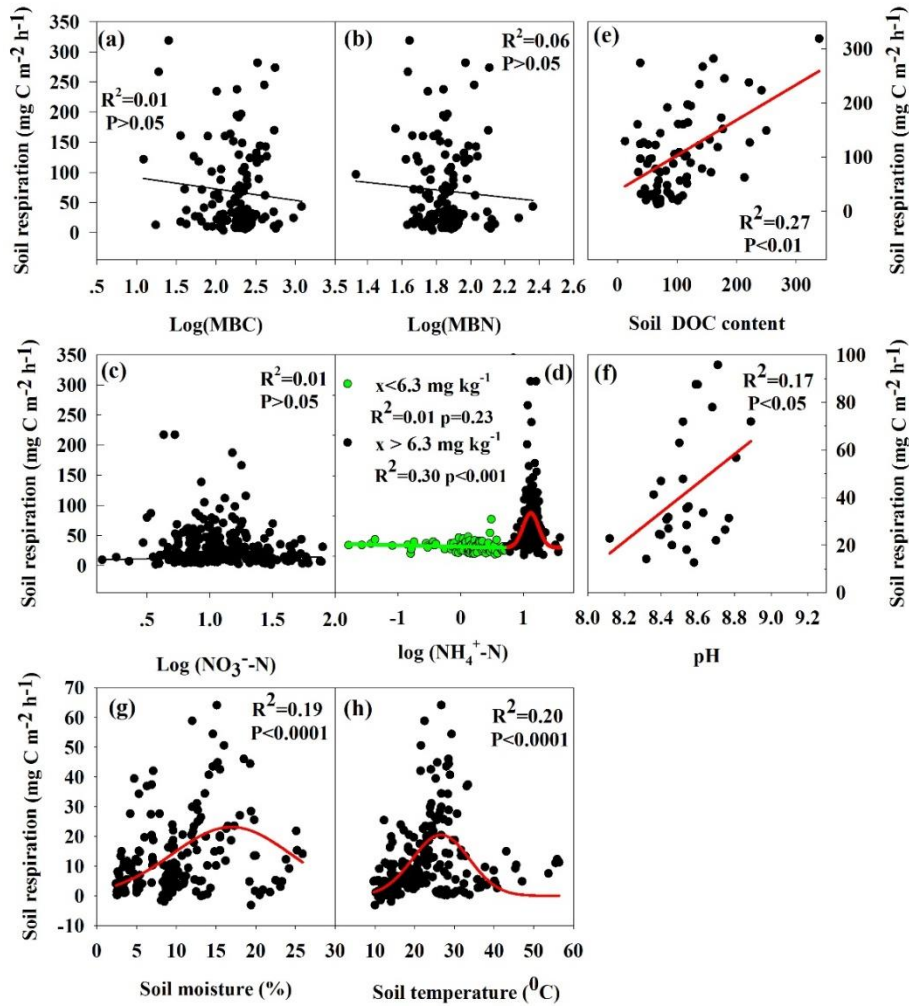


图 9. 土壤呼吸与土壤微生物量碳 (a)、微生物量氮(b)、土壤可溶性有机碳(e)、土壤硝态氮含量(c)、土壤铵态氮(d)、pH (f)、土壤湿度(g)和土壤温度(h)。

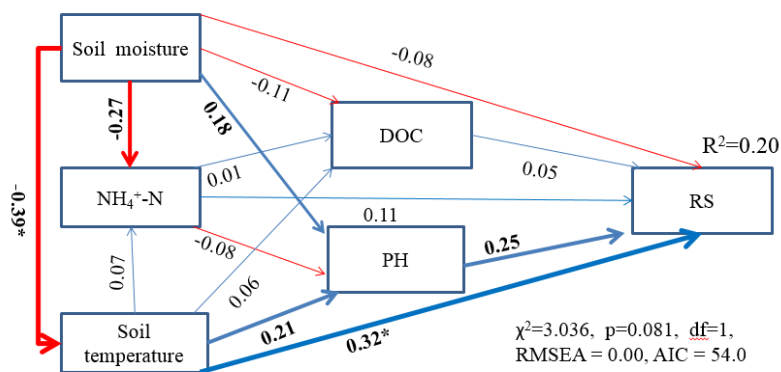


图 10. 结构方程模型分析荒漠土壤关键因素对土壤呼吸的影响

9) 揭示了沙质草地优势植物对土壤细菌群落组成的影响机制

半干旱沙质草地退化植被恢复过程中，植被-土壤-微生物系统发生了相应的变化，直接或间接影响着生态系统的功能及其稳定性。土壤微生物决定生态系统

的养分循环、能量流动等关键过程。因此，研究沙质草地退化植被恢复对土壤微生物多样性及其群落组成的影响具有重要的生态学意义。通过对半干旱沙质草地退化植被恢复过程中的优势植物：沙米 *Agriophyllum squarrosum*(AS)、差巴嘎蒿 *Artemisia halodendron* (AH)、狗尾草 *Setaria viridis* (SV)、灰绿藜 *Chenopodium acuminatum* (CA)和虫实 *Corispermum macrocarpum* (CM)对土壤微生物多样性和群落组成影响进行研究，结果表明，沙质草地退化植被的恢复降低了土壤细菌多样性（图 11）。植被特征和土壤因子显著影响沙质草地土壤微生物群落组成，其中土壤水分和土壤全氮含量是影响沙质草地生态系统土壤微生物多样性和群落组成的主要环境因子。沙质草地退化植被恢复过程中，优势植物种的变化，通过改变土壤理化性质，间接影响了土壤微生物多样性及其群落结构组成，揭示了沙质草地植物与环境因子的相互作用对土壤细菌群落组成的影响机制。该成果 2018 年发表在 *Ecology and Evolution* 杂志上。

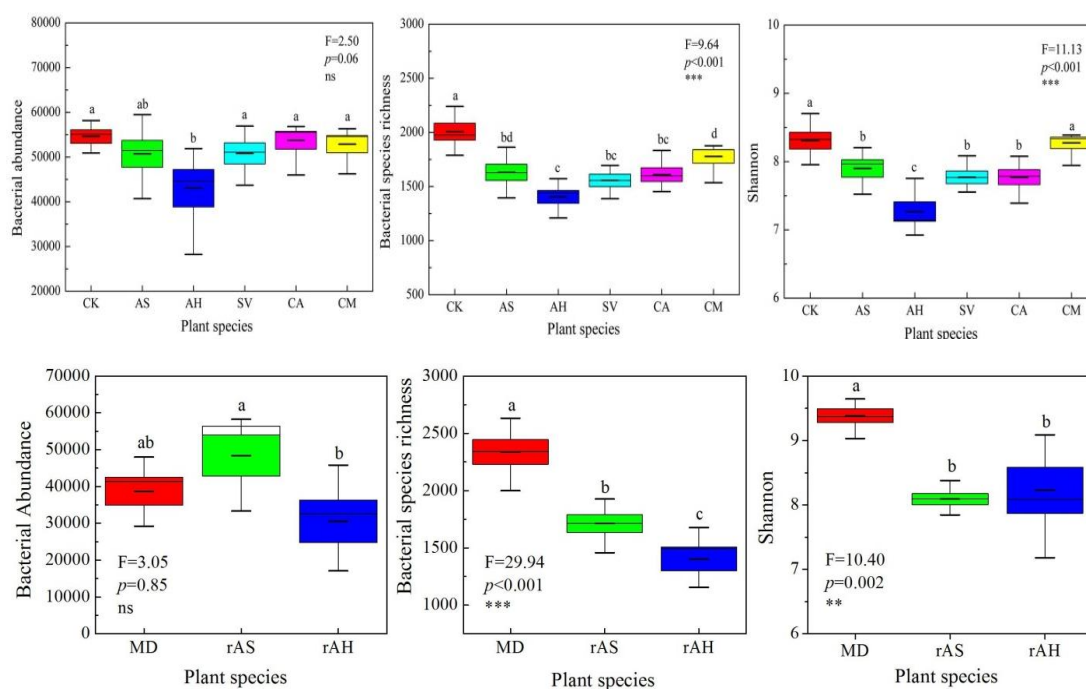


图 11. 沙质草地优势植物对土壤细菌多样性的影响

10) 揭示了寒旱区土种绵羊应对寒冷环境的特殊产热机制

阿勒泰羊是新疆最古老的绵羊品种之一，其饲养管理方式粗放，终年放牧，很少补饲。经过成百上千年的自然和人工选择，阿勒泰羊已经形成了耐粗饲、抗严寒、生长快的特点。湖羊原产于我国太湖流域，其具有高效的生产性能，因而

在上世纪 70 年代被引入新疆阿勒泰地区。阿勒泰羊和湖羊由于形成产地的不同而对寒冷环境形成了不同的适应机制，在长期寒冷胁迫环境下，阿勒泰羊形成了更耐寒的遗传机制。根据研究发现：①对于同一绵羊品种而言，阿勒泰羊和湖羊在冷应激条件下尾脂产热最为活跃（图 12）。②对于不同绵羊品种而言，阿勒泰羊在-5℃环境下对于寒冷应激较轻，因而并没有产生传统的依赖 UCP1 型产热，而以钙信号通路和 IP6K1 诱导的脂肪分解通路的非 UCP1 依赖型产热为主。并且这两种非 UCP1 依赖型产热方式在绵羊耐寒性研究中报导较少，因此具有十分重要的研究意义（图 13）。③研究发现了 IP6K1、RYR1 和 SERCA2b 等在非传统产热通路里显著差异的表达靶基因（图 14）。以上研究结果对于绵羊耐寒性代谢机制的研究和分子遗传标记的筛选具有重要的指导意义。

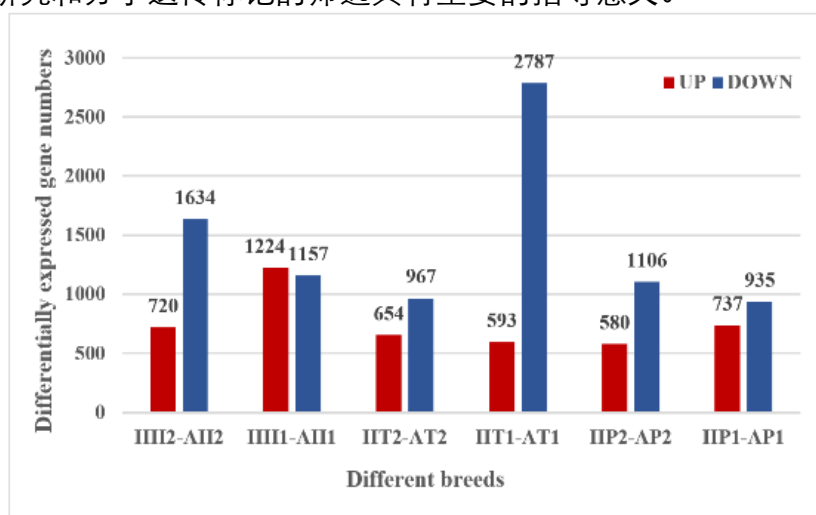


图 12. 寒冷应激对相关基因表达量的影响

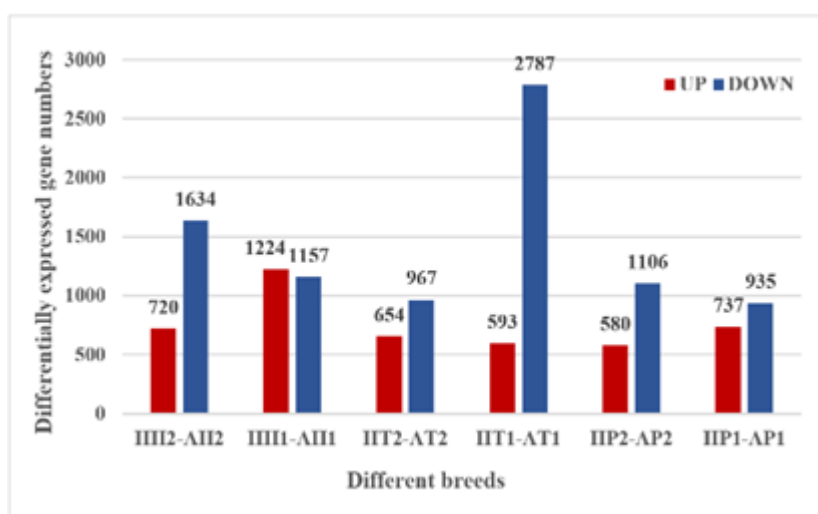


图 13. 寒冷应激相关基因在不同绵羊品种间的表达差异

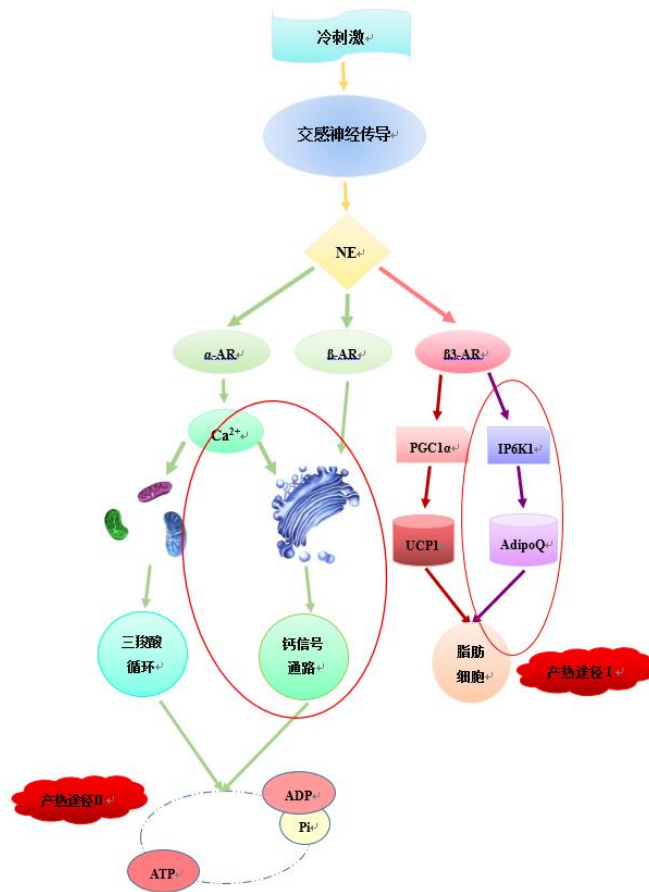


图 14. 绵羊特殊的产热通道

11) 沙蓬表皮毛减少突变体*astcl1*的初步定位分析

引种驯化沙蓬这一潜势作物对于我国干旱区的生态修复和粮食安全意义深远。人工诱变已被广泛运用于作物育种，该技术将有助于我们快速改良沙蓬草本性状，加强其农艺性状，培育适宜栽培的品系，加速驯化进程。沙米表面密被表皮毛，严重影响种子采集。通过人工诱变，已获得一株表皮毛减少突变体*astcl1*，其表型变异由隐性单基因突变控制。随着测序技术的发展，由于缺乏基因组信息造成的研究壁垒持续削弱。针对这一单一驯化性状增强的沙蓬突变体，结合最新测序定位技术和近缘物种共线性绘图，初步实现了目的基因的粗定位。相关研究结果发表于 Zhang et al. 2018, Journal Plant Physiology 231: 86-95。

12) 发现了二穗短柄草磷缺乏应答调控机理

二穗短柄草是新型的禾本科模式植物，磷缺乏显著抑制其生长和光合作用，然而对于磷缺乏应答调控机制研究较少。通过施加不同浓度磷素，选取磷素缺乏但没有出现明显生长抑制的早期阶段，采用转录组测序，深入分析了二穗短柄草

地下部分的基因表达差异。结果表明, 1740个基因受缺磷调控, 其中包括一些重要的磷转运蛋白、磷酸酶以及SPX结构域蛋白。通过对不同转录因子家族分析发现, ERF、bHLH和WRKY家族相关基因呈现差异表达较多。统计检验表明WRKY家族以及JA信号相关基因显著富集。以上结果表明磷缺乏应答、肌醇磷酸以及JA信号存在关联, 相关研究结果发表于Zhao et al. 2018, *Plant Physiology and Biochemistry* 122:113-120.。

13) 解释了青藏高原区域十字花科物种的系统发育关系与扩散方式

十字花科广泛分布于世界各高山区域, 具有较高的遗传多样性, 约有3,700个物种, 分属于321个属, 51个族, 有很多种是重要的油料、蔬菜和模式生物, 具有重要的经济价值和科研价值。作为生物多样性的热点区域之一, 青藏高原被认为是十字花科植物的分布核心区域之一。然而, 关于青藏高原隆升对十字花科植物的物种扩散以及多样性的发生等问题尚不明确。通过广泛采集分布于青藏高原及其周边的十字花科物种, 利用一个双亲遗传的核糖体内部转录间隔区片段(nrITS)和两个母系遗传的叶绿体基因(cpDNA)的序列变异式样, 深入探讨了青藏高原区域十字花科物种的系统发育关系, 证实由于十字花科进化早期发生的快速的适应性辐射分化事件, 不同分子标记所构建的系统发育关系并不一致。同时, 基于~700个十字花科nrITS序列构建系统发育关系并进一步探讨单系族的多样化及分散模式发现, 东亚地区可能也是十字花科的多样性中心之一, 并且其分化和扩散很大程度上受到青藏高原隆升的影响。该研究首次在时间和空间尺度上解析了青藏高原隆升与植物物种的多样性分化以及扩散方式之间的关系, 从系统发育的角度为探讨地质运动对物种多样性及其扩散方式的影响提供了新的思路, 并将对油料和蔬菜的野生种质资源现状评估提供参考。相关研究结果发表于Qian Chaoju et al. *Journal of Systematics and Evolution*. 2018. 56(3): 202-217.

14) 解淀粉芽孢杆菌生物防治及抗逆诱导机理研究

解淀粉芽孢杆菌在植物根际定殖的分子生物学机制。解淀粉芽孢杆菌气态挥发物对植物耐受性的诱导的基因表达。研究结果表明 FZB42 能通过释放气态挥发物对拟南芥产生显著促生作用。构建突变体抑制 2,3-丁二醇合成后仍然对拟南芥有促生作用, 说明可能还有其他气态信号分子在作用。解淀粉芽孢杆菌提高植

物抗盐水平的基因表达研究。盐胁迫下 FZB42 显著增加拟南芥生物量，证明 FZB42 诱导了拟南芥抗盐性增加了其盐耐受性。危害药材种植最为严重的当归、党参的根腐病，当归和黄芪的麻口病，进行病原微生物分离鉴定，明确致病微生物的种类。在解淀粉芽孢杆菌生物防治、诱导植物抗逆机理和百合、枸杞，当归等中药材病害防治和检测等领域取得了一系列研究成果。

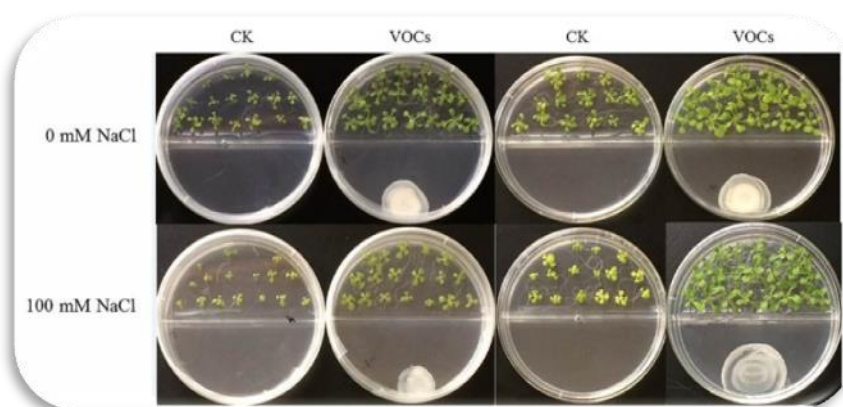


图 15. 解淀粉芽孢杆菌气体挥发物提高拟南芥盐胁迫耐受性



图 16. 甘肃省渭源县会川镇当归实验

15) 以色列进化谷 I 十字紫罗兰的同域微环境适应性物种形成机制研究

同域物种形成是进化生物学的热点领域，也是难点，关键是研究模型稀缺。位于以色列 Lower Nahal Oren 的 Mount Carmel 的进化谷 I 在相距 100-400 米的两个山坡之间，其微环境差异显著，生境多样化，生物多样性高，为我们研究同域物种形成的分子机制提供了绝佳模型。为了探讨同域物种形成发生的分子生态基础，中科院西北院马小飞研究员与以色列海法大学 Eviator Nevo 院士合作，深入分析了进化谷 I 两坡间不同生态型的十字紫罗兰的遗传变异和表型变异模式。比

较转录组分析表明，两个生态型之间共有 1,064 个差异表达的 unigenes，主要涉及四个非生物/生物胁迫响应途径中，包括类黄酮生物合成、 α -亚麻酸代谢、植物 - 病原体相互作用和亚油酸代谢。此外， Ka / Ks 分析共检测到 9 个参与两个生态型的适应性分化的基因，这些基因多参与转录后调控、光保护反应、能量代谢过程，说明两坡不同微环境差异已造成两个生态型显著的适应性遗传差异。其中，有 4 个基因 (*SPDS1*, *FCLY*, *Tic21* 和 *BGLU25*) 在十字紫罗兰和拟南芥间也检测到适应性选择信号，说明这些基因不仅参与两个生态型十字紫罗兰的同域物种形成过程，还可能与植物的种间分化有关。通过开花时间监测我们发现两个生态型间的开花时间相差约 3 个月，花期完全不重叠，说明其基因流受到完全阻碍。基于以上结果，我们推测，由于长期适应两坡不同的微环境，这 9 个基因的分子功能在两种生态型之间已发生分歧，对下游参与胁迫的基因和通路进行差异调节，从而进一步导致两种生态型间的开花时间发生分化，最终通过自然选择阻断生态型间的基因交流导致生殖隔离的建立，促进同域物种的形成。该成果受到中科院百人计划、国家重点研发计划、自然科学基金和以色列 Ancell Teicher 研究基金会的支持。这一结果发表已发表在 Qian et al. *Frontier in Genetics*.2018 上 (见封面彩图)。

16) 低温植物 ω -3 去饱和酶基因触发的综合调控赋予烟草多重胁迫耐受性

ω -3 脂肪酸去饱和酶 (FADs) 主要通过亚麻酸 (C18:3) 诱导的膜稳定作用促进植物的抗逆境，但缺乏对其在逆境适应中作用的全面分析，本研究从耐低温植物高山离子芥 (*Chorispora bungeana*) 中分离出一个微粒体 ω -3 FAD 基因 (CbFAD3)，并阐明其功能。CBFAD3 与拟南芥在 FAD3 上具有很高的同源性，受非生物胁迫上调，酵母异源表达证实了其相同功能性。过度表达 CbFAD3 的烟草叶和根中均增加了亚麻酸 C18:3 含量，维持了膜的流动性，增强了植物对寒冷、干旱和盐胁迫的耐受性。尤其是增加的亚麻酸 C18:3 诱导持续增强了质膜 Ca^{2+} -ATPase 活性，从而改变胁迫诱导的 Ca^{2+} 信号。活性氧清除系统与亚麻酸 C18:3 水平呈正相关，在转基因植株中也被激活。微芯片分析表明 CbFAD3 过表达的植物增加了应激反应基因的表达，其中大部分受 C18:3、 Ca^{2+} 或 ROS 的影响。

总之, CbFAD3 通过 C18:3 诱导的膜、Ca²⁺、ROS 和应激反应基因的整合调节赋予烟草对多种胁迫的耐受性。这一结果发表已发表在 Journal of Experimental Botany (Shi et al 2018)。

17) 中百 1 号百合良种繁育推广

中百 1 号是从可食用的海原地方百合资源中经过优良筛选而来的株系, 和兰州百合一样具有洁白细腻、口味香甜的基本特征, 叶片的形状、姿态、着生方式及花序类型、花的着生姿态、花型、花色等基本形态也与兰州百合一致。但与兰州百合相比, 在兰州市榆中县园子岔种植时, 农艺性状方面, 中百 1 号植株显著高于兰州百合, 中百 1 号平均株高为 53.6cm, 而兰州百合为 33.2cm; 中百 1 号叶片着生密度比兰州百合大, 叶片比兰州百合叶片长; 单鳞茎比兰州百合重, 中百 1 号平均单鳞茎重为 436.2g, 而兰州百合为 206.9g; 中百 1 号鳞片比兰州百合长, 较兰州百合薄。在品质性状方面, 中百 1 号鳞茎淀粉含量高于兰州百合, 中百 1 号为 148.7mg/g 鲜重, 兰州百合为 135.3mg/g 鲜重; 鳞茎 AsA 含量中百 1 号远高于兰州百合, 中百 1 号是 248.8nmol/g 鲜重, 兰州百合为 100.8nmol/g 鲜重; 总氨基酸含量中百 1 号也高于兰州百合, 中百 1 号为 15.9mg/g 鲜重, 兰州百合为 13.4mg/g 鲜重; 中百 1 号鳞茎还原性糖低于兰州百合, 中百 1 号是 55.4mg/g 鲜重, 兰州百合是 57.3mg/g 鲜重; 可溶性糖含量也低于兰州百合。2018 年繁育食用百合新品种“中百 1 号”脱毒苗 50 万株, 鳞片籽球 10 万个, 为新品种示范推广奠定了基础 (见封底彩图)。

五、实验室人才队伍建设

实验室现有研究员 18 名 (其中杰青 1 名, 中科院“百人计划”7 人, 人事部跨世纪百千万人才工程国家级人选 1 人, 甘肃省领军人才 1 人), 副研究员 16 名, 助理研究员 34 名, 支撑系列高级工程师 3 人, 工程师 6 人, 共 77 人。

表二 实验室固定科研人员

序号	姓名	性别	职称	专业	学位	研究方向	入职时间
1	李新荣	男	研究员	生态学	博士	恢复生态学	1987-

2	赵学勇	男	研究员	生态学	博士	恢复生态学	1987-
3	刘玉冰	女	研究员	分子生物学	博士	微生物生态学	2006-
4	陈国雄	男	研究员	遗传学	博士	分子遗传学	1986-
5	马小飞	男	研究员	分子生态学	博士	分子生态学	2011-
6	王若愚	男	研究员	病毒学	博士	微生物学	2011-
7	王新平	男	研究员	生态水文学	博士	生态水文学	1992-
8	周海燕	女	研究员	生理生态学	博士	生理生态学	1985-
9	谢忠奎	男	研究员	生态学	博士	农业生态学	1986-
10	刘立超	男	研究员	生态学	博士	生态学	1990-
11	张铜会	男	研究员	生态学	博士	自然地理学	1986-
12	李玉霖	男	研究员	生态学	博士	生态学	1996-
13	张志山	男	研究员	生态学	博士	生态学	2004-
14	左小安	男	研究员	生态学	博士	生态学	2005-
15	何明珠	男	研究员	生态学	博士	土壤生态学	2006-
16	李玉强	男	研究员	生态学	博士	生态学	2005-
17	李小军	男	研究员	生态学	博士	生态学	2008-
18	杨 果	男	研究员	畜牧	博士	畜牧学	2016
19	刘新平	男	副研究员	生态学	博士	生态学	2005-
20	赵 昕	女	副研究员	生理生化学	博士	生理生态学	2006-
21	王亚军	女	副研究员	生态学	博士	农业生态学	1999-
22	谭会娟	女	副研究员	生理学	博士	植物生理学	2005-
23	潘颜霞	女	副研究员	生态学	博士	水文生态学	2010-
24	贾荣亮	男	副研究员	生态学	博士	生态学	2010-
25	王 进	男	副研究员	细胞生物学	博士	细胞生物学	2005-
26	赵鹏善	男	副研究员	分子生物学	博士	分子生物学	2011-
27	黄 磊	男	副研究员	生态学	博士	生态学	2011-
28	赵 洋	男	副研究员	生态学	博士	生态学	2013-
29	黄文达	女	副研究员	生态学	博士	生态学	2012-
30	胡宜刚	男	副研究员	生态学	博士	自然地理学	2010-
31	回 嵘	女	副研究员	生态学	博士	植物生态学	2013-

32	王少昆	男	副研究员	生态学	博士	生态学	2011-
33	毛伟	男	副研究员	生态学	博士	生态学	2012-
34	潘成臣	男	副研究员	生态学	博士	生态学	2005-
35	樊恒文	男	高级工程师	科研管理	本科	科研管理	1987-
36	李爱霞	女	高级工程师	会计	本科	会计	1987-
37	张玉宝	男	高级工程师	分子生物学	博士	分子生物学	2007-
38	黄承红	女	助理研究员	分子生物学	博士	分子生物学	2006-
39	陈翠云	女	助理研究员	分子生物学	博士	分子生物学	2009-
40	石玉兰	女	助理研究员	分子生物学	博士	分子生物学	2008-
41	郭志鸿	男	助理研究员	分子生态学	博士	分子生态学	2007-
42	何玉惠	女	助理研究员	生态学	博士	生态学	2009-
43	罗亚勇	男	助理研究员	生态学	博士	自然地理学	2012-
44	连杰	男	助理研究员	生态学	博士	生态学	2013-
45	王增如	男	助理研究员	生态学	博士	生态学	2011-
46	张鹏	男	助理研究员	生态学	博士	生态学	2001-
47	高艳红	女	助理研究员	生态学	博士	自然地理学	2012-
48	曲浩	男	助理研究员	生态学	博士	生态学	2012-
49	虎瑞	女	助理研究员	生态学	博士	土壤生态学	2013-
50	苏洁琼	女	助理研究员	生态学	博士	生态学	2013-
51	杨昊天	男	助理研究员	生态学	博士	生态学	2014-
52	张亚峰	男	助理研究员	生态学	博士	生态水文学	2014-
53	李启森	男	助理研究员	生态学	本科	科技推广	1985-
54	陈怀顺	男	助理研究员	生态学	本科	科技推广	1986-
55	李清	男	助理研究员	生态学	本科	科技推广	1988-
56	高永平	男	工程师	气象监测	本科	气象监测	2006-
57	云建英	女	工程师	数据管理	本科	数据管理	1984-
58	赵金龙	男	工程师	农业管理	本科	农业管理	1984-
59	冯静	女	工程师	生态学	学士	科研管理	2007-
60	苏娜	女	工程师	生态学	学士	科研管理	2008-
61	冯丽	女	工程师	生态学	博士	生态学	2011-

62	邱 阳	男	助理研究员	生态学	博士	生态学	2014-
63	刘美玲	女	助理研究员	生态学	博士	生理生态学	2014-
64	罗永清	男	助理研究员	生态学	博士	自然地理学	2014-
65	陈 敏	男	助理研究员	生态学	博士	生态学	2015-
66	赵 霞	女	助理研究员	微生物学	博士	微生物生态学	2016-
67	钱朝菊	女	助理研究员	生态学	博士	分子生态学	2017-
68	赵杰才	男	助理研究员	生态学	博士	育种学	2016-
69	马旭君	男	助理研究员	生理生态学	博士	恢复生态学	2017-
70	周建伟	男	助理研究员	草业科学	博士	畜牧	2017-
71	张成琦	男	助理研究员	地球系统科学	博士	环境变化碳循环	2017-
72	周 琴	女	助理研究员	分子生物学	博士	分子生物学	2018-
73	刘良旭	男	助理研究员	生态学	博士	生态学	2017-
74	宋 光	男	助理研究员	生态学	博士	生态学	2018-
75	段育龙	男	助理研究员	生态学	博士	生态学	2018-
76	王立龙	男	助理研究员	生态学	博士	生态学	2018-
77	岳 平	男	助理研究员	生态学	博士	生态学	2018-

六、2018 年实验室新增科研项目

2018 年在各项在研项目顺利进行的同时，新增 29 项，其中中科院战略性先导科技专项 1 项，国家重点研发计划课题 1 项，国家自然科学基金面上及青年基金 4 项，其他项目 23 项，经费合计 4296.3 万元。

表三 2018 年新争取课题/项目统计表

序号	课题名称	类 别	主持人	起始年限	总经费(万元)
1	荒漠化土地植被恢复重建关键技术研发与集成示范	中国科学院战略性先导科技专项(A 类)子课题	李新荣	2018-2023	1584
2	盆地荒漠地下咸水利用与荒漠化治理技术	国家重点研发计划课题	李新荣	2018-2021	300

3	干旱风沙区高等级公路“生态廊道”建设标准及效益评估	中科院地方合作	何明珠	2018-2020	300
4	甘肃道地药材主产区重金属污染现状评估和防控措施	中科院西北院 STS 项目	何明珠	2018-2020	150
5	科尔沁沙地生态产业优化与示范	国家重点研发计划课题	张铜会	2019-2021	185
6	库伦旗特色产业扶贫关键技术试验示范	中国科学院 STS 项目	张铜会	2019-2021	350
7	库伦旗草牧业-肉牛养殖一体化脱贫与产业发展模式试验示范	中国科学院 STS 项目	刘新平	2019-2021	350
8	基于功能性状研究半干旱沙地植物叶片和细根凋落物可分解性的关联性	国家自然科学基金	赵学勇	2019-2023	60
9	沙蓬表皮毛减少突变体 Astcl1 的克隆及其对不同干旱自然环境的适应性研究	国家自然科学基金	赵鹏善	2019-2023	60
10	指针式灌溉对半干旱区景观功能多样性的影响	国家自然科学基金	连杰	2019-2021	25
11	干旱与半干旱生态脆弱区凋落物分解响应降水格局变化的对比研究	国家自然科学基金	曲浩	2019-2022	61
12	沙米适应性及初步驯化研究	中国科学院青年创新促进会会员	赵鹏善	2018-2021	80
13	浑善达克沙地生态建设与资源高效利用技术集成与试验示范	内蒙古科技计划项目	李玉霖	2019-2020	70
14	天然草地适宜放牧率的判断指标体系及适宜放牧率研究	青海省科技成果转化专项	周建伟	2018-2021	40
15	复合缓释解淀粉芽孢杆菌微肥制剂的示范与推广	宁夏农业综合开发办公室	王若愚	2018-2020	53
16	库伦旗优质饲草种植技术示范	中国科学院科技扶贫专项	王亚军	2018-2020	60

17	库伦旗肉牛高效饲养技术集成与示范	中国科学院科技扶贫专项	杨 果	2018-2020	55
18	优质滩羊标准化产业体系建立与新技术示范推广	宁夏农业综合开发办公室	杨 果	2017-2018	50
19	沙米的有效成分提取工艺技术与产品开发研究	甘肃省重点研发计划项目	马小飞	2018-2020	30
20	黑河流域全景评价	中科院战略性先导科技专项专题	左小安	2018-2020	200
21	日粮能氮调控对藏羊尿素循环及其转运载体 UT-B 的影响	西北院青年人才成长基金	周建伟	2018-2020	10
22	干旱荒漠草原植被生产力对降水波动的响应机制	西北研究院青年人才成长基金	刘良旭	2018-2020	10
23	沙蓬适应我国北方沙漠异质性环境的遗传机制研究	西部青年学者 B 类项目	钱朝菊	2018-2021	15
24	荒漠生态恢复区主要灌木对脉冲降雨响应的试验和模型研究	西北退化生态系统恢复与重建教育部重点实验室开放课题	黄 磊	2018-2020	20
25	荒漠化治理新业态培育	国家重点研发计划	李玉霖	2017-2020	30
26	贫困旗县产业发展规划与跟踪研究	中科院地理所	张铜会	2016-2018	20
27	内蒙古库伦旗乡镇科技扶贫实施方案建议报告	中科院科发局	张铜会	2017-2018	80
28	沙地植物过程对生境变化的响应	中国科学院青年创新促进会	左小安	2018-2021	30
29	科尔沁沙化土成效监测	奈曼旗林业局	李玉霖	2018-2020	18.3

七、实验室获得主要科研成果

1、科研奖励成果

- 1) 李新荣研究员荣获 2018 中国科学院“感动中国”年度先锋人物荣誉称号。

- 2) 国家科学技术进步二等奖：风沙灾害防治理论与关键技术应用。主要完成人：王涛、屈建军、王文彪、赵学勇、李新荣、赵哈林、蒋富强、王进昌、汪万福、尹成国。
- 3) 内蒙古科技进步二等奖：内蒙古退化沙地生态系统恢复与资源有效利用技术。主要完成人：完成人员：赵学勇、王晓江、张文军、左合君、蒙仲举、曲浩、毛伟。
- 4) 环保科技二等奖：宁蒙灌区农田退水污染全过程控制技术及应用。主要完成人：杨正礼、杨世琦、赵忠、李友宏、张炳宏、吴海卿、张志山、张晴雯、张学军。
- 5) 2018年7月5-7日,北京召开的2017年度国家生态系统观测研究共享服务平台内部评价考核会议上,沙坡头站被评为优秀国家站。

2、专利

表四 实验室2018年授权、受理专利

序号	专利名称	专利类型	专利号	技术联系人
授 权				
1	一种区分生物土壤结皮及其下层土壤基础呼吸的方法	发明专利	ZL201510473029.6	李新荣
2	一种干旱沙区固沙植物栽植方法	发明专利	ZL201510280853.X	李新荣
3	一种生物土壤结皮中藻类生物量的测定方法	发明专利	ZL201510473242.7	赵洋
4	一种百合X病毒LVX半定量检测金标卡的制备方法.	发明专利	ZL201510951206.7.	张玉宝
5	一种百合草莓潜隐环斑病毒SLRSV半定量检测金标卡的制备方法.	发明专利	ZL201510951189.7	张玉宝
6	沙米愈伤组织及其诱导增殖方法	发明专利	ZL201600044976.7	赵昕
7	野外全自动增减雨装置	发明专利	ZL201510186556.9	王增如

8	一种基于箱式法和考虑降水影响的干旱区碳通量估算方法	发明专利	ZL201610117048.x	王增如
9	一种提高人工培育藓类结皮抗旱能力的方法	发明专利	ZL201611191838.9	贾荣亮
10	荒漠区土壤水分数据批量自动分析程序	软件著作权	ZL2018SR892659	罗亚勇
11	生态环境治理修复进程管理系统	软件著作权	ZL2018SR826525	曲 浩
12	一种与土壤贯通的半封闭式多功能植树袋	实用新型	ZL201720096491.3	王增如
13	一种野外模拟地下滴灌的便携式装置	实用新型	ZL201720096492.8	王增如
14	一种基于土壤水分入渗动态的地下滴灌模拟试验装置	实用新型	ZL201720236561.0	王炳尧
15	一种悬挂直插式地下滴灌灌溉系统	实用新型	201721103518.3	王炳尧
16	一种羊消化代谢笼	实用新型	ZL201721392832.8	杨 果
17	一种生态用防沙挡板	实用新型	ZL20172745838.2	曲 浩
18	一种标准土壤剖面样品存放展示柜	实用新型	ZL201720578429.8	苏 娜
19	一种开合式便携取土器	实用新型	ZL201720843819.3	高永平
20	一种可伸缩式微地形地貌测绘仪	实用新型	ZL201720843911.X	高永平
21	一种改良的通风橱排风管道	实用新型	ZL201721457857.1	苏 娜
22	一种便于PE管试验土样砂土装载的装置	实用新型	ZL201820723853.1	何钊全
23	一种便于小块农田同步覆膜施肥的机具	实用新型	ZL201820724195.8	何钊全
受 理				
1	野外植物根系远程监测系统	发明专利	2018100004321.7	马雄忠

2	一种兰州百合椰子饮料及其制备方法	发明专利	201810118351.0	邱 阳
3	一种兰州百合雪梨饮料及其制备方法	发明专利	201810118330.9	邱 阳
4	一种特异性检测百合隐症病毒的试剂盒及其检测方法	发明专利	201810641454.5	张玉宝
5	一种特异性检测百合斑驳病毒的试剂盒及其检测方法	发明专利	201810641531.7	张玉宝
6	一种特异性检测百合黄瓜花叶病毒的试剂盒及其检测方法	发明专利	201810641533.6	张玉宝
7	检测百合拟南芥菜花叶病毒的试剂盒及其检测方法	发明专利	201810641534.0	张玉宝
8	一种提高沙区人工培育藓结皮抗高温能力的方法	发明专利	201811412980.0	贾荣亮
9	一种可拆卸移动式羊自动称重栏	实用新型	201821169778.5	周者不

2018 年实验室科研人员所获得奖励

- 李新荣研究员荣获 2018 中国科学院“感动中国”年度先锋人物荣誉称号；
- 李新荣研究员荣获中国科学院“新时代科技报国优秀共产党员”；
- 李新荣、刘立超、张志山研究员入选甘肃省第一层次领军人才；
- 左小安研究员获得第 22 届“甘肃青年五四奖章”；
- 左小安研究员获得了第九届“甘肃青年科技奖”；
- 左小安研究员获得了中科院西北研究院优秀共产党员称号；
- 张亚峰博士入选中国科学院青年创新促进会会员；
- 赵昕荣获中科院寒旱所大型仪器设备公共服务所级中心先进个人奖；
- 受中国科学院公派留学项目资助，李小军研究员、王进副研究员、胡宜刚副研究员、毛伟助理研究员、张玉宝高级工程师等于 2017 年-2018 年分别赴美国、澳大利亚、新西兰等国家进行为期 6 个月到 1 年的访问与交流。

八、实验室研究生培养

2018 年实验室继续重视人才培养。2018 年新招 8 名硕士研究生、12 名博士研究生；毕业博士生 5 人，硕士生 7 人。目前在读研究生 64 人。

- 博士生张继伟、硕士生牛亚毅获得荣获中国科学院大学博士生国家奖学金；
- 博士生宋光和硕士生赵芸被评为中国科学院大学 2018 学年“优秀毕业生”；
- 博士生宋光被评为北京市“优秀毕业生”；
- 博士生赵丽娜和硕士生李昭环获得中国科学院大学 2017-2018 学年“优秀学生干部”；
- 14 位研究生获得中国科学院大学 2017-2018 学年“三好学生”奖。

表五 实验室学科站点设置

研究生类别	专业代码	学科名称	研究方向
博士	071300	生态学	寒旱区生态学、植物生理学、农业生态学、极端环境下植物基因工程、恢复生态学、分子生态、植物地理
硕士	070501	自然地理学	生态水文学
	071300	生态学	生态学、生态农业、干旱区生态、植物基因工程
	085238	生物工程	寒旱区抗逆植物培育及原理、典型逆境动植物筛选、细胞与酶工程、寒旱区土壤与土地资源

2018 年毕业答辩博士、硕士研究生

1) 题目：两个大麦角质层蜡质突变体的遗传定位

答辩人：周琴 申请学位：理学博士

导师：陈国雄 研究员

答辩委员会主席：李新荣 研究员

2) 题目：解淀粉芽孢杆菌诱导植物耐盐的分子机理研究

答辩人：刘少芳 申请学位：理学博士

导师：王若愚 研究员

答辩委员会主席：李新荣 研究员

3) 题目：温带荒漠生物土壤结皮对草原植物侵入与定居的影响

答辩人：宋 光 申请学位：理学博士

导 师：李新荣 研究员

答辩委员会主席：赵文智 研究员

4) 题目：西北干旱荒漠区表层土壤水文过程的时空变异规律

答辩人：石 薇 申请学位：理学博士

导 师：王新平 研究员

答辩委员会主席：赵文智 研究员

5) 题目：内蒙古典型草原与荒漠草原植物功能多样性对极端干旱事件的响应

答辩人：岳喜元 申请学位：理学博士

导 师：左小安 研究员

答辩委员会主席：王 涛 研究员

6) 题目：沙区不同类型生物土壤结皮对表层土壤理化性质及碳循环关键过程的影响

答辩人：都 军 申请学位：理学硕士

导 师：李小军 研究员

答辩委员会主席：李新荣 研究员

7) 题目：典型沙尘源区及沉降区生物气溶胶中微生物群落多样性研究

答辩人：魏文斐 申请学位：工程硕士

导 师：刘立超 研究员

答辩委员会主席：李新荣 研究员

8) 题目：混合盐胁迫对两种枸杞叶片生理特性的影响

答辩人：张雯莉 申请学位：理学硕士

导 师：刘玉冰 研究员

答辩委员会主席：李新荣 研究员

9) 题目：腾格里沙漠人工固沙植被演替过程中生物土壤结皮 NDVI 变化特征

答辩人：赵 芸 申请学位：理学硕士

导 师：贾荣亮 副研究员

答辩委员会主席：李新荣 研究员

10) 题目：科尔沁沙地植被-土壤碳、氮、磷化学计量特征研究

答辩人：宁志英 申请学位：理学硕士

导 师：李玉霖 研究员

答辩委员会主席：王 涛 研究员

11) 题目：沙质草地生态系统碳通量特征及其影响因素

答辩人：牛亚毅 申请学位：理学硕士

导 师：李玉强 研究员

答辩委员会主席：王 涛 研究员

12) 题目：邻苯二甲酸介导的兰州百合“自毒”基因应答及他感协同作用研究

答辩人：华翠平 申请学位：工程硕士

导 师：王亚军 副研究员

答辩委员会主席：王 涛 研究员

表六 2018 年博士生开题、考核、中期报告

序号	姓名	报告题目	导师
1	马雄忠	阿拉善高原红砂与珍珠根系生长动态研究	王新平
2	程清平	基于水资源的黑河流域全景评价	左小安

3	焦丹	冷应激对绵羊能量代谢通路的分子作用机制	谢忠奎
4	于海伦	入侵植物刺萼龙葵和光梗蒺藜草生态适应性对比研究	赵学勇
5	岳靓	解淀粉芽孢杆菌诱导植物抗旱的分子机制研究	王若愚
6	张润霞	干旱荒漠区城镇化对土地利用/覆被变化与土壤侵蚀的影响-以兰州新区为例”	赵学勇
7	张涛	青藏高原“黑土滩”退化草地中“秃斑块”的水热空洞效应及其尺度分析	谢忠奎
8	赵生龙	干旱荒漠草原植被结构与功能对不同放牧强度的响应机制	张铜会
9	孙靖尧	生物土壤结皮的微尺度空间格局及其机理	李新荣
10	赵丽娜	生物土壤结皮微生物群落结构及其功能演替	李新荣 刘玉冰
11	陈娟丽	沙地与荒漠草原三种共有草本植物对水分胁迫的生理响应	赵学勇
12	范兴科	基于简化基因组测序技术研究红砂的生态物种形成历史	马小飞
13	何钊全	科尔沁沙地灌溉农田作物节水技术及潜力研究	张铜会
14	李文美	干旱胁迫下兰州百合的适应机制研究	谢忠奎
15	吕朋	科尔沁沙地退化植被恢复及管理对土壤氮矿化的影响	左小安
16	王旭洋	北方农牧交错带土壤有机碳时空动态及其影响机制	李玉强
17	王艳莉	砂蓝刺头对沙地生境变化的生活史对策及响应机制	李新荣
18	尹晓月	基于多组学探究沙米局域适应性的分子代谢机制	马小飞
19	张继伟	沙蓬表皮毛生物学功能及 astc11 基因定位	陈国雄
20	张晶	科尔沁沙质草地植物功能性状变化规律及其影响机制	左小安
21	张蕊	荒漠草原生态系统群落碳收支对降水变化的响应	赵学勇
22	韩亚楠	半干旱区农田生态系统中微生物降解地膜的研究	谢忠奎
23	卢翔	胞外多糖在解淀粉芽孢杆菌 FZB42 促进植物抗干旱作用中的研究	王若愚
24	周媛媛	植物固沙对沙漠生态系统碳通量的影响	李新荣
25	刘璐璐	退耕还林政策对农户生计可持续性及其生计安全的影响—以甘肃会宁县为例	李锋瑞

26	杨 琨	欠发达地区城市化过程中失地农民可持续生计问题的实证研究 ——以兰州市安宁区为例	李锋瑞
27	CONSTANTINE UWARE MWE	Investigation on root rot disease in wolf berry plants, and a systematic study on disease biocontrol(a case study of Chinese wolf Berry)	王若愚
28	刘 洋	植物根际促生菌 PGPR 参与当归抗病的分子机理研究	王若愚
29	王瑞雄	科尔沁沙地植被-土壤协同演变规律的研究	赵学勇
30	华翠平	兰州百合连作土壤中主要自毒物质的自毒效应及降解研究	谢忠奎
31	周珊珊	沙米药材道地性形成的分子机制研究	马小飞
32	魏海莲	兰州百合多糖动态累积规律及调控机制研究	谢忠奎
33	宁志英	沙质草地植物叶片和细根功能性状与凋落物可分解性间的关联性	赵学勇
34	牛亚毅	沙地生态系统碳平衡及其对氮磷养分添加的响应	李玉强
35	田 原	气态挥发物(VOCs)介导的 PGPR 在植物个体间迁移的机制研究	王若愚
36	胡 亚	全球变化对荒漠草原植物叶片解剖结构、生理特性及代谢组的影响	左小安
37	漆婧华	咸海周边地区微生物群落结构多样性变化及其生态学意义	李新荣
38	李昌盛	荒漠绿洲不同景观单元植被与土壤系统演变特征及内在机制	李新荣
39	徐冰鑫	我国北方沙区植被与土壤空间格局及相互关系	张志山
40	李荣麟	甘肃西南地区表土植硅体组合及植硅体-气候因子模型的研究	李新荣

表七 2018 年终硕士生开题、考核、中期报告

序号	姓名	报告题目	导师
1	李云飞	沙区土壤有机碳截存及矿化对植被恢复的响应	李小军
2	许 华	荒漠土壤微生物碳、氮、磷生态化学计量特征对降水控	何明珠

		制的响应	
3	李昭环	纳米复合材料对于沙漠生物土壤结皮的促进作用研究	刘立超
4	毛忠超	西北干旱区荒漠-绿洲过渡带稳定性研究	张志山
5	王明明	半干旱沙地固沙植被对土壤水动态的影响模拟	刘新平
6	杨利贞	荒漠人工植被区典型植物叶片吸水策略研究	黄磊
7	张子谦	青藏高原地区土壤冻融过程的遥感监测算法研究	李玉霖
8	赵成政	砾石覆盖农田生态保育研究-以甘肃砂田为例	王亚军
9	吕文聪	砾石覆盖对土壤侵蚀过程的影响及机制研究	谢忠奎
10	杨红玲	凋落物化学成分多样性对土壤有机碳矿化的激发效应	李玉霖
11	车力木格	半干旱沙地一年生植物生殖生长对降水变化的响应	刘新平
12	龚相文	科尔沁地区植被净初级生产力及生态承载力时空动态研究	李玉强
13	姬凯茜	基于转录组分析冷胁迫下绵羊骨骼肌相关基因的表达差异	杨果
14	吕星宇	固沙植被演替进程中土壤微生物功能群和酶活性的生态化学计量研究	张志山
15	马晓俊	土壤微生物多样性、微生物量及酶活性对固沙植被过程的响应	李小军
16	王炳绕	直插式地下滴灌的土壤湿润体特征值变化规律研究及田间应用	刘立超
17	周丽靖	生物炭对农田退化土壤的改良作用研究	王亚军

九、2018 年实验室发表专著和学术论文

2018 年实验室出版专著两部。发表论文 91 篇，其中 SCI 论文 66 篇，中文核心期刊 25 篇。Change Biology, Soil Biology and Biochemistry, Frontiers in Plant Science, Science of the Total Environment, Geoderma 等国际 TOP 刊物。

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十、学术会议和学术交流活动

10.1 国内学术会议与培训活动

10.1.2 2018 年逆境重点实验室学术年会

2018 年 7 月 1 日至 3 日,甘肃省寒区旱区逆境生理与生态重点实验室学术研讨会在兰州召开。中国科学院西北生态环境资源研究院常务副院长赖远明院士出席会议。

实验室主任李新荣研究员首先致欢迎辞。赖远明介绍了西北研究院历史沿革、研究特色、发展规划等。并欢迎专家们来西北研究院开展学术交流。

本次研讨会主题为“生态恢复的微生物响应机理及其应用”。国内外多名专家学者作了大会报告,介绍相关领域最新科研进展。其中,Uffe Nielsen 博士作了“*Soil fauna and ecosystem services*”报告、兰州大学肖洒教授作了“高山植物保育作用研究”报告、武汉大学陈兰洲教授作了“藻类修复荒漠化土壤技术及机理”报告。实验室研究员李新荣、马小飞、王若愚、刘玉冰,副研究员王少昆分别就“中国风沙区生态重建与恢复对中亚-西亚地区沙漠化治理的启示”“沙米的生态适应性与驯化策略”“解淀粉芽孢杆菌在植物抗病抗逆中的研究及应用”“生物土壤结皮微生物群落及其生态功能的演替”“科尔沁沙地植被恢复对土壤微生物群落的影响”等科研进展作了汇报。

西北研究院科研人员及兰州大学、西北师大等高校师生 70 多人听取学术报告。

专家们的进展报告条分缕析、深入浅出、精彩纷呈。与会师生们展开热烈讨论，获益匪浅。会后特邀专家到沙坡头沙漠研究试验站开展实地考察调研，为生态恢复微生物研究的深入合作奠定基础。

10.2 国际合作交流

1) 为了深入研究家畜采食行为对科尔沁沙地沙丘草地土地沙漠化的影响，2018年奈曼站与日本鸟取大学干燥地研究中心合作，共同建立了“牧户级放牧行为观测试验场”，联合开展家畜采食行为对沙丘草地植被空间格局、植被组成、优势物种变化、土壤机械组成和养分状况等植被特征和土壤属性的影响。

2) 为了揭示降水变化对中国北方不同类型草地生态系统结构与功能的影响，奈曼站与美国科罗拉多州立大学 Alan K. Knapp 教授和 Melinda D. Smith 教授合作，沿北方农牧交错带建立了荒漠草原、典型草原、沙质草地和草甸草原联网控制试验样地，通过模拟降水变化研究草原植被生产力、物种组成、优势种功能性状、土壤碳氮循环等响应和适应过程。

3) 应兰州大学生命科学学院尚占环教授和中科院西北生态环境资源院杨果研究员联合邀请，以色列本-古里安大学(Ben-Gurion University of the Negev)草食动物营养专家 Allan Degen 和 Michael Kam 教授于 2018 年 5 月 1 日-5 月 2 日来实验室进行学术访问。期间，杨果研究员及其课题组与来宾就国际合作、师生互访、绵羊抗逆营养研究等方面进行了深入交流与探讨。会后，双方就学生联合培养、国际合作等方面达成协议。本次学术交流由杨果研究员主持，王亚军副研究员、周建伟助理研究员以及 10 余名研究生参与。通过这次活动，加深了我实验室与国内外高校在农业领域的合作与交流，促进了畜牧与生态学科的建设与发展。

10.3 举办国内外项目/学术会议

1) 3 月 21 日由沙坡头站王新平研究员主持的国家重点研发计划战略性国际科技创新合作重点专项“丝绸之路经济带沿线国家流沙固定及植被恢复关键技术研发与示范”中哈合作研讨会在兰州召开。哈萨克斯坦植物生物学与生物技术研究

所 Yerlan Turuspekov 教授做 “IPBB research activities and participation in joint international DSVR Program” 报告。

2) 4 月 23-25 日, 由中国科学院西北生态环境资源研究院主办的国家科技基础资源调查专项“中国荒漠主要植物群落调查”项目技术培训会议在甘肃兰州召开。项目组科研人员和学生 60 余人参加活动。会议由项目首席科学家赵学勇研究员主持。会议邀请新疆农业大学安沙舟教授、内蒙古农业大学兰登明教授、中国科学院辰山植物园陈彬工程师和中国科学院西北生态环境资源研究院翟晓慧博士分别从荒漠植物调查方法、荒漠植物分类与标本制作、野外调查规划、物种数据与信息管理方法、中国荒漠区划及指标体系进行系统培训。报告人的精彩报告使课题骨干收获颇多。最后, 赵学勇研究员就项目实施方案和技术指导手册听取了大家的意见和建议。报告结束后, 报告人和参会人员就感兴趣的科学问题展开热烈的讨论交流。

3) 7 月 13 日, 沙坡头站第三期论坛举办, UNCCD 亚太地区协调处处长杨有林、中国林业科学研究院荒漠化研究所所长卢琦、中国科学院合肥物质科学研究院蔡冬清研究员分别以“土地退化、荒漠化及干旱治理措施及履约”、“沙漠有功劳, 服务价更高”、“农业纳米材料”为题为科研人员做了精彩的报告。

4) 7 月 16 日, 由中国通量观测研究联盟 (ChinaFLUX)、沙坡头站、中科院地理所、中国生态系统研究网络 (CERN)、国家生态系统观测研究网络 (CNERN)、以及北京力高泰科技有限公司和 LI-COR Biosciences 联合组织承办的 ChinaFLUX 第十三次通量观测理论与技术培训班在中卫召开, 参会人员近 150 人。

5) 7 月 15-21 日, 由人力资源和社会保障部资助、宁夏人力资源和社会保障厅主办、沙坡头站承办的专业技术人才知识更新工程 2018 年高级研修项目—“丝绸之路经济带沿线流沙固定及生态恢复”高级研修班在宁夏中卫市顺利举办。

6) 8 月 7 日, 宁夏沙坡头生态保护和建设院士工作站沙坡头站揭牌仪式在沙坡头举行。国际著名冰川学家、地理学家和气候学家秦大河院士、宁夏回族自治区人力资源与社会保障厅副厅长马力、气象局副局长杨兴国、中科院西安分院副院长

杨青春、中卫市副市长蔡菊、宁夏农业综合开发办公室主任许学禄、宁夏回族自治区人社厅留学人员与专家服务中心侯晓东主任、中卫市人社局局长孙尚金以及中科院西北生态环境资源研究院丁永建研究员、康世昌研究员、吴青柏研究员、赵林研究员、任贾文研究员、山地所王根绪研究员、北京师范大学效存德教授、港中旅（宁夏）沙坡头旅游景区有限责任公司总经理韩忠胜等参加了揭牌仪式。宁夏回族自治区人力资源与社会保障厅聘请秦大河院士为“自治区特聘专家”，副厅长马力向秦大河院士颁发聘书。

7) 9月27日至28日，中国科学院西北生态环境资源研究院（简称西北研究院）2018年度野外台站工作会议在内蒙古通辽召开。会议由西北研究院奈曼沙漠化研究站承办。西北研究院院长王涛、副院长冯起，中科院科发局资环处研究员杨萍、西北研究院23个野外台站、基地负责人、管理与支撑部门负责人及野外台站相关科研人员70余人参加会议。会议由冯起主持。会上，王涛传达了特色研究所评估工作进展，阐述了野外台站建设与特色所工作密切关系。并着重介绍了基于野外台站的重大成果“寒旱区生态环境资源工程特色野外台站监测研究网络”对西北研究院科技创新的服务和数据积累，及对祁连山国家公园、三江源国家公园建设的科技支撑工作。冯起在讲话中强调了野外台站是立院之本。并要求各野外台站高度重视，按照要求认真准备即将到来的野外站评估和国家站申报工作。23个野外台站、基地负责人还分别就台站基本概况、2018年度平台建设、工作进展、取得成果、数据提交情况、安全工作措施及下一步工作计划等方面作了详细汇报。随后参会人员参观了奈曼沙漠化研究站。

8) 10月13-14日，国家重点研发计划“西北荒漠-绿洲区稳定性维持与生态系统综合管理技术研发与示范”（2017YFC0504300）2018年专题讨论会在沙坡头站召开。

10.4 实验室人员学术交流记录

- 1) 1月8-9日，李新荣研究员作为咨询专家参加中科院水保所野外台站会议。
- 2) 1月8-11日，谭会娟、潘颜霞在深圳大亚湾参加了长期生态观测数据的整理、应用及开放共享培训班。

- 3) 1月9日, 张亚峰博士参加第四届西部生态环境资源青年学术论坛暨兰州分会第七期优秀青年科学家论坛, 并做了“荒漠灌丛对降水的再分配及树干茎流对灌丛沃岛效应的贡献”学术报告。
- 4) 1月9-13日, 黄文达在深圳参加“长期生态观测数据的整理、应用及开放共享”培训班与研讨会。
- 5) 1月19日, 赵学勇在北京参加科技部的2017年典型脆弱生态恢复专项项目总结会议, 作会议报告“对跟踪的11个项目进行了亮点介绍”。
- 6) 1月26-28日, 李新荣研究员在厦门参加中国生态学会常务理事会议。
- 7) 1月31-2月2日, 李新荣参加中科院南京土壤研究所国家重点实验室学术年会, 做特邀报告“中国风沙危害区生态重建与恢复的生态水文学基础”。
- 8) 2月, 张玉宝参加了在新西兰举行的第13届澳大利亚植物病毒学研讨会, 在大会上宣读了论文, 促进了国际合作与交流。
- 9) 2月5-6日, 李新荣研究员在北京参加CERN重点设施建设交流会议
- 10) 2月8日, 张铜会在北京参加中国科学院科技扶贫领导小组第一次工作会议。
- 11) 3月20-21日, 王少昆副研究员在兰州参加战略性国际科技创新合作重点专项“丝绸之路经济带沿线国家流沙固定及植被恢复关键技术研发与示范”中哈合作研讨会, 并在会上做了题为“Microbial organic compound-an ecological amendment in degraded sandy land restoration”的学术报告, 获得哈萨克斯坦学者的关注, 并建立后期合作意向。
- 12) 3月23日, 李新荣研究员在兰州参加国家重点研发计划“西北荒漠-绿洲区稳定性维持与生态系统综合管理技术研发与示范”年度会议
- 13) 3月25日-4月5日, 王新平、潘颜霞、虎瑞、张亚峰四人访问蒙古科学院地理与地质生态研究所, 在该所Elsen野外站附近进行野外考察, 选择样地。
- 14) 3月26-37日, 张铜会在兰州参加中国科学院库伦旗2018年科技扶贫工作会议作会议报告“库伦旗科技扶贫试验示范”。
- 15) 4月1-2日, 张铜会在兰州参加科尔沁沙地生态产业优化与示范课题2018年工作推进会, 作会议报告“科尔沁沙地生态产业优化与示范课题”。
- 16) 4月12-14日, 李新荣研究员在天津, 参加国家自然科学基金委第197期“双清论坛”, 做了“中国风沙区生态恢复与重建对中亚-西亚沙化防治的启示”的特邀报告
- 17) 4月23-25日, 左小安研究员作为技术咨询专家参加了国家科技基础资源调查专项“中国荒漠主要植物群落调查”项目的野外调查和取样技术培训会。
- 18) 4月26-28日, 罗永清博士在大连参加第五届生态毒理学学术研讨会。

- 19) 5 月, 周建伟博士受邀参加兰州大学草地农业生态系统国家重点实验室“青年论坛”。
- 20) 5 月 3-5 日, 沙坡头站李新荣、张志山、黄磊、回嵘、谭会娟在南京参加了第十七届中国生态学大会, 张志山和黄磊分别做了“固沙灌木的冠层截留及雨影效应”和“干旱露天煤矿排土场植被恢复重建关键技术与模式研究”的报告。
- 21) 5 月 3-6 日, 奈曼站王少昆、陈娟丽、张蕊、宁志英、牛亚毅、黄文达、杨红玲、左小安在南京参加第十七届中国生态学大会暨中国生态学学会第十次全国会员代表大会。并就“草地植物功能多样性对放牧的响应”进行了交流。王少昆副研究员在会议上做了题为“基于有机混合物对退化沙地修复的试验示范”的学术报告; 张蕊博士提交了题为“降水变化对荒漠草原区针茅群落日尺度碳交换的影响”的会议论文。
- 22) 5 月 14 日, 赵学勇在北京参加傅伯杰院士工作站会议, 作报告“乌梁素海国家湿地保护与利用”。
- 23) 5 月 21-24 日, 胡宜刚、谭会娟、潘成臣副研究员参加了在湖南桃源举办的“2018 年生物监测新技术与新版规范培训研讨班”。
- 24) 5 月 24-27 日, 潘颜霞副研究员参加中科院青促会汶川地震十周年综合科学考察
- 25) 5 月 24 日, 左小安在兰州参加中科院青促会优秀会员科研交流会, 作大会报告: 半干旱沙地生态格局、过程和机制。
- 26) 5 月 24 日, 左小安研究员受中科院西北研究院青促会小组邀请参加了“中科院青促会优秀会员科研交流会”, 并做了有关半干旱沙地生态格局、过程和机制的学术报告。
- 27) 6 月 2-9 日, 王新平研究员参加在美国夏威夷召开的 AOGS 会议, 在水文科学分会场 (HS30-A003) 做了“Event-based rainfall characteristics at Shapotou in north China”报告。
- 28) 6 月 21-23 日, 李新荣研究员在兰州参加甘肃省地理学会年会。
- 29) 6 月 22-23 日, 罗亚勇在杨凌参加 2018 年植被动力学暑期学校。
- 30) 6 月 24-30 日, 杨红玲在上海参加第十四届复旦大学生态学期高级讲习班。
- 31) 6 月 25 日, 何明珠研究员参加中国治沙暨沙产业学会防沙治沙新材料专业委员会 2018 年年会。
- 32) 6 月 25 日-7 月 5 日, 王新平、潘颜霞、虎瑞、张亚峰四人在蒙古进行合作研究、建设样地、架设仪器、扎设草方格等。

- 33) 7月5日, 赵学勇在通辽参加中日蒙合作项目会议, 作会议报告: Combating desertification in Horqin Sandy Land。
- 34) 7月5日, 程清平在北京参加大数据驱动的美丽中国全景评价与决策支持课题启动会
- 35) 7月5-7日, 李新荣、张志山北京参加2017年度国家生态系统观测研究共享服务平台内部评价考核会议。
- 36) 7月5-8日, 王少昆副研究员在通辽市参加中蒙日关于脆弱生态系统生态评估的“Discussion Workshop on Ecological Vulnerability Assessment”的学术论坛, 并在会议上做了“A New Approach of Ecological Restoration in Degraded Sandy Land Restoration—Using Microbial Organic Compound”的学术报告。
- 37) 7月6日-8日, 谭会娟、贾荣亮、回嵘、宋光、王艳莉在甘肃瓜州参加第五届“甘肃生态论坛”。
- 38) 7月9-10日, 王少昆副研究员和马旭君助理研究员在巴彦淖尔市中科院乌拉特荒漠草原研究站参加“中科院西北研究院所级中心技术人员能力提升培训”。
- 39) 7月11-13日, 毛伟博士在中科院沈阳应用生态研究所的额尔古纳草原站参加了“中美极端干旱联网研究”学术讨论会, 就4年的联网研究数据的应用和共享进行了深入的交流。
- 40) 7月12-14日, 毛伟参加中美“草原生态系统对极端气候事件的响应”国际研讨会, 并就深入开展联网研究及论文发表进行交流。
- 41) 7月14-15日, 李新荣研究员在张掖参加沙产业论坛, 特邀报告
- 42) 7月14-16日, 李新荣在张掖河西学院参加“绿洲论坛”, 并作大会报告。
- 43) 7月22-25日, 潘成臣在烟台参加“一带一路”现代农业产业技术国际学术会议。
- 44) 7月28-30日, 李新荣研究员参加中科院西北研究院敦煌站学术会议
- 45) 8月2日, 左小安在兰州参加大数据驱动的美丽中国全景评价与决策支持研讨会, 作大会报告“黑河流域全景评价指标体系的思考与进展”。
- 46) 8月12-15日, 国家标本资源共享平台植物子平台2019年度工作会暨第四期标本数字化技术培训班在内蒙古大学顺利召开。沙坡头站沙漠植物标本室冯丽工程师参加了此次培训。
- 47) 8月12-17日, 张铜会在呼和浩特参加帮扶干部打好精准脱贫攻坚战专题培训班作参加会议中国科学院—库伦旗定点帮扶工作介绍。
- 48) 8月15日, 北京市通州区科委到奈曼旗举办“科技扶贫”对接研讨会。奈曼站罗亚勇助理研究员、罗永清助理研究员受邀参会并介绍了奈曼站科普教育的

相关情况。

- 49) 8月15日, 罗亚勇在奈曼参加北京市通州区科委对口帮扶奈曼旗对接考察座谈会, 作报告“奈曼沙漠化研究站科普教育基地合作项目简介”。
- 50) 8月18-22日, 马旭君在呼和浩特参加第一届中国菌根学青年学术论坛暨丛枝菌根真菌分类鉴定培训班。
- 51) 8月20-22日, 罗亚勇在奈曼参加蒙药特色产业与奈曼旗可持续发展暨第二届占布拉道尔吉蒙医药发展战略研讨会, 作报告“奈曼旗蒙医药发展的科技瓶颈和产业发展思考”。
- 52) 8月22-23日, 程清平在兰州参加“时空三极环境”项目第一、第五课题联合启动会。
- 53) 8月25日, 刘新平在通辽参加中国科学院科技扶贫项目启动会, 作会议报告“库伦旗草牧业-肉牛养殖一体化脱贫与产业发展模式试验示范”。
- 54) 8月25日, 张铜会在通辽参加中国科学院科技扶贫项目启动会, 作会议报告“库伦旗特色扶贫产业关键技术试验示范”。
- 55) 8月27-29日, 左小安研究员和王少昆副研究员在西安参加了“2018年中国地理学大会”, 并就“荒漠草地生物地球化学过程及其模型模拟研究”进行了讨论。
- 56) 8月29-31日, 刘玉冰、赵丽娜参加2018年全国污染生态学学术研讨会暨中国生态学会污染生态专业委员会四届二次会议。
- 57) 8月30日, 赵学勇在北京参加中国科学院联合考察项目会议, 作会议报告“Long-term research and monitoring along the Sino-Mongolia Transect”。
- 58) 9月2日, 左小安研究员在兰州参加了“大数据驱动的美丽中国全景评价与决策支持”研讨会, 并作了“黑河流域全景评价指标体系的思考与进展”的学术报告。
- 59) 9月3-4日, 左小安研究员在北京参加了“地球大数据支撑SDGs与美丽中国评价专题论坛”, 并就“黑河流域全景评价指标体系”的完善进行了讨论。
- 60) 9月10-21日, 王新平、潘颜霞、虎瑞、张亚峰四人访问哈萨克斯坦生物与生物技术研究所、哈萨克斯坦农业部土壤与农业化学研究所, 在Birlik站进行野外调查研究
- 61) 9月18日, 张铜会在通辽参加通辽中直机关2018年扶贫工作推进会议作会议报告库伦旗科技扶贫进展汇报。
- 62) 9月19日, 左小安研究员受甘肃农业大学林学院的邀请, 为了林学院广大师生做了有关“半干旱沙地生态格局、过程和机制”的学术报告, 同时与林学院

有关从事植物功能性状的老师就未来林学院相关方向的研究和发展进行了深入的讨论。

- 63) 9月20日,李新荣研究员参加西北师大教育部重点实验室年会。
- 64) 9月21-23日岳平在右玉参加国家重点研发计划课题进展的研讨会。
- 65) 9月26-30日,李新荣在阿根廷门多萨参加中阿(NSFC-CONICET)土地退化/荒漠化与生态系统修复双边研讨会。
- 66) 9月29-30日,王新平研究员参加在西安召开的2018年中国地理学大会。
- 67) 10月8-10日李玉霖、段育龙、王立龙在长春参加“美丽中国”项目评审会,李玉霖作特邀报告“东北农牧交错带农草畜水复合生态工程发展模式及示范”。
- 68) 10月10-11日,何明珠研究员参加在定西召开的2018中国(甘肃)中医药产业博览会。
- 69) 10月10-13日,马小飞研究员在云南省昆明市参加中国植物学会八十五周年学术年会,“水文与土壤微生物生态”专题主持人,做报告“沙米的生态适应性分析”。
- 70) 10月11-12日,张铜会在呼和浩特参加内蒙古中直机关2018年定点帮扶工作座谈会议,作会议报告“中科院-库伦旗2018年科技扶贫进展汇报”。
- 71) 10月16-17日,张铜会在合肥参加第四届现代农业推广与技术转移国际会议。作大会报告“Poverty alleviation Using Science and Technology Measures in Agro-pastoral Ecotone, Inner Mongolia, China”。
- 72) 10月26日,刘新平、赵学勇、马小飞、王少昆、罗亚勇、张蕊、冯静、苏娜、岳平在长沙参加中国地理学会-沙漠分会2018年学术研讨会。左小安作大会报告:北方荒漠-草原植被对降水变化响应的野外观测与模拟实验对比研究;岳平作学术报告“温带沙质荒漠温室气体通量对水分、温度和氮沉降升高的响”;王明明分会场报告“半干旱草地生物量积累过程对降水变化的响应模拟——以科尔沁沙质草地为例”。
- 73) 10月30-11月1日,李新荣研究员在北京参加“中国沙漠誌”编写会议,在中国林科院做了“恢复生态学发展战略”报告。
- 74) 10月30日-11月4日,黄文达在杭州参加East Asia Plant Diversity and Conservation 2018 Program and Information。
- 75) 11月1日,赵学勇在北京参加科技部2018年典型脆弱生态修复专项年度总结会议,作会议报告“11个跟踪项目结果总结汇报”。
- 76) 11月8日,赵学勇在成都参加草地学会在程度召开的会议,作会议报告“科尔沁沙地人工草地的变化与功能”。

- 77) 11 月 8-11 日, 周建伟博士在广州参加中国畜牧兽医学会家畜生态学分会学术年会并作学术报告, 报告题目“日粮能氮调控对藏羊氮平衡和尿素循环的影响”。
- 78) 11 月 11-12 日, 李玉霖、赵学勇、左小安、李玉强、刘新平、王少昆、连杰、罗永清、陈敏、岳平、刘良旭、云建英在北京参加 2018 年奈曼站-乌拉特站学术委员会会议。
- 79) 11 月 12-13 日, 陈敏、周建伟博士在兰州参加第五届西部生态环境资源青年学术论坛, 分别作大会报告“开花物候和生殖限制对荒漠优势植物传粉过程的影响”和“牦牛对低氮营养胁迫的适应性机制研究”。
- 80) 11 月 13-15 日, 程清平在北京参加黑河集成预测项目。
- 81) 11 月 13 日, 岳平在兰州参加第五届“西部生态环境资源青年学术论坛”暨“祁连山青年论坛”, 作学术报告“温带沙质荒漠温室气体通量对水分、温度和氮沉降升高的响应”。
- 82) 11 月 16-17 日, 谭会娟副研究员参加在长沙召开的数据出版与台站综合信息系统交流会。
- 83) 11 月 17 日, 左小安在兰州参加西北师范大学地理与环境学院学术报告会作大会报告“北方荒漠-草原植被对降水变化响应的观测与模拟实验对比研究”。
- 84) 11 月 18 日, 李玉霖、赵学勇、刘新平、左小安、李玉强、王少昆、陈敏、宁志英、岳平、何钊全在银川参加荒漠化与生态恢复 2018 年学术研讨会。作汇报性报告“科尔沁沙地农田作物节水技术及潜力研究”。
- 85) 11 月 18 日, 张铜会在北京参加中科院-通辽市科技扶贫工作座谈会。作会议报告“通辽市院地合作及库伦旗科技扶贫工作进展汇报”。
- 86) 11 月 27-28 日, 左小安在成都参加四川农业大学林学院学术报告会作大会报告“北方荒漠-草原植被对降水变化响应的野外观测与模拟实验对比研究”。
- 87) 11 月 30 日, 赵学勇在北京参加水土保持学会会议, 作会议报告“科尔沁沙地退化与恢复问题”。
- 88) 11 月 30 日-12 月 1 日, 程清平在兰参加“大数据驱动的美丽中国全景评价与决策支持”2018 年度总结会, 作大会报告“黑河流域全景评价指标体系构建进展”。
- 89) 12 月 5 日-7 日, 杨红玲在南京参加 2018 年“世界土壤日”中国活动。主题为土壤污染防治暨“第一届全国土壤修复大会”。

十一、大事记

- 1) 3月17-23日,应陈国雄研究员邀请哈萨克斯坦植物研究所 Yerlan Turuspekov 教授来访,开展沙蓬驯化学术交流。
- 2) 4月19日,中卫市人大常委会副主任刘林森一行10余人到沙坡头站参观。
- 3) 4月20日,中科院西北研究院宜树华研究员到沙坡头站小红山样地参观。
- 4) 4月21日,中卫市林业局副局长刘任涛一行4人来沙坡头站参观。
- 5) 4月24日,广东揭阳市退休教师陈泽龙来沙坡头站参观顺带讨论固沙问题;北京植物所高秀丽一行来沙坡头站在流沙、固定沙丘上采样。
- 6) 4月25日,天水师范学院刘艳梅副教授一行6人来沙坡头站选择样地。
- 7) 4月28日,中科院西北研究院网络室赵雪茹一行3人到沙坡头站参观蓝藻结皮固沙样地并为蓝藻固沙科普准备基础材料。
- 8) 5月1日,河南科技大学陈应武副教授和中科院西北研究院沙漠室牛清河来沙坡头站开展试验。
- 9) 5月1-3日,以色列古里安大学及兰州大学动物营养学专家来皋兰站考察与交流。
- 10) 5月5日,北京林业大学饶良毅教授、中国林科院郝玉光研究员、程磊磊、周海川等专家一行10人到奈曼站进行学术交流和科学考察。
- 11) 5月11日,兰州大学千人计划贺缠生教授一行7人来沙坡头站参观交流。
- 12) 5月11-12日,中科院科技摄影联盟负责人、新华社摄影记者金立旺,中科院科技摄影联盟(上海)负责人、《文汇报》原摄影部主任谢震霖,中科院科学传播局新闻联络处业务主管王晓亮,西北研究院办公室副主任岳晓等一行到沙坡头站调研和积累素材。
- 13) 5月18日,国家民族事务委员会主管的《中国民族》杂志社的3名记者在中卫市委宣传部相关工作人员的陪同下到沙坡头站搜集素材。
- 14) 5月19日,中科院西北研究院特色所考核视频材料拍摄组到沙坡头站开始拍摄。
- 15) 5月22日,武汉外国语学校师生28人组成的西北研学旅团到沙坡头站参观。
- 16) 5月23日,深圳卫视《探秘时刻》栏目组到沙坡头站为治沙系列纪录片搜集素材;西北研究院国资处、审计处、财务处一行7人到沙坡头站对 Lysimeter 群项目进行检查。
- 17) 5月30日,新华社驻银川记者沙坡头站一行4人到沙坡头站搜集素材。
- 18) 5月31日,西北研究院国资处和监察审计处相关负责人对沙坡头沙坡头站承担的“中国北方沙区水量平衡自动模拟监测系统-Lysimeter 群”工程进行中期验收。

- 19) 6月1日, 青岛农业大学植物医学学院学生2人到沙坡头站开展苹果蠹蛾的分布与药理、性诱剂对苹果蠹蛾影响的合作研究。
- 20) 6月2日, 中科院地理所生态网络综合中心刘宇博士一行到沙坡头站考察。
- 21) 6月4日, 中卫市委宣传部主任胡立华带领“2018年拉美国家新闻官员与记者研修班”的国外学员一行54人到沙坡头站参观。学员主要来自巴拿马、秘鲁、玻利维亚、赤道几内亚、多米尼加、哥伦比亚、哥斯达黎加、乌拉圭等。
- 22) 6月8日, 浙江大学社会学系郦菁副教授、美国加利福尼亚大学伯克利分校 Christopher Kong Ho Chan 博士一行到沙坡头站参观; 天水师范学院刘艳梅副教授到沙坡头站进行合作研究。
- 23) 6月9-10日, 西南林业大学石漠化研究院副院长王妍副教授、生态与水土保持学院副院长刘云根副教授和杨波助教到沙坡头站开展学术交流。王妍副教授做了“岩溶湖滨湿地流域景观演变与环境效应研究”的报告。
- 24) 6月10日, 新华社记者来沙坡头站拍摄, 为6月17日“世界防治荒漠化与干旱日”准备治沙工作素材。
- 25) 6月11日, 宁夏电视台卫视频道记者来沙坡头站采访李新荣研究员。
- 26) 6月16-17日, 中央电视台导演刘彬一行6人到沙坡头站为宁夏回族自治区60周年大庆电视政论片《家园》系列纪录片的拍摄搜集素材。
- 27) 6月20-21日, 北京市图强第二小学150余名师生来到沙坡头站参观学习。
- 28) 6月26日, 中卫市人社局、市委组织部到沙坡头站考察沙坡头站黄磊同志; 西北研究院沙漠室张克存研究员到沙坡头站开展工作; 兰州大学陈宁博士一行4人到沙坡头站采样。
- 29) 6月27-28日, 中国科学院院士许智宏、苏国辉、中科院华南植物园王瑛研究员、宁夏农林科学院秦垦研究员一行8人到沙坡头站。座谈会上, 许智宏院士就国际现代农业发展态势, 优良植物基因的保护和开发、农业产业结构的调整等方面进行了解读。苏国辉院士和王瑛研究员以“药食同源枸杞子: 神经保护”和“淫羊藿野生资源挖掘和可持续利用”为题到沙坡头站科研人员和研究生做了精彩的学术报告。
- 30) 6月29日, 宁夏西部云基地科技有限公司员工到沙坡头站参观。
- 31) 6月30日, 中科院传播局宣传片拍摄组到沙坡头站拍摄; 西北研究院所级中心康建芳5人来沙坡头站拍摄影像数据。
- 32) 7月3日, 兰州大学肖洒教授、悉尼大学 HPPER NSELSEN 一行4人到沙坡头站参观考察。
- 33) 7月4日, 东南大学6人来沙坡头站参观; 宁夏老科协副会长吕林昌带领新疆老科协一行7人到沙坡头站考察。

- 34) 7月6日,中卫市政协副主席刘学禄一行10人到沙坡头站参观。
- 35) 7月9日,美国科罗拉多州立大学 Alan K. Knapp 教授和 Melinda D. Smith 教授,及新墨西哥大学 Scott L. Collins 教授一行3人来我院进行学术交流。Alan K. Knapp 教授作了题为“Understanding grassland productivity response to changing precipitation regimes”的报告,与会师生与 Alan K. Knapp 教授就如何设置更加贴近实际的干旱实验、干旱频率的波动是否影响不同功能群物种的生长等问题进行了讨论; Melinda D. Smith 教授做了题为“Drought-Net: A global network to assess terrestrial ecosystem sensitivity to drought”的精彩报告,就如何设置全球或者区域尺度上的联网实验和大家进行了热烈讨论; Scott L. Collins 教授等人与参会师生讨论了学术论文的撰写,数据共享和挖掘、学生的培养和交流、及未来可能潜在的国际合作进行了讨论。
- 36) 7月7-9日,中国科学院西北生态环境资源研究院王涛院长一行20人来乌拉特站考察指导工作。
- 37) 7月9-10日,中国科学院西北生态环境资源研究院所级中心一行25人来乌拉特站召开了中科院兰州区域仪器中心技术交流会,乌拉特站站长左小安研究员做了题为“乌拉特荒漠草原研究站-研究、监测与示范”的报告,介绍了建站背景、研究方向与内容、研究基础以及野外站仪器需求等。
- 38) 7月10日,中科院遗传所段子渊研究员和西高所赵凯研究员考察皋兰站并开展学术交流。
- 39) 7月12日,宁夏电视台采访李新荣研究员。
- 40) 7月13-14日,《中国北方半干旱荒漠区沙漠化防治关键技术与示范》项目组薛娴研究员等一行18人,《中国荒漠主要植物群落调查》项目组赵学勇研究员等一行7人,中科院西北院皋兰站站长谢忠奎研究员一行5人对奈曼站进行访问交流。主要对沙地生态环境问题展开深入交流和项目合作。
- 41) 7月13日,中央民委一行30人来沙坡头站参观。
- 42) 7月13-16日,宁夏银川唐徕回民中学56名师生进行科学实践。
- 43) 7月14日,中科院成都山地所一行12人来沙坡头站参观。
- 44) 7月16日,西北师范大学生科院“拾木沉沙”社会实践团6人来沙坡头站参观。
- 45) 7月16日-19日,“丝绸之路经济带沿线流沙固定及生态恢复高级研修班”学员90余人到沙坡头站参观。
- 46) 7月18日,宁夏广播电视台2人来沙坡头站采访李新荣研究员。
- 47) 7月19日,西安新汇译测控投资有限公司4人来沙坡头站参观 lysimeter 群;中科院地理所孙晓敏研究员、张雷明、朱治林副研究员;北京师范大学刘绍民教授;国家林业局西北规划院副院长周环水等一行6人到沙坡头站考察。

- 48) 7月20日, 参加 ChinaFLUX 第十三次通量观测理论与技术培训的科研人员 37 人到沙坡头站参观。
- 49) 7月21-23日, 重庆大学环境生态工程专业师生 24 人到沙坡头站实习。
- 50) 7月22日, 宁夏黄河文化专题片拍摄组到沙坡头站开展前期工作。
- 51) 7月23日, 中卫市政协副主席刘学禄联系广东省政协考察中卫市沙漠生态环境治理情况座谈会会务准备事宜。
- 52) 7月24日, 宁夏回族自治区政协副主席马力、中卫市市长万新恒、市委常委高振宇等陪同由王荣同志率领的广东省政协考察团一行 10 人到沙坡头沙坡头站考察, 并进行“广东省政协考察中卫市沙漠生态环境治理情况座谈会”。
- 53) 7月24日, “中国—阿拉伯国家现代农业节水技术国际研修班”20 余人到沙坡头站参观和现场交流; 宁夏黄河文化专题片拍摄组到沙坡头站确定 25 日拍摄细节, 并完成沙坡头站区拍摄。
- 54) 7月24日, 全国政协副主席秘书长、民进中央副主席朱永新一行 10 余人, 在内蒙古自治区、通辽市部分领导成员和相关部门人员陪同下来奈曼站调研。主要对奈曼站研究、监测、示范台站运行情况进行了深入交流与讨论。
- 55) 7月25日, 中山大学地理科学专业师生 33 人进行综合自然地理学课程野外实习; 宁夏黄河文化专题片拍摄组到沙坡头站拍摄。
- 56) 7月26日, 宁夏大学生态中心师生 10 余人开展研究生野外实习。
- 57) 7月27日, 国家海洋局第一海洋研究所王宗灵研究员一行 4 人到沙坡头站参观。
- 58) 7月28日, 中科院生态环境中心卫伟研究员一行 4 人到沙坡头站参观; 中科院油气中心张生银研究员一行 5 人到沙坡头站参观。
- 59) 7月10-12日, 甘肃农业大学资环学院生态学专业 60 名大一学生到沙坡头站进行生态学教学实习。
- 60) 7月29日, 中科院近物所王彦瑜研究员一行 3 人到沙坡头站参观。
- 61) 7月31日, 中科院兰州分院副院长陈改学 3 人到沙坡头站参观。
- 62) 8月1日, 南京大学生命科学学院 7 位研究生开展野外专业实习。
- 63) 8月3日, 北京林业大学水保学院“美丽中国环保科普”行动小组 6 人到沙坡头站实习。
- 64) 8月4日-8日, 《冰冻圈科学系列丛书》编撰会议在沙坡头举行。
- 65) 8月5日, 深圳卫视记者来沙坡头站拍摄纪录片, 采访李新荣研究员。
- 66) 8月6日, 由商务部主办、宁夏农林科学院承办的“阿拉伯国家防沙治沙技术培训班”学员 29 人到沙坡头站现场考察学习。

- 67) 8月6-8日, 深圳卫视《探秘时刻》栏目组到沙坡头站进行治沙系列纪录片的拍摄。
- 68) 8月7日, 秦大河院士和丁永建研究员分别以“冰冻圈科学与可持续发展”和“干旱区山区流域水量平衡研究”为题到沙坡头站科研人员和学生做了精彩的学术报告。
- 69) 8月8日, 通辽市科学技术局党组书记包志敏一行5人到奈曼站考察调研, 主要对奈曼站的科普工作和示范推广情况进行了深入交流与讨论。
- 70) 8月8日, 宁夏回族自治区常委一行30余人到沙坡头站检查自治区大庆慰问工作准备情况; 中卫市市委书记何健, 副书记马河清等人到沙坡头站看望秦大河院士。
- 71) 8月9日, 财政部国际财金合作司司长陈诗新一行13人到沙坡头站考察。
- 72) 8月12日, 西北研究院沙漠室杨保研究员4人来沙坡头站; 太原市小店区政府人员一行19人来沙坡头站参观; 中国矿业大学暑期科学实践6人到沙坡头站。
- 73) 8月13日, 佛山电视台一行3人到沙坡头站做前期拍摄准备。
- 74) 8月14-20日, 美国乔治·华盛顿大学 Ginger R. H. Allington 到奈曼站进行学术交流。并做了题为“Understanding landscape change in dryland socio-environmental systems”的学术报告, 报告结束后与奈曼站在站师生开展了深入学术讨论。
- 75) 8月15日, 中卫市林业检疫人员5人来沙坡头站; 佛山电视台“珠江形象大使”宁夏沙坡头站拍摄在沙坡头拍摄草方格扎设。
- 76) 8月24日, 中国科学院南海海洋研究所三亚站站长黄晖研究员等一行5人来奈曼站考察调研。双方就三亚站和奈曼站未来的发展合作进行了深入交流和讨论。
- 77) 8月25日, 甘肃省政协副主席一行4人来沙坡头站参观; 中科院西北研究院办公室主任张景光一行17人来沙坡头站参观。
- 78) 8月28日, 中科院遗传发育所栾城站站长沈彦俊研究员、太行山站副站长曹建生研究员、南皮站副站长孙宏勇研究员等一行9人到沙坡头站考察。
- 79) 8月29日, 陕西师范大学4位本科生来沙坡头站参观。
- 80) 8月30日, 中国气象局副局长余勇一行8人到沙坡头站调研。参加调研的还有宁夏回族自治区气象局局长杨兴国、中卫市副书记马和清、副市长曾申平、中卫市气象局等; 中卫市委副书记马和清10人来沙坡头站检查观摩点; 国家开发银行10余人到沙坡头站参观。

- 81) 8月31日,王若愚研究员邀请美国纽约 Albany 药学院马卓研究员来实验室进行学术交流,并作学术报告。
- 82) 9月1日,中科院合肥物质科学研究院技术生物所3人来沙坡头站参观。
- 83) 9月3日,应急管理部副部长尚勇一行到沙坡头站调研。参加调研的还有中卫市委书记何健、中卫市旅游局局长范家宏等;宁夏电视台60周年大庆宣传片拍摄组4人来沙坡头站拍摄。
- 84) 9月4日,中组部带领新西兰奥克兰大学微生物学专家一行4人到沙坡头站参观。
- 85) 9月6日,西部省区老年科协120多人到沙坡头参观。
- 86) 9月8日,甘肃省水利科学研究院副院长马成祥带领“2018年发展中国家雨水集蓄利用技术培训班”59人到沙坡头站参观学习。利用甘肃省在雨水集蓄利用方面的优势解决亚、非、拉干旱半干旱地区人畜饮水问题及发展当地旱作农业。
- 87) 9月10日,宁夏回族自治区人民政府党委副书记一行25人来沙坡头站。
- 88) 9月14日,《联合国防治荒漠化公约》秘书处副执秘普拉迪普在国家林业局治沙办国际处贾晓霞处长、宁夏回族自治区林业厅平学志副厅长等陪同下一行9人到沙坡头站考察。
- 89) 9月15日,广东省环保厅的环境教育立法调研组一行8人到沙坡头站;中科院西北研究院乌拉特站副站长王少昆等4人来沙坡头站参观;河海大学岩土工程科学研究所何稼副教授等4人来沙坡头站。
- 90) 9月21日,值宁夏回族自治区成立60周年之际,中央军委委员、军委政治工作部主任、中央代表团副团长苗华率中央代表团第五分团,带着党中央的亲切关怀,视察了中国科学院沙坡头沙漠研究试验站包兰铁路人工固沙植被防护体系和科技成果展厅,代表党中央和国务院赠送了民族团结瓷瓶。在参观完展厅后,苗华同志代表以习近平总书记为核心的党中央向科研人员表示亲切的慰问,高度赞扬了沙坡头站六十多年来对科研精神的传承与坚持,鼓励青年一代继续坚持和发扬“沙坡头精神”。随行人员有国家民委专职委员张京泽,西部战区政委吴社洲,全国工商联副主席王永庆,司法部党组成员、政治部主任冯力军,生态环境部副部长庄国泰,水利部副部长田学斌,应急部副部长、中国地政局局长郑国光,银保监会副主席周亮,中央军委办公厅副主任、新疆维吾尔自治区副主席芒力克·斯依提等中央代表团成员。陪同人员有宁夏回族自治区党委常委、组织部部长盛荣华,党委常委、宁夏军区政委潘武俊,自治区政府副秘书长王小成,中卫市委书记、市人大常委会主

任何健，市委副书记、市长万新恒，中国科学院西北生态环境资源研究院院长王涛、党委书记谢铭等。

- 91) 9月21日，中国科学院西北生态环境资源研究院院长王涛、党委书记兼副院长谢铭、办公室主任张景光一行4人视察中国科学院沙坡头沙漠研究试验站。王涛向全沙坡头站人员做了题为“西北生态环境资源研究院特色所建设工作进展”的报告。
- 92) 9月22日，宁夏大学林学院80余人到沙坡头站参观。
- 93) 9月29日，辽宁省农科院风沙地改良利用研究所所长于国庆、副所长吕林有、阜新种羊场场长孙陶、科技科副科长李亚男等6人来奈曼站考察调研。主要对风沙地改良利用、草牧业发展、以及不同模式下土壤质量提升机理研究等方面开展项目合作。
- 94) 10月8-9日，以色列自然资源农业部Newe-Ya'ar研究中心的Zalmen Henkin教授访问，参观了乌拉特站的试验平台和实验场地，做了““Long-term research on herbage production, composition and quality in a grazed Mediterranean grassland””的学术报告。

The β -Ketoacyl-CoA Synthase HvKCS1, Encoded by *Cer-zh*, Plays a Key Role in Synthesis of Barley Leaf Wax and Germination of Barley Powdery Mildew

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(Received November 12, 2017; Accepted January 24, 2018)

The cuticle coats the primary aerial surfaces of land plants. It consists of cutin and waxes, which provide protection against desiccation, pathogens and herbivores. Acyl cuticular waxes are synthesized via elongase complexes that extend fatty acyl precursors up to 38 carbons for downstream modification pathways. The leaves of 21 barley *eceriferum* (*cer*) mutants appear to have less or no epicuticular wax crystals, making these mutants excellent tools for identifying elongase and modification pathway biosynthetic genes. Positional cloning of the gene mutated in *cer-zh* identified an elongase component, β -ketoacyl-CoA synthase (CER-ZH/HvKCS1) that is one of 34 homologous KCSs encoded by the barley genome. The biochemical function of CER-ZH was deduced from wax and cutin analyses and by heterologous expression in yeast. Combined, these experiments revealed that CER-ZH/HvKCS1 has a substrate specificity for C₁₆–C₂₀, especially unsaturated, acyl chains, thus playing a major role in total acyl chain elongation for wax biosynthesis. The contribution of CER-ZH to water barrier properties of the cuticle and its influence on the germination of barley powdery mildew fungus were also assessed.

Keywords: *Blumeria graminis* f. sp. *Hordei* • Cuticular wax • *Hordeum vulgare* • β -Ketoacyl-CoA synthase • Very-long-chain fatty acids.

Abbreviations: *Bgh*, *Blumeria graminis* f. sp. *Hordei*; BSTFA, *N,O*-bis(trimethylsilyl)trifluoroacetamide; CDS, coding sequence; CER, *ECERIFERUM*; DMSO, dimethylsulfoxide; EmBL, emerged leaf blade; EST, expressed sequence tag; EZ, elongation zone; FID, flame ionization detection; GC, gas chromatography; KCS, β -ketoacyl-CoA synthase; MS, mass spectrometry; NEZ, non-elongation zone; POLI, point of leaf

insertion; qPCR, quantitative real-time PCR; SC, synthetic complete; SEM, scanning electron microscopy; TLC, thin-layer chromatography; VLCFA, very-long-chain fatty acid.

Introduction

The lipidic cuticle coats the primary aerial surfaces of land plants, providing a robust water barrier that protects shoots from desiccation, and repels water and particulates from the epidermis. The cuticle also serves as the first line of defense against pathogens and herbivores, and reflects harmful UV radiation. It consists of two main components, cutin and cuticular wax. Cutin is a polymer of oxidized long-chain fatty acids and glycerol linked by ester bonds. The cutin matrix embeds and covers the outer epidermal cell walls, providing the structural backbone of the cuticle. Cutin is permeated and overlaid with cuticular waxes that are predominantly acyl aliphatics, including modified very-long-chain fatty acids (VLCFAs) and polyketide aliphatics. On some plant surfaces, cuticular waxes form intricate wax crystals; these epicuticular crystals impart a glaucous appearance to the pertinent organ and contribute to the reflective properties of the cuticle (Holmes and Keiller 2002).

Because of the importance of the cuticle for plant health, cuticular waxes have been intensively studied. The cuticle additionally presents a convenient means of investigating associated processes of broad interest in plant biology such as secretion and VLCFA synthesis. Wax-deficient '*eceriferum*' (*cer*) mutants with fewer or no epicuticular crystals can be easily selected and used to dissect the processes of cuticular wax metabolism, regulation or secretion, and to study stress phenomena. Barley (*Hordeum vulgare*) organs and *Arabidopsis* (*Arabidopsis thaliana*) stems are two systems that have been

Hydrological response of biological soil crusts to global warming: A ten-year simulative study

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Funding information

This research was supported by the National Natural Scientific Foundation of China, Grant/Award Number: Grant no. 41621001, 41530746.

Abstract

Biological soil crusts across the desert regions play a key role in regional ecological security and ecological health. They are vital biotic components of desert ecosystems that maintain soil stability, fix carbon and nitrogen, influence the establishment of vascular plants, and serve as habitats for a large number of arthropods and microorganisms, as well as influencing soil hydrological processes. Changes in temperature and precipitation are expected to influence the functioning of desert ecosystems by altering biotic components such as the species composition of biological soil crusts. However, it remains unclear how these important components will respond to the prolonged warming and reduced precipitation that is predicted to occur with climate change. To evaluate how the hydrological properties of these biological soil crusts respond to these alterations, we used open-top chambers over a 10-year period to simulate warming and reduced precipitation. Infiltration, dew entrapment, and evaporation were measured as surrogates of the hydrological functioning of biological soil crusts. It was found that the ongoing warming coupled with reduced precipitation will more strongly affect moss in crustal communities than lichens and cyanobacteria, which will lead to a direct alteration of the hydrological performance of biological soil crusts. Reductions in moss abundance, surface cover, and biomass resulted in a change in structure and function of crustal communities, decreased dew entrapment, and increased infiltration and evaporation of biological soil crusts in desert ecosystems, which further impacted on the desert soil water balance.

KEYWORDS

biological soil crusts, dew entrapment, evaporation, infiltration, open-top chamber, warming and reduced precipitation

1 | INTRODUCTION

Global climate change profoundly affects the composition, structure, and functioning of terrestrial ecosystems (Lu, Siemann, Shao, Wei, & Ding, 2013; Maestre, Salguero-Gomez, & Quero, 2012). Such changes can affect organisms both directly via physiological stress (Belnap, Phillips, Flint, Money, & Caldwell, 2008; Hui et al., 2014; Maestre et al., 2015) and indirectly via the changing relationships among species (Harley, 2011), as well as through the increased risk

of biological invasions (Bellard et al., 2013; Lu et al., 2013). Future climate scenarios predict an alteration of the timing and amount of precipitation in desert environments (Belnap, Phillips, & Miller, 2004). In addition, many climatic models have predicted increases in drought frequency and duration, coupled with a substantial warming in arid desert ecosystems (Dai, 2013; Trenberth et al., 2014), where biological soil crusts (BSCs) are key biotic components (Zelikova, Housman, Grote, Neher, & Belnap, 2014). A model from China

中国荒漠与沙地生物土壤结皮研究

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2018-04-22 收稿, 2018-05-08 修回, 2018-05-14 接受, 2018-06-21 网络版发表

国家自然科学基金创新研究群体项目(41621001)和国家自然科学基金重点项目(41530746)资助

摘要 生物土壤结皮广泛分布于干旱半干旱区, 其盖度占该区域地表活体覆盖的40%以上, 是联结荒漠地表生物与非生物成分的“生态系统工程师”和荒漠/沙地生态系统健康的重要标志, 也是干旱区地球表面过程研究中生物学与地球科学交叉研究的热点科学问题。21世纪初, 相关研究绝大多数来自国外, 且集中在热带荒漠、寒漠和欧洲草原, 很少有来自中国和温性荒漠的报道。本文评述了2000年以来中国学者在这一研究领域开展的系列创新性研究, 涉及生物土壤结皮组成、分布和演替, 对环境胁迫及全球变化的生理生态学响应, 与土壤生态、水文过程, 与维管植物和土壤动物关系, 对干扰响应和人工培养及在生态恢复实践中的应用等, 介绍了中国学者对国际生物土壤结皮研究所做的贡献。

关键词 荒漠生态系统, 生物土壤结皮, 土壤生态与水文过程, 生态恢复

生物土壤结皮(biological soil crust, BSC)是由蓝藻、绿藻、地衣、藓类和微生物, 以及相关的其他生物体通过菌丝体、假根和分泌物等与土壤表层颗粒胶结形成的十分复杂的地表覆盖体, 是荒漠生态系统的重要组成部分^[1,2]。其盖度占全球干旱、半干旱地区裸地面积的70%, 发挥着极其重要的生态系统功能。截至2000年, 对BSC研究主要来自于美国、澳大利亚、德国、西班牙和以色列, 很少有来自中国的报道, 中国和中亚地区的研究几乎处于空白状态^[3]。基于这一现状, 中国学者从20世纪90年代末开始对BSC的形成、结构、群落组成、演替特征、时空分布和生态系统功能开展了大量的研究^[4,5]。补充和完善了国际BSC在温性荒漠区的研究不足, 填补了相关认知空白, 并从跟踪研究发展到并行研究, 促进了中国荒漠生态系统生态学和干旱区生态水文学的发展, 在国际上产生了重要影响。本文主要评述了2000年至今

我国学者在这一领域取得的重要进展, 展示了对全球BSC研究所做出的贡献。

1 BSC群落组成、分布和演替

不同于热荒漠(hot desert)和寒漠(cold desert), 发育在中国温性荒漠和沙地的BSC, 其种类组成多样, 群落多以藻类、地衣和藓类镶嵌分布。电子显微镜扫描结果证明, 这些隐花植物在地表利用菌丝体、假根和地表的依托支撑结构及分泌的多聚糖, 束缚和胶结了土壤细小颗粒, 形成了BSC^[6-13]。Hu等人^[14]从微米尺度上发现了藻类在BSC中呈精细“层片”分布和发育特征, 由表及里分别为矿物质保护层(0~20 μm)、富藻层(20~1000 μm)和疏藻层(1000~5000 μm)等3层结构, 并发现随着BSC的拓殖发展, 维持BSC结构的主要胶结方式也由胞外多聚糖的黏结作用逐渐转变为蓝藻和荒漠藻的藻丝体、地衣菌丝体以及藓

引用格式: 李新荣, 谭会娟, 回嵘, 等. 中国荒漠与沙地生物土壤结皮研究. 科学通报, 2018, 63: 2320-2334

Li X R, Tan H J, Hui R, et al. Researches in biological soil crust of China: A review (in Chinese). Chin Sci Bull, 2018, 63: 2320-2334, doi: 10.1360/N972018-00390



ORIGINAL RESEARCH

Pollinator activity and pollination success of *Medicago sativa* L. in a natural and a managed population

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Funding information

China National Key Research and Development Plan, Grant/Award Number: 2016YFC0500506; National Natural Science Foundation of China, Grant/Award Number: 31600252; CAS "Light of West China" Program, Grant/Award Number: Y729821001 and National Natural Science Foundation of China, Grant/Award Number: 41501572.

Abstract

Medicago sativa L. is an important cash crop in the arid region of northwest China. Pollinator activity is an essential aspect of pollination success, but the relationships between pollinator visitation rate and seed set still need further study of *M. sativa*. We investigated the following characteristics of *M. sativa* in natural and managed populations: floral traits, pollinator activity, and breeding system. Our results indicated the management could affect the number of flowers produced; however, there was no detectable effect on the seed set per flower. We found the percentage of seeds among pollinated flowers in the managed population was significantly higher than that in the natural population. Moreover, the increase in the proportion of pollinated flowers could significantly increase seed set per flower, and pollinator visitation rate was the important limiting factor for seed set in both populations. *Andrena lebedevi* Popov was found to be the most frequent pollinator in both populations. Outcrossing was dominant in the breeding system and insect pollination played an important role in outcrossing. Our study suggested that proper management (artificial selection) could promote pollination success of *M. sativa*.

KEYWORDS

breeding system, pollination, pollinator activity, pollinator visitation rate, seed set

1 | INTRODUCTION

Plants are immobile, and therefore, rely on abiotic or biotic vectors to transport pollen for sexual reproduction (Ashman et al., 2004). Pollination is a key biological process in terrestrial communities, and it affects a variety of evolutionary processes, such as selection on floral attraction and plant mating systems (Ashman & Morgan, 2004). For many plant species, pollination is the first stage in sexual reproduction, and an essential prerequisite for the development of fruits and seeds (Ashman et al., 2004; Kevan, Clark, & Thomas, 1990). The plant pollination process provides important indicators for designing conservation and sustainability strategies for a population (Rodríguez-Oseguera, Casas, Herrerías-Diego, & Pérez-Negrón, 2013).

In recent years, plant-pollinator interaction has been the focus of much discussion and debate (Fenster, Armbruster, Willson, Dudash, & Thomson, 2004; Gómez, Abdelaziz, Lorite, Munõz-Pajares, & Perfectti, 2010). Plant species that depend on animal pollinators for their reproduction have developed many different phenotypic traits, such as floral display, flower architecture and nectar (Arias-Cóyotl, Stoner, & Casas, 2006; Nores, López, Rudall, Anton, & Galetto, 2013). Insect mediated pollination, the transfer of pollen within or between flowers via insect vectors, is one such ecosystem service that benefits human populations and agriculture (Fisher, Turner, & Morling, 2009). During this process, the quantity of pollen deposited on the stigma is limited by pollinator visitation frequency and affects pollination success rates (Ashman

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RESEARCH ARTICLE

Open Access



Pollen limitation and resource limitation affect the reproductive success of *Medicago sativa* L.

Min Chen*  and Xiao-An Zuo*

Abstract

Background: A large proportion of the flowers and ovules of plants do not develop into fruits and seeds. Plant reproduction may be limited because of pollen limitation and resource limitation. *Medicago sativa* L. is an ecologically important species in northwest China. We conducted a pollen supplementation experiment to determine the degree of pollen limitation in this species and detect the possible effects of resource allocation on pollen supplementation. We crossed two factors, pollen level (natural condition and hand pollinated) and resource level (control, water added, and fertilizer added), to estimate the effects of pollen addition and resource limitation on the opening of flowers and seed set. We also analyzed the floral characters, visitation frequency of pollinators and pollinator activity to estimate the effect of pollinators on the reproduction of *M. sativa*.

Results: Our results indicated that addition of pollen to some flowers did not divert resources from other flowers and that the addition of pollen boosted the seed set per flower, with no effect on flower number. The primary effect of resource limitation was on the number of flowers produced; however, there was no significant effect on seed set per flower. These findings showed that pollen limitation was an important limiting factor for seed set. In addition, *Andrena lebedevi* Popov was identified as the most effective pollinator, and pollinator visiting and activity affected reproduction success in *M. sativa*.

Conclusions: We found outcrossing was dominant in the breeding system and insect pollination played an important role in outcrossing. These findings have identified the dominant factor influencing seed set of *M. sativa*. This study aspires to contribute to a better understanding of pollen limitation, resource limitation and reproductive success.

Keywords: Pollen limitation, Resource limitation, Pollinators, Seed set, *Medicago*

Background

Many plant species often produce more flowers and ovules than fruits and seeds [1, 2]. Several hypotheses have been presented to explain this phenomenon, including pollen and resource limitation [3, 4]. Pollen and resource limitation have received special attention because inadequate pollen and an insufficient availability of resources can reduce the reproductive success of plants [5]. An insufficient amount of pollen and compromised pollen quality have been demonstrated to result in

reduced fruit and seed set, a phenomenon referred to as pollen limitation [6, 7]. Many studies have also indicated that plants are assumed to be limited by resources if the addition of resources increases fruit or seed set [8, 9]. In most flowering plants, pollen limitation and resource limitation are important constraints on reproduction [10, 11].

Pollination is the first stage in sexual reproduction, and pollination traits have an important influence on plant reproductive success [12]. Plant–pollinator interactions have been viewed as a key process in most flowering plant species [13]. In animal-pollinated plants, pollen delivery and the visiting frequency and activity of pollinators are major biotic factors

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Research papers

Ecohydrological effects of biological soil crust on the vegetation dynamics of restoration in a dryland ecosystem

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ARTICLE INFO

This manuscript was handled by Corrado Corradini, Editor-in-Chief, with the assistance of Philip Brunner, Associate Editor

Keywords:

Drylands
Long-term restoration
Infiltration
Ecohydrological model
Biocrust
Layered soils

ABSTRACT

When restoring dryland ecosystems, growing biological soil crust (biocrust) may greatly change the redistribution of rainfall in layered soils. However, ecohydrological modelling studies generally ignore biocrust and thus, the ecohydrological effects of biocrust on restorations remain largely unexplored. Using a long-term restoration case (located in the southeast edge of the Tengger Desert, northern China), we developed an ecohydrological model with explicit consideration of the infiltration in three layered soils (biocrust, shallow and deep sand layers) to investigate influences of biocrust on restoration dynamics in drylands. The proportion of infiltration that reaches ‘annual grass’ (including biocrust and shallow sand layers, 0–30 cm) and ‘shrub’ layers (30–150 cm) with biocrust significantly increased and decreased relative to the values without biocrust, respectively. Meanwhile, biocrust significantly decreased soil water content in deep sand layer, but not in shallow sand layer. As more water was used by transpiration than evaporation, the ecosystem with biocrust reached a final grass-dominated state (high grass cover of 40%, low shrub cover of 4%) rather than a shrub-dominated state (grass cover of 3%, shrub cover of 20%). This study suggests that we need to account for the roles of biocrust on rainfall infiltration to better understand vegetation and restoration dynamics in dryland ecosystems.

1. Introduction

Drylands cover about 41% of earth’s land surface, and are home to about 38% of the global population (MEA, 2005). About 10%–20% of drylands have been degraded, and more are under serious threat of further degradation because of global environmental change and more intensified anthropogenic influences (MEA, 2005). Degradation adversely affects dryland ecosystem functions and the associated services such as water resource supply, water quality, and carbon sequestration (Petrie et al., 2015; Sala and Maestre, 2014; Ylännä et al., 2015). Therefore, it is urgent to prevent further degradation and to restore the degraded ecosystems in drylands.

Rainfall is an important factor and may be the sole water resource for dryland ecosystems (D’Odorico et al., 2013; Li et al., 2014a; Schlesinger et al., 1990). Therefore, the availability and redistribution of rainfall play a significant role in influencing the dynamics of vegetation and restoration (D’Onofrio et al., 2015; Li et al., 2014b; Rietkerk et al., 2004). Among the factors influencing the availability and

redistribution of rainfall, biological soil crust (covering a large part of the world’s terrestrial land surface; biocrust hereafter) may be the dominant one in many cases (Belnap, 2006; Belnap and Lange, 2003; Lebron et al., 2007; Li, 2012). Biocrust generally has a greater water holding capacity (e.g., over 15%–gravimetric soil water content) than the underlying sand (e.g., about 4%), and thus, can intercept more rainfall relative to sand (Belnap, 2006; Li, 2012). Meanwhile, biocrust promotes the growth of the underlying soil, which is also characterized by a high water holding capacity (unless indicated otherwise, biocrust also includes the subsurface soil, hereafter) (Belnap and Lange, 2003; Li et al., 2010). Although the thickness of biocrust generally only ranges in millimeters and centimeters, it still largely alters the redistribution of rainfall in soil because of the relatively low amount and intensity of rainfall events in drylands (Belnap, 2006; Chamizo et al., 2016; Corradini et al., 2011a). Theoretical and empirical studies have discussed the role of biocrust in regulating the ecohydrological properties of soils in drylands (Assouline et al., 2015; Belnap, 2006; Kidron and Benenson, 2014; Rodriguez-Caballero et al., 2015; Xiao et al., 2015).

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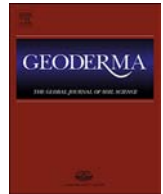
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<https://doi.org/10.1016/j.jhydrol.2018.06.076>

Received 21 April 2018; Received in revised form 25 June 2018; Accepted 27 June 2018

Available online 30 June 2018

0022-1694/ © 2018 Published by Elsevier B.V.



Soil carbon storage along a 46-year revegetation chronosequence in a desert area of northern China

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ARTICLE INFO

Handling editor: Jan Willem Van Groenigen

Keywords:

Soil inorganic carbon
Root-derived carbon
Deep soil carbon
Recovery time
Tengger Desert

ABSTRACT

Soil contains the majority of terrestrial carbon; however, most studies only focus on soil organic carbon (SOC) in the first meter or even shallower layers, and soil inorganic carbon (SIC) and root-derived carbon (RDC) are often overlooked. Here, we investigated the distribution of soil carbon at a depth of 0–3.0 m over a 46-year revegetation chronosequence on moving sand dunes and evaluated the potential influence of soil water content on soil carbon. The SOC density increased significantly along the 0–3.0 m profile, and showed a faster increasing rate in shallow layer (0–0.4 m) than that of the deep layers below 0.4 m. Although the SIC density did not increase significantly, it accounted for > 65% of the total soil carbon in shallow layer and at least 82% in deep layer. The live and dead RDC increased significantly over the chronosequence in both shallow and deep layers. The RDC accounted for a small amount of the total soil carbon at an average of 3.19%. The SOC was closely linked with live RDC in both the shallow and deep layers. The soil water content was only positively correlated with the SOC in the shallow layer. The SOC storage in the shallow layer required 57.4 years to reach the level at the natural vegetation site, whereas the storage in the deep layers required > 100 years. Our results indicated that soil carbon accumulation is a slow process in both shallow and deep layers after revegetation, and the most notable increase in soil carbon was accounted by SOC. We suggest that SOC, SIC and RDC should be considered when assessing the effects of revegetation on soil carbon in water-limited ecosystems.

1. Introduction

Soil represents an important and effective carbon reservoir in terrestrial ecosystems, and it is expected to have a more substantial sink capacity than the associated vegetation; thus, soil has a considerable ability to sequester carbon for the mitigation of elevated atmospheric CO₂ (Schlesinger, 1990; Batjes, 1996; Lal, 2004a, 2004b; Schmidt et al., 2011). Soil in water-limited ecosystems, which account for 47.2% of the global terrestrial surface, is estimated to contain approximately 241 Pg soil organic carbon (SOC) in the top one meter and an even larger soil inorganic carbon (SIC) pool (Eswaran et al., 2000). Therefore, the soil carbon storage in these ecosystems must be quantified and its potential response to environmental changes, e.g. vegetation and soil changes, should be determined.

Complete assessments of the SOC, SIC, and RDC pool are particularly lacking, especially in water-limited ecosystems. Due to the faster sequestration rate of SOC, most studies have focused on SOC, only a few studies have documented the distribution and dynamics of SIC (Diaz-

Hernandez et al., 2003; Hirmas et al., 2010; Chang et al., 2012). However, SIC is a main constituent of soil carbon in these ecosystems, and recent studies have suggested that SIC sequestration through both biological and non-biological processes may be underestimated (Wohlfahrt et al., 2008; Lal, 2009; Li et al., 2015). Root system is also a frequently neglected carbon reservoir. Actually, the cumulative contribution of RDC is comparatively larger and the residence time of root tissues in soil is longer than other plant tissues (Rasse et al., 2005; Pierret et al., 2016). Considering the high belowground production of root systems, which are normally large and deep in water-limited ecosystems (Chapin et al., 1993), RDC should not be overlooked when assessing soil carbon.

Most individual studies and large-scale investigations only focused on the first meter of soil (Batjes, 1996), or at even shallower depths, generally due to difficulties and costs associated with deeper sampling. However, many previous studies have detected larger amounts of soil carbon in deeper soil profiles in water-limited ecosystems (Harrison et al., 2011; Rumpel and Kogel-Knabner, 2011; Harper and Tibbett,

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<https://doi.org/10.1016/j.geoderma.2018.03.024>

Received 18 December 2017; Received in revised form 1 February 2018; Accepted 21 March 2018
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Effect of global warming on soil respiration and cumulative carbon release in biocrust-dominated areas in the Tengger Desert, northern China

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Received: 9 August 2018 / Accepted: 14 October 2018
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Abstract

Purpose Global warming is expected to have profound effects on terrestrial carbon (C) fluxes, consequently influencing future climate. Biocrusts are important sources of C in the C cycle of desert ecosystems, where vascular plants are restricted by limited soil moisture. This study was conducted in order to evaluate the expected increases in temperature on soil respiration in biocrust-dominated areas.

Materials and methods In a field warming experiment, we evaluated the impact of increased temperature on soil respiration in biocrust-dominated (moss-crust and lichen-crust) areas in Shapotou, China. In addition, the impacts of precipitation, soil temperature, and moisture on soil respiration were investigated.

Results and discussion The effect of warming on soil respiration varied with soil water availability. Our results showed that soil respiration in moss-crust and lichen-crust areas in the warming treatment was significantly lower than that in the control. The observed inhibition of soil respiration by the increase in soil temperature was likely due to the reduction in soil moisture caused by the increased water evaporation rate under higher soil temperature. Warming also decreased cumulative C release in moss-crust and lichen-crust areas. Moreover, cumulative C release showed marked seasonal variations, with the highest C release occurring in summer and the lowest in winter. Over the seasonal cycle, soil respiration rates were positively correlated with precipitation, soil temperature, and volumetric soil water content.

Conclusions The results of this study indicate that warming may increase the sensitivity of soil respiration to water availability in biocrust-dominated areas in desert ecosystems, suggesting that biocrust should be considered in projections of future C budget.

Keywords Biological soil crust · Precipitation · Seasonality · Soil respiration · Stimulated warming · Cumulative C release

Responsible editor: Zucong Cai

Electronic supplementary material The online version of this article (<https://doi.org/10.1007/s11368-018-2171-4>) contains supplementary material, which is available to authorized users.

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1 Introduction

Biological soil crusts (biocrusts) are widely distributed communities comprising cyanobacteria, green algae, lichens, mosses, and other microorganisms that live within or immediately on the top of the uppermost millimeters of the soil surface. Biocrusts develop widely on the soil surface in desert regions, where no vascular plants grow, and are often a substantial component of the total terrestrial surface (Belnap and Lange 2003). Due to their environmental sensitivity, biocrusts serve as indicators of environmental changes in temperature and soil moisture, and they can influence ecological processes, including seed germination and plant establishment (Li et al. 2010). Biocrusts also play an important role in carbon (C) cycling in terms of C uptake and release C to the atmosphere

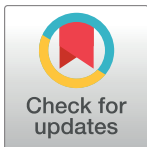
RESEARCH ARTICLE

Diel hysteresis between soil respiration and soil temperature in a biological soil crust covered desert ecosystem

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OPEN ACCESS

Citation: Guan C, Li X, Zhang P, Chen Y (2018) Diel hysteresis between soil respiration and soil temperature in a biological soil crust covered desert ecosystem. PLoS ONE 13(4): e0195606. <https://doi.org/10.1371/journal.pone.0195606>

Editor: Ben Bond-Lamberty, Pacific Northwest National Laboratory, UNITED STATES

Received: November 13, 2017

Accepted: March 26, 2018

Published: April 6, 2018

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Data Availability Statement: All relevant data are within the paper and its Supporting Information file.

Funding: This work was supported by National Natural Science Foundation of China (grant No. 41621001, 41530746) and the West Light Program for Talent Cultivation of Chinese Academy of Sciences. The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

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

Abstract

Soil respiration induced by biological soil crusts (BSCs) is an important process in the carbon (C) cycle in arid and semi-arid ecosystems, where vascular plants are restricted by the harsh environment, particularly the limited soil moisture. However, the interaction between temperature and soil respiration remains uncertain because of the number of factors that control soil respiration, including temperature and soil moisture, especially in BSC-dominated areas. In this study, the soil respiration in moss-dominated crusts and lichen-dominated crusts was continuously measured using an automated soil respiration system over a one-year period from November 2015 to October 2016 in the Shapotou region of the Tengger Desert, northern China. The results indicated that over daily cycles, the half-hourly soil respiration rates in both types of BSC-covered areas were commonly related to the soil temperature. The observed diel hysteresis between the half-hourly soil respiration rates and soil temperature in the BSC-covered areas was limited by nonlinearity loops with semielliptical shapes, and soil temperature often peaked later than the half-hourly soil respiration rates in the BSC-covered areas. The average lag times between the half-hourly soil respiration rates and soil temperature for both types of BSC-covered areas were two hours over the diel cycles, and they were negatively and linearly related to the volumetric soil water content. Our results highlight the diel hysteresis phenomenon that occurs between soil respiration rates and soil temperatures in BSC-covered areas and the negative response of this phenomenon to soil moisture, which may influence total C budget evaluations. Therefore, the interactive effects of soil temperature and moisture on soil respiration in BSC-covered areas should be considered in global carbon cycle models of desert ecosystems.

Introduction

Soil respiration accounts for the largest proportion of the total ecosystem respiration [1], and its global integration is an order of magnitude larger than that of anthropogenic CO₂ releases from burning fossil fuels and deforestation [1,2]. However, soil respiration processes are not

Article

Water-Yield Relationship Responses of Maize to Ridge-Furrow Planting Systems Coupled with Multiple Irrigation Levels in China's Horqin Sandy Land

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Received: 26 August 2018; Accepted: 6 October 2018; Published: 9 October 2018



Abstract: Water scarcity threatens the sustainability of irrigated agriculture in semi-arid regions, and ridge-furrow planting systems (RFPS) can be a prospective rainwater harvesting approach. In this study, we aimed to develop a promising water-saving strategy to boost maize productivity and water use efficiency (WUE). In 2017, we carried out a field experiment to study the effects of various RFPS with multiple irrigation levels on the yield-water relationship of maize (*Zea mays* L.). Eleven treatments were set up: RFPS with film mulching on both ridges and furrows and without water supply after seed emergence, abbreviated as QF; RFPS with film mulching on continuous ridges, abbreviated as MD, including SMD, MMD, and LMD (S, M, and L—three water supply (irrigation plus precipitation) levels of 650 mm, 500 mm, and 350 mm during the whole growing season); RFPS without film mulching, abbreviated as DD, including SDD, MDD, and LDD; conventional flat planting with no film mulching, abbreviated as GG, including SGG, MGG, and LGG; localized full irrigation (actual amount of irrigation excessively exceeding the quantity needed), abbreviated as NM. A positive linear relationship ($R^2 = 0.95-1$), a quadratic curve, and a negative linear relationship were observed between the irrigation water level and actual crop evapotranspiration (ET_c), grain yield, and WUE, respectively. The ET_c of QF (292 mm) was substantially lower than that of the other treatments ($p < 0.01$), saving 649 mm of irrigation water and increasing the yield by 2.24% compared with those of NM. Meanwhile, the WUE and irrigation water use efficiency (IWUE) of QF reached maximums of 6.3 and 47.36 kg m⁻³, respectively, which were significantly higher than those of other treatments ($p < 0.001$). The results showed that planting in an RFPS with film mulching on both ridges and furrows (a ridge-to-furrow ratio of 50:30, with a 38 mm irrigation level) is suitable for maize to obtain high yield and reduce irrigation water use significantly.

Keywords: ridge-furrow planting systems; evapotranspiration; crop coefficient; yield; water use efficiencies

1. Introduction

In arid and semi-arid regions, the annual crop evapotranspiration (ET_c) greatly exceeds the total precipitation, and approximately 50% of the total evapotranspiration occurs through the soil surface. Farmland irrigation is obtained mainly from groundwater [1], and over-exploitation of this resource can result in water unavailability. The total water requirement for maize (*Zea mays* L.), the third

CHANGES IN ANTIOXIDANT ENZYME ACTIVITIES AND BERRY COMPOSITIONS OF WINE GRAPES (MERLOT) SUBJECTED TO WATER STRESS WITH DRIP IRRIGATION

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ABSTRACT

Water is not only a limiting factor, but also one of the most important mediators of grape berry compositions in semi-arid land. Differences in superoxide dismutase (SOD), catalase (CAT), proline (Pro), malondialdehyde (MDA), and wine grape berry composition were investigated under water stress with drip irrigation. Merlot vines were proposed to the three levels of irrigation threshold (70-75%, 60-65% and 50-55% of field capacity (FC)) at the stage of germination, flowering and enlargement. The sweet taste and the favorable aromatic flavor were improved significantly from the germination to the enlargement stage to which slight water stress (60-65% of FC) was applied, wherein an optimal berry composition was achieved at the flowering stage which was mostly responsible for a positive relationship with high SOD activity. Such as, sugar-acid ratio, total sugar, tannins, total phenols, and anthocyanins of berries increased by 183.85%, 47.79%, 66.67%, 100%, 57.52% in comparison to normal irrigation threshold (70-75% of FC), respectively. When Merlot vines were stressed at 50-55% of FC from germination to flowering stage, berry composition, diameter and cluster mass were higher than in normal irrigation (70-75% of FC), resulted from the linear positively correlations between berry diameter, dry matter and Pro content, activities of SOD, CAT observed.

KEYWORDS:

Water stress, Merlot, Antioxidant enzyme activities, Berry composition and appearance.

INTRODUCTION

Drought stress, being defined as the absence of adequate soil moisture, is a major limiting factor for plants to grow normally, and seed germination, seedling, vegetative and flowering of the plant all are sensitive to water stress [1], therefore, the efficiency of applied water use of plants is of vital importance.

The by-products accumulation of normal cell metabolism, viz. reactive oxygen species (ROS), resulting in lipid peroxidation (in terms of MDA content), membrane injury, and enzyme inactivation through oxidative damage, such as superoxide radical (O_2^-), hydrogen peroxide (H_2O_2), hydroxyl radical (OH^\cdot), and singlet oxygen (O^1), is a biochemical change of plants subjected to water stress [2, 3]. ROS is scavenged by the principal antioxidant system of plants, including antioxidant enzymes, such as, SOD, CAT [4], which were broadly used for characterizing drought resistance, wherein, SOD is a primary defense line because it detoxify O_2^- into H_2O_2 [5]. Drought increased osmotic solutes, such as the soluble sugars and the Pro, have been observed previously [6-8]. The Pro could be affected by leaf age and position, as well as maintained the membrane integrity through reducing oxidation of membrane lipids [7]. Thereby, the maintenance of turgor via osmotic adjustment is used as a mechanism of drought tolerance.

Grapevine (*Vitis vinifera*) is regarded as the most vital fruit crop worldwide. Wines with high concentration, intense color, soft tannins, fruitiness, and low acidity are produced numerously. Grape berry contains abundant secondary metabolites which affect wine quality through determining its color, aroma, and flavor [9], such as, organic acids favorably affecting human metabolism, sugars, and flavonoids [10]. Generally, at veraison, grape leaf growth has practically ended and sugar starts to accumulate quickly in berries, and is time for treating berries with auxin prior to veraison [11]. Anthocyanins, as the predominant plant pigments and a class of flavonoids, are responsible for grape colors ranging from red to violet [12], wine color, mouthfeel and astringency, as does tannin content and composition. Besides, phenolic compounds are vital in red wine color and taste, as well as are rich in grape juice [13, 14].

Water is the main challenge to grape ripening in dry lands with irregular rainfall distributions, and remarkably affects grape berry compositions [15, 16], determines berry size, increasing with berry solute content [17]. Though grapevine is a greatly

THE PHYSIOLOGICAL-MORPHOLOGICAL (LEAF-LEVEL) RESPONSES OF SOYBEAN (*GLYCINE MAX* L. MERR.) TO THREE REGIMES OF DEFICIT IRRIGATION AND FERTILIZER COUPLING IN HORQIN SANDY LAND, NORTHEASTERN CHINA

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ABSTRACT

In regions with sandy soil texture and water scarcity, it is little to know the coupling effect of deficit irrigation with fertilization on soybean growth. The three combined effects of deficit irrigation (DI) and nitrogen fertilization (NF) on the leaf-level physiological and morphological parameters were identified. Irrigation was started once soil water content (SWC) was below 60% (T1), 50% (T2), 40% (T3), or 70% (CK) of field capacity (FC), respectively; meanwhile, 54 kg N ha⁻¹ (T1), 67.5 kg N ha⁻¹ (T2), or 81 kg N ha⁻¹ (T3) was assigned at the beginning of the blooming stage. The results showed that the net photosynthetic rate (P_N) and leaf water use efficiency (LWUE) was highest in T3. The leaf area (LA), plant height (SH), and leaf fresh mass (LFM) of T1, T3 increased by 32.69%, 16.05%, 29.10%, 14.93%, 62.49%, 71.43%, respectively, in comparison to CK. Relative water content (RWC, including leaf and pod) was lower in T1, T3 than in CK significantly, which was negative linear relationship with leaf water potential (ψ_w), and decreased continuously across growth stage. Ultimately, the average pod dry mass (PDM) in T3, T1 was up to 1.93g, 1.85g, CK just was 0.26g. Our results suggested that combination of 324mm irrigation and 54 kg N ha⁻¹ optimally elevated VG, and 81mm water combining with 81 kg N ha⁻¹ coupling most favoured RG and dry matter accumulation (DM) in comparison to single 405mm irrigation, maximizing the use efficiency of water, nitrogen and increasing vegetative growth (VG) and reproductive growth (RG).

KEYWORDS:

Gas exchange, Leaf morphology, Leaf water status, Nitrogen, Water stress.

INTRODUCTION

Due to its high protein, numerous mineral elements, and physiologically active substances that are beneficial to human health, soybean (*Glycine max* L. Merr.) is used as a vital source of quality protein and edible oil [1]. Soybean is popularly cultivated in the Horqin Sandy Land, located in the semiarid area of southeast Inner Mongolia, which was once severely desertified [2]. In this region, the frequency and amount of rainfall is considered to be a primary limitation to plants growth, owing to its volatility. As a result, irrigation is greatly dependent on groundwater. But, excessive irrigation depletes groundwater reserve. The measurement of photosynthesis can be used as an index of metabolic response to water stress [3], when leaf gas exchange activity is limited due to stomatal or nonstomatal limitations [4]. Another response is manifested in growth development limitations *via* inhibition of cellular expansion needed for, leaf area development and main stem elongation [5], as well as in reduction in yield potential [6]. An effective irrigation regime conserving limited water could be achieved via a DI strategy, i.e., one that applies less water than required by plants for increasing growth and ensuring stability in yields [7]. Reducing irrigation during drought tolerance periods to stabilize growth and yield is the primary objective of DI [8]. Therefore, it was an urgent necessity to confirm the effect of DI on plant physiological parameters. In previous studies, resistance to abiotic conditions was mainly expressed in stomatal morphology and dynamics [9]. Although the reduction in stomatal conductance occurred at 90 days after the plants were subjected to WS with 50% FC, the plants remained alive [10]. Taking into account the intensity and duration of WS, a remarkable decrease was also observed in ψ_w and LRWC [11]. Furthermore, the decrease in photosynthetic efficiency, stomatal and nonstomatal limitations, and inhibition of photochemical processes were strongly



Transcriptome analysis in *Malus halliana* roots in response to iron deficiency reveals insight into sugar regulation

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Received: 7 February 2018 / Accepted: 6 August 2018 / Published online: 12 August 2018
© Springer-Verlag GmbH Germany, part of Springer Nature 2018

Abstract

Iron (Fe) deficiency is a frequent nutritional problem limiting apple production in calcareous soils. The utilization of rootstock that is resistant to Fe deficiency is an effective way to solve this problem. *Malus halliana* is an Fe deficiency-tolerant rootstock; however, few molecular studies have been conducted on *M. halliana*. In the present work, a transcriptome analysis was combined with qRT-PCR and sugar measurements to investigate Fe deficiency responses in *M. halliana* roots at 0 h (T1), 12 h (T2) and 72 h (T3) after Fe deficiency stress. Total of 2473, 661, and 776 differentially expressed genes (DEGs) were identified in the pairs of T2 vs. T1, T3 vs. T1, and T3 vs. T2, respectively. Several DEGs were enriched in the photosynthesis, glycolysis and gluconeogenesis, tyrosine metabolism and fatty acid degradation pathways. The glycolysis and photosynthesis pathways were upregulated under Fe deficiency. In this experiment, sucrose accumulated in Fe-deficient roots and leaves. However, the glucose content significantly decreased in the roots, while the fructose content significantly decreased in the leaves. Additionally, 15 genes related to glycolysis and sugar synthesis and sugar transport were selected to validate the accuracy of the transcriptome data by qRT-PCR. Overall, these results indicated that sugar synthesis and metabolism in the roots were affected by Fe deficiency. Sugar regulation is a way by which *M. halliana* responds to Fe deficiency stress.

Keywords RNA-Seq · Fe deficiency · Sugar · Glycolysis · Apple · *Malus halliana*

Introduction

Iron (Fe) is an essential micronutrient for plants (Briat et al. 2015; Zargar et al. 2015a). Low uptake of Fe alters plant chloroplast structure, blocks the synthesis of chlorophyll and reduces photosynthesis (Niebur and Fehr 1981; Briat et al. 2015). Fe availability is very low in calcareous soils, which is caused by high pH and poor aeration (McGeorge et al. 1935). Moreover, calcareous soils account for approximately 30% of the world's cultivated soils, and Fe deficiency is a

widespread agricultural problem affecting crop yields (Mori 1999). An approach to preventing this problem is to use Fe deficiency-tolerant rootstocks (Rombolà and Tagliavini 2006). *Malus halliana* shows Fe deficiency-tolerant characteristics. The investigation of responses of *Malus halliana* to Fe deficiency may provide new insights into its regulation and adaptation mechanisms.

Under Fe deficiency, non-graminaceous plants experience changes in metabolic levels, including increases in several enzymes involved in the glycolytic pathway, the citrate cycle and the pentose phosphate pathway (Abadía et al. 2002; Zocchi 2006; López-Millán et al. 2009). Transcriptomic and proteomic studies have also reported an upregulation of enzymes related to the glycolytic pathway and citrate cycle in roots in Fe-deficient environments (Thimm et al. 2001; Jelali et al. 2010; Anita et al. 2012). Alteration of glycolysis seems to be an important mechanism for the adaptation of plants to Fe deficiency (Mai and Bauer 2016). Accordingly, Fe deficiency induces an accumulation of organic acids, mainly malate and citrate, that can affect Fe availability (Abadía et al. 2002). Moreover, root sugar accumulation under Fe deficiency results from starch degradation and/or

Communicated by S. Hohmann.

Electronic supplementary material The online version of this article (<https://doi.org/10.1007/s00438-018-1479-5>) contains supplementary material, which is available to authorized users.

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Environmental determinants of genetic diversity in *Salix gordejvii* (Salicaceae) in three Sandy Lands, northern China

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1. Introduction

Genetic differentiation in desert species is related to the spatial scale of environmental heterogeneity and to the balance between selection and gene flow (Xu et al., 2003). Genetic variation among populations of desert species for quantitative traits is well established (Scheiner, 1993), and this variation often occurs along different climatic gradients, such as changes in temperature and precipitation (Lovejoy and Hannah, 2005), suggesting strong local adaptation to climate (Sork et al., 2010). Understanding the environmental parameters that drive adaptation among populations is important in predicting how species may respond to global climatic changes and how gene pools might be managed to conserve adaptive genetic diversity (Bradbury et al., 2013).

Globally, desertified lands occupy approximately 3.6×10^7 km² in area, which amounts to about 24.1% of Earth's land surface and desertification affects about one-sixth of the world's population (Wang et al., 2012). Land degradation and desertification have become increasingly severe environmental and socio-economic problems throughout the world, while China is one of the most seriously affected countries (Wu and Ci, 2002). There are four large Sandy Lands in the agro-pastoral transitional zone in northern China, from east to west are Hulunbel Sandy Land, Horqin Sandy Land, Hunshandak Sandy Land and Mu Us Sandy Land, area reached 10,000 km², 139,300 km², 21,400 km² and 40,000 km² (Wu and Ci, 2002). There are environment gradient changes in the four Sandy Lands. There are different water and heat conditions in every Sandy Land, from east to west, mean annual temperature reached 0–2.5 °C, 3–7 °C, 1–3 °C and 5–9 °C, mean annual rainfall reached 280–400 mm, 350–500 mm, 100–200 mm and 200–400 mm (Wang et al., 2014; Cheng et al., 2004; Wang, 2003; Zhao et al., 2003). Horqin Sandy Land, Hunshandak Sandy Land and Mu Us Sandy Land were three of the four largest sandy areas in China and

provided a source of sand for sandstorms occurring in Northern China (Li et al., 2005). So it is an important exploration of the genetic diversity level and genetic variation in typical sand-fixation plants in this region.

Salix gordejvii Chang et Skv. (Salicaceae) is widely distributed in the Sandy Land in northern China (Su et al., 2005; Zhang et al., 2006). It has an important role in restoring the degraded ecosystem. In desertification control, it also serves as the pioneer species for vegetation re-establishment and moving sand fixation because it has several highly valuable ecological traits, including high drought tolerance, anti-wind erosion utility and sand burial-resistance (Wu, 2003; Zhang et al., 2006; Cui et al., 2011). *S. gordejvii* inhabits semi-fixed and fixed dunes. In terms of life history traits, *S. gordejvii* is long-lived, perennial, insect-pollinated, reproduces by seed and cottage propagation, and has a broad ecological amplitude (Fu, 1993). Previous studies on *S. gordejvii* have focused on aspects of its root morphological characteristics and variations (Huang et al., 2010; Liu et al., 2016), root ecology (Huang et al., 2008; Liu et al., 2014; Cui et al., 2011), physiological adaptations (Su et al., 2009; Ma et al., 2015; Liu et al., 2003), nutrient absorption (Yuan et al., 2005), and water use efficiency (Niu et al., 2006; Yue et al., 2013). The relationship between the genetic diversity of *S. gordejvii* and different Sandy Lands has not yet been reported, however.

The association between genetic and environmental gradients is well-established evidence of natural selection (Endler, 1986; Mannel et al., 2010). Climate is one of the most important drivers of local adaptation in desert species. Standing levels of genetic diversity and structure within and among natural populations of desert species are determined by the interplay between climatic heterogeneity and the balance between selection and gene flow. To investigate this hypothesis, we assessed *S. gordejvii* population genetic variation in different Sandy Lands in Northern China using inter-simple sequence repeat

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<https://doi.org/10.1016/j.actao.2018.08.007>

Received 1 November 2017; Received in revised form 8 July 2018; Accepted 12 August 2018

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Changes in winter snow depth affects photosynthesis and physiological characteristics of biological soil crusts in the Tengger Desert

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Abstract

Water availability is a major limiting factor in desert ecosystems. However, a winter snowfall role in the growth of biological soil crusts is still less investigated. Here, four snow treatments were designed to evaluate the effects of snow depth on photosynthesis and physiological characteristics of biological soil crusts. Results showed that snow strongly affected the chlorophyll fluorescence properties. The increased snow depth led to increased contents of photosynthetic pigments and soluble proteins. However, all biological soil crusts also exhibited a decline in malondialdehyde and soluble sugar contents as snow increased. Results demonstrated that different biological soil crusts exhibited different responses to snow depth treatment due to differences in their morphological characteristics and microhabitat. In addition, interspecies differentiation in response to snow depth treatment might affect the survival of some biological soil crusts. Further, this influence might lead to changes in the structural composition and functional communities of biological soil crusts.

Additional key words: biological soil crusts; chlorophyll fluorescence; photosynthetic pigments; soluble sugar; water availability.

Introduction

Climate change impacts ecosystems worldwide, with semiarid and arid ecosystems particularly vulnerable because many fundamental aspects of their structure and function are closely connected with variations in temperature, CO₂, and precipitation (Salguero-Gómez *et al.* 2012). Water availability is a major limiting factor in desert ecosystems; even small changes in precipitation are expected to have a strong impact on species composition and biodiversity in the soil profile (Sala and Lauenroth 1982). Snow is an important source of precipitation, it influences soil temperature and moisture, insulates soil from severe freezing, and is a protective cover for many plants, since air temperatures in winter are often considerably lower than soil temperatures (Mondoni *et al.* 2012). In addition, as available stored water is released when snow melts, it can improve plant growth and development (Olsen *et al.* 2011). However, because of anthropogenic climate change, snow frequency, cover, depth, and cover duration can be changed considerably. Since global air temperatures are predicted to increase in

winter (IPCC 2007), snow cover is expected to become thinner and melt earlier. As a result, a number of studies have focused on a decline in snow cover and advance in snow melt timing across a variety of arctic, subarctic, and alpine environments (Wipf and Rixen 2010). Evans and Fonda (1990), for example, examined community pattern expressed as a function of snow depth and snow cover duration, in order to look at their effect on soil moisture, soil temperature, and the growing season, while Tan *et al.* (2014) suggested that a decrease in snow cover can alter soil microbial activities, and hence element biogeochemical cycling in alpine forest ecosystems. However, changes in snow depth and cover duration are not consensus, as snow depth has increased in some areas (Callaghan *et al.* 2011). Indeed, an increase in snow depth can lead to enhanced ecosystem respiration during the late winter. Bosiö *et al.* (2014) analyzed the effect of increased snow cover on plant photosynthesis, showing higher absorption of photosynthetically active radiation on account of increased soil moisture and nutrients.

Received 24 August 2017, accepted 1 January 2018, published as online-first 21 June 2018.

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Abbreviations: BSC – biological soil crusts; Car – carotenoid; Chl – chlorophyll; F_v/F_m – the maximum photochemical efficiency; MDA – malondialdehyde; Yield – the effective photochemical quantum yield of PSII.

Acknowledgments: This study was jointly supported by the National Natural Science Foundation of China (Nos. 41621001, 41701104, 41530746) and West Light Program for Talent Cultivation of Chinese Academy of Sciences.



Effects of enhanced ultraviolet-B radiation, water deficit, and their combination on UV-absorbing compounds and osmotic adjustment substances in two different moss species

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Received: 18 November 2017 / Accepted: 4 March 2018 / Published online: 16 March 2018
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Abstract

A simulation experiment was conducted to explore the influence of enhanced ultraviolet-B (UV-B) radiation, water deficit, and their combination on UV-absorbing compounds and osmotic adjustment substances of mosses *Bryum argenteum* and *Didymodon vinealis* isolated from biological soil crusts (BSCs) growing in a revegetated area of the Tengger Desert, China. Four levels of UV-B radiation and two gradients of water regime were employed. Compared with their controls, amounts of total flavonoids, chlorophyll, carotenoids, soluble sugars, and soluble proteins significantly decreased ($p < 0.05$), but proline content significantly increased ($p < 0.05$), when exposed to either enhanced UV-B or water deficit. The negative effects of enhanced UV-B were alleviated when water deficit was applied. There were increases in UV-absorbing compounds and osmotic adjustment substances when exposed to a combination of enhanced UV-B and water deficit compared with single stresses, except for the proline content in *D. vinealis*. In addition, our results also indicated interspecific differences in response to enhanced UV-B, water deficit, and their combination. Compared with *B. argenteum*, *D. vinealis* was more resistant to enhanced UV-B and water deficit singly and in combination. These results suggest that the damage of enhanced UV-B on both species might be alleviated by water deficit. This alleviation is important for understanding the response of BSCs to UV-B radiation in future global climate change. This also provides novel insights into assessment damages of UV-B to BSC stability in arid and semiarid regions.

Keywords Biological soil crusts · Ultraviolet-B · Water deficit · Interaction · Total flavonoid · Proline

Abbreviations

BSCs Biological soil crusts
N Nitrogen
UV-B Ultraviolet-B

Car Carotenoid
Chl Chlorophyll
ANOVA Analysis of variance

Responsible editor: Philippe Garrigues

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Introduction

Biological soil crusts (BSCs) are widely and diffusely spread in arid and semiarid regions as an association of soil particles and diminutive organisms, formed by fungi, bacteria, cyanobacteria, green algae, lichens, and mosses closely integrated with soil particles (Belnap and Lange 2003). As a key functional component of arid and semiarid regions, BSCs provided various ecosystem services, such as enhancing soil stabilization, preventing wind and water erosion, accelerating carbon and nitrogen (N) cycles by increasing microbial biomass and fixing carbon, supplying microhabitat and livelihood for soil animals, and increasing interactions with vascular plants (Elbert et al. 2012; Jia et al. 2012; Li et al. 2012;

High rainfall frequency promotes the dominance of biocrust under low annual rainfall

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Received: 9 June 2018 / Accepted: 9 November 2018
© Springer Nature Switzerland AG 2018

Abstract

Aims Global climate change may greatly alter the structure and stability of drylands, creating an urgent need to recover their functions and services. Biological soil crust (biocrust), an interface between the soil and atmosphere, plays a crucial role in ecohydrological processes, and thus in influencing the restoration dynamics of dryland ecosystems. Previous studies have generally investigated the influences of biocrust on ecohydrological processes as an exogenous factor. However, it remains unclear how biocrusts, as an integral part of many ecosystems (i.e., as a system state variable), will change under global climate change.

Methods This study developed a new ecohydrological model with biocrust cover as a system state variable, and explored the response of dryland ecosystems to altered rainfall regimes.

Results Biocrust cover responded with an inverted U-shaped curve relationship to increasing annual rainfall and linearly to increasing rainfall frequency. Vascular plant (grass and shrub) cover showed an increasing trend with increasing annual rainfall and a decreasing trend to increasing rainfall frequency. Therefore, biocrust usually dominated over vascular plants (i.e., high biocrust cover and low vascular plant cover) under low annual rainfall. Furthermore, an increasing rainfall frequency would amplify the range of environmental (rainfall) conditions dominated by biocrust from an annual rainfall 0–100 mm under a rainfall frequency of 0.025 day⁻¹ to 0–500 mm under a rainfall frequency of 1 day⁻¹.

Conclusions This study developed a model framework to predict dryland dynamics for surfaces covered by biocrust under global climate change. We suggest that restoration efforts could target at biocrust-dominated state in deserts, especially in a (future) drier climate.

Responsible Editor: Hans Lambers.

Electronic supplementary material The online version of this article (<https://doi.org/10.1007/s11104-018-3880-6>) contains supplementary material, which is available to authorized users.

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Keywords Biological soil crust · Rainfall frequency · Global climate change · Drylands · Ecohydrological model · Layered soils

Introduction

Drylands are the largest terrestrial biome of the Earth covering around 40% of the terrestrial land surface and



The differential effects of sand burial on CO₂, CH₄, and N₂O fluxes from desert biocrust-covered soils in the Tengger Desert, China



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ARTICLE INFO

Keywords:

Biocrusts
Sand burial
Greenhouse gas
Desert

ABSTRACT

Biocrusts are a crucial component of desert ecosystems, playing a significant role in greenhouse gas fluxes when they cover soils. However, little is known about whether, and how sand burial, one of the most common disturbances affecting the biodiversity and ecological function of biocrusts, influences fluxes of CO₂, CH₄, and N₂O from the desert biocrust-covered soils. Based on measurements of the fluxes of three greenhouse gases from soils covered with two kinds of biocrusts separately dominated by mixed (i.e., approximately 50% algal coverage and 50% lichen coverage of *Endocarpon pusillum* Hedw., here cyanobacteria are classed as algae) and moss (i.e., 100% coverage of *Didymodon vinealis* (Brid.) Zand.) crusts respectively, followed by zero (control), 1 mm (shallow burial), and 10 mm (deep burial) burial depths of sand, we studied the effects of short (20 days) and relatively long periods (one year) of sand burial on the fluxes of three greenhouse gases as well as their relationships with soil temperature and moisture at Shapotou on the southeastern edge of the Tengger Desert. The results of this study showed that sand burial had a significantly positive effect on emission fluxes of CO₂ and a negative effect on uptake of CH₄ by soils covered with the two types of biocrusts ($P < 0.05$), but had a differential effect on N₂O fluxes depending on burial depth. Shallow burial dramatically increased N₂O emissions from the biocrust-covered soils ($P < 0.05$), but the opposite was observed under deep burial. As burial time increased, the increase of CO₂ emissions decreased, but changes in fluxes of CH₄ and N₂O varied with biocrust types and burial depths, respectively. In addition, results showed that CO₂ fluxes from the two biocrusts were closely related to soil temperature and moisture; thereby increased with the raised soil temperature at 5 cm depth and soil moisture caused by sand burial. In contrast, CH₄ and N₂O emissions were not clearly related to temperature or moisture. Overall, the increase in global warming potential caused by sand burial indicates that this kind of deposition may aggravate the greenhouse effect of desert areas covered with biocrusts.

1. Introduction

The existence of global climate change is widely accepted (IPCC, 2013). Greenhouse gases, as important drivers of this change, have recently become one key research focus of environmental sciences. Desert regions make potentially marked contributions to the volume of global greenhouse gases and play an important role in climate change feedback because of their huge areas and stored amounts of soil carbon and nitrogen (Lal and Kimble, 2000; Wohlfarth et al., 2008). A number of studies have suggested that desert soils are the main contributors to soil respiration and contribute significantly to N₂O and CH₄ fluxes in desert (Peterjohn and Schlesinger, 1990, 1991; Strieg et al., 1992; Hartley and Schlesinger, 2000; Abed et al., 2013). However, due to their fragility and susceptibility, desert regions are more susceptible to climate change compared with other ecosystems. Small absolute

changes can lead to huge impacts on desert ecosystem function and therefore feedback into climate change (Lal and Kimble, 2000; Belnap et al., 2003).

In many desert areas around the world, soil surfaces are often covered with biocrusts (Li, 2012). The biological community of these crusts comprises cyanobacterium, algae, lichen, moss, fungi, and other bacteria in differing proportions, which may dominate living desert cover to 70% or more (Belnap et al., 2003). Thus, desert biocrusts make important contributions to the circulation of energy, materials, and nutrient flows in these regions and greatly benefit ecosystem productivity. An increasing number of studies have shown that biocrusts comprise major pools of soil organic carbon and nitrogen in deserts (Belnap et al., 2003; Evans and Lange, 2003; Elbert et al., 2012; Li et al., 2012) and play dominant roles in soil respiration (Castillo-Monroy et al., 2011) and nitrogen cycling in many such ecosystems (Evans and

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<http://dx.doi.org/10.1016/j.catena.2017.09.031>

Received 15 March 2017; Received in revised form 5 September 2017; Accepted 29 September 2017

0341-8162/ © 2017 Published by Elsevier B.V.



Antagonistic effects of drought and sand burial enable the survival of the biocrust moss *Bryum argenteum* in an arid sandy desert

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Received: 22 September 2017 – Discussion started: 1 November 2017

Revised: 24 January 2018 – Accepted: 25 January 2018 – Published: 23 February 2018

Abstract. Biocrust moss is an essential soil surface bio-cover. It can represent the latest succession stage among the diverse range of surface-dwelling cryptogams (e.g., cyanobacteria, green algae, and lichen, which are also referred to as biocrusts), and it can make a major contribution to soil stability and fertility in many arid sandy desert ecosystems. The soil surface represents a very large ecological niche that is poikilohydric in nature. Biocrust moss is therefore highly susceptible to drought and sand burial, which are two ubiquitous stressors in arid sandy deserts. However, little information is available regarding the mechanism by which biocrust moss can survive and flourish in these habitats when stressed simultaneously by the two stressors. The combined effects of drought and sand burial were evaluated in a field experiment using the predominant biocrust moss, *Bryum argenteum* Hedw., in the Tengger Desert, China. Drought was simulated by applying distilled water in three artificial rainfall regimes at 8-day intervals in spring and autumn: 4 and 6 mm (average rainfall, control), 2 and 3 mm (double drought), and 1 and 1.5 mm (4-fold drought), respectively. The effect of sand burial was determined by applying six treatments, i.e., sand depths of 0 (control), 0.5, 1, 2, 4, and 10 mm. The four parameters of chlorophyll *a* content, PSII photochemical efficiency, regeneration potential, and shoot upgrowth were evaluated in the moss. It was found that the combined effects of drought and sand burial did not exacerbate the single negative effects of the four parameters tested. Drought significantly ameliorated the negative effects of deep-sand burial on the retention of chlorophyll *a* content, PSII photochemical efficiency, and the regeneration potential of *B. argenteum*. Sand burial diminished and even re-

versed the negative effects of drought on the maintenance of chlorophyll *a* content, PSII photochemical efficiency, and regeneration potential. Although drought and sand burial imposed an additive negative effect on shoot upgrowth, which suggested a trade-off between growth ability and stress tolerance, their mutually antagonistic effect on the physiological vigor of *B. argenteum* provided an opportunity for the biocrust moss to overcome the two co-occurring stressors. In addition to providing a strong stress tolerance, drought and sand burial may provide an important mechanism for the biodiversity maintenance of biocrust mosses in arid sandy ecosystems.

1 Introduction

Drought is the most common stressor constraining biological activity in dryland ecosystems (Whitford, 2002; Huxman et al., 2004). The predicted increase in the frequency and severity of droughts is likely to generate more profound consequences for community structure and ecosystem functioning in arid and semiarid ecosystems (IPCC, 2007; Smith, 2011; Weber et al., 2016). In arid sandy ecosystems, drought generally occurs alongside another ubiquitous disturbance, sand burial, due to the lowering of the threshold friction velocities of the upper soil surface (Belnap and Gillette, 1998; Li, 2012). Sand burial can alter various physical factors such as moisture, temperature, aeration, and other aspects of the plant and soil microenvironment. It can therefore act as a filter eliminating sensitive species, and it plays a significant role in determining the composition and distribution

Article

Extrapolation of Leaf Measurements to Obtain the Whole-Canopy Transpiration of C₃ and C₄ Xerophytic Shrubs

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Received: 9 May 2018; Accepted: 7 June 2018; Published: 20 June 2018



Abstract: Quantifying the water balance within areas with sparse vegetation requires frequent measurement of transpiration in water-limited, arid, desert ecosystems. Field experiments were conducted in Shapotou, northwestern China, to examine the feasibility of up-scaling the transpiration of C₃ and C₄ xerophytic shrubs (*Reaumuria soongorica* and *Salsola passerina*, respectively) from the leaf to the canopy level throughout the growing season in 2015. The large weighing lysimeter method and LI-6400XT portable photosynthesis system were used to make relatively long-term measurements of transpiration. The results indicated that meteorological factors coupled with stomatal conductance affected the transpiration rate of the two shrubs at the leaf level, and that the vapor pressure deficit other than net radiation and the air temperature affected the transpiration rate of *S. passerina* at the canopy level. Precipitation and vegetation characteristics determined the transpiration amount of the C₃ and C₄ xerophytic shrubs. The leaf gas exchange measurements were arithmetically scaled up to the canopy level based on the leaf area. The validity of the extrapolation was evaluated by comparing the upscale values of transpiration with the calculated values obtained from lysimeter measurement. The up-scaling approach accurately ($\pm 0.005 \text{ mm h}^{-1}$, RMSE = 35%) obtained canopy transpiration from the leaf measurements. Our study suggests that the up-scaling method based on leaf area can be adopted to determine the canopy transpiration of C₃ and C₄ xerophytic shrubs in arid desert environments.

Keywords: transpiration; Lysimeter; LI-6400XT; *Reaumuria soongorica*; *Salsola passerina*

1. Introduction

Transpiration (T) is the process whereby water is transported from the soil to the plant, via the roots, and to the atmosphere through the plant. It serves as an important component of evapotranspiration (ET) and is a dominant force in the global water cycle, as it accounts for 61% ($\pm 15\%$ s.d.) of ET at the ecosystem scale and accounts for more than two-thirds of total surface water ET for 85% of the catchments examined [1,2]. Partitioning T from ET is essential to understanding the links between hydrological and ecological systems, because biological water use is inexorably coupled with ecosystem productivity, yet it is difficult and problematic to use a single method to determine their partitioning [3]. Remarkably, the ratio of T to ET ranged from 6% to 60% due to seasonal patterns of precipitation, the differential water use of different plant types and varying ET contributions in a Chihuahuan Desert shrub-dominated community [4]. The ability to independently measure soil evaporation (E) and canopy T is important for the detection of sparse vegetation water balance [5]. However, areas covered by sparse vegetation, such as the Shapotou area of Tengger

Evapotranspiration of xerophytic shrub *Salsola passerina* and *Reaumuria soongorica* in an arid desert ecosystem of NW China

Yanxia Jin, Xinping Wang, Yafeng Zhang, Yanxia Pan, Haojie Xu, Rui Hu and Wei Shi

ABSTRACT

Understanding the actual evapotranspiration (ET) variation of the sparsely distributed xerophytic shrubs is crucial to accurately upscale community ET to ecosystem scale. Here we quantified the actual ET of two dominant xerophytic shrubs of Tengger Desert in northwestern China, i.e. *Salsola passerina* and *Reaumuria soongorica*, by using four large weighing lysimeters. The results showed that with the increase in precipitation from 140 to 171 mm in the year 2015/2016, the daily mean evaporation (E) of the bare area, and ET of the single shrub communities of *S. passerina*, *R. soongorica*, and the associated shrub community (*S. passerina* + *R. soongorica*) increased 50, 60, 44, and 47%, respectively; correspondently, the total E and ET increased 49, 61, 44, and 47%, respectively. The variation of soil moisture within 0–40 cm depth plays a vital important role in regulating the E and ET. The new shoot length, as one of important parameters of the xerophytic shrub, was significantly exponentially related to the cumulative ET. From the long- and short-term perspective, event-based precipitation and wind speed is the dominant driving factor on changes in E and ET, respectively. Relative humidity is the main influencing factor for E and ET after a large rainfall event within 8 days.

Key words | arid desert ecosystem, evapotranspiration, *Reaumuria soongarica*, *Salsola passerina*, weighing lysimeter

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INTRODUCTION

Evapotranspiration (ET), including soil evaporation (E) and plant transpiration (T), is a fundamental process of ecological, hydrological and atmospheric systems and a major component of water balance especially in the desert area, where ET accounts for more than 95% of precipitation. The controlling factors of ET are various in different ecosystems, and dynamic from intra-annual to decade time scales (Wilcox *et al.* 2003; Huxman *et al.* 2005; Ryu *et al.* 2008). ET is one of the most problematic components of the hydrological cycle, and is one of the most difficult variables to be accurately quantified since it exhibits high spatial and temporal variability (Gebler *et al.* 2015).

Numerous methods have been acquired to measure or estimate ET (Shuttleworth 2008). At regional or global scales, the remote sensing approach has been increasingly used to map the spatial distribution of ET (Kramber *et al.* 2010; Mariotto *et al.* 2011; Anderson *et al.* 2012a, 2012b; Wang *et al.* 2013; Xiong *et al.* 2015). Nevertheless, using the remote sensing method to accurately estimate ET in arid regions with large barren or sparsely vegetated areas is still a challenge for the areas characterized by high spatial heterogeneity of aerodynamic and land surface properties (Vinukollu *et al.* 2011; Tian *et al.* 2013). At scales smaller than 1 km², soil water balance, Bowen ratio energy balance



Afforestation with xerophytic shrubs accelerates soil net nitrogen nitrification and mineralization in the Tengger Desert, Northern China

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ARTICLE INFO

Keywords:

Afforestation
Vegetation restoration
Net N mineralization
Soil inorganic N
Tengger Desert

ABSTRACT

Afforestation with xerophytic shrubs in drylands to curb desertification and land degradation has been increasingly implemented worldwide. However, the effects of this restoration practice on soil nitrogen mineralization and availability in desert areas remain poorly understood. We investigated the seasonal patterns of soil inorganic N pools and net N nitrification and mineralization in mobile sand dune and three shrublands (afforested in 1956, 1964 and 1981, respectively) in the Tengger Desert by using the *in situ* incubation method. Our results showed that afforestation significantly increased the soil inorganic N pools, and net nitrification and mineralization rates. Annual average values of $\text{NH}_4^+\text{-N}$, $\text{NO}_3^-\text{-N}$ and total inorganic N were 2.64–4.06, 3.37–7.74 and 3.06–6.12 times greater in afforested sites than those in mobile sand dunes, with $\text{NO}_3^-\text{-N}$ being predominant in all sites and its proportion being increased with stand age. In mobile sand dune, annual soil net N nitrification and mineralization rates were 1.25 and 1.87 $\text{mg N m}^{-2} \text{d}^{-1}$, respectively, while those in afforested sites were 5.32–11.89 and 5.98–15.16 times higher, respectively, with nitrification predominated the N mineralization process. Marked seasonality in inorganic N pools, net N nitrification and mineralization were observed with the highest values in summer and the lowest in winter, which were closely linked to afforestation-induced changes in soil temperature and moisture as well as surface litter, content of clay and silt, C: N and OC of soil. The contrasting results for soil N transformations were observed during non-growing season, that was net N immobilization for the mobile sand dune without afforestation and the shrubland established in 1981, while net N mineralization for the shrublands established in 1964 and 1956, the latter two sites account for 2.65% and 9.68% of their total mineralization, respectively. These results suggested that afforestation with xerophytic shrubs has positive effects on soil nitrogen availability and cycling in desert region. It also implied that the afforestation-triggered recovery of biogeochemical cycling of N was a long-term process, and therefore soil habitat conservation is a vital issue in desert ecosystems.

1. Introduction

Soil nitrogen (N) availability is a key factor influencing plant growth in drylands where N is the first limiting nutrient (Robertson and Groffman, 2007; Schlesinger and Bernhardt, 2013; Delgado-Baquerizo et al., 2014). However, N availability is actually determined by net N mineralization which transforms organic N to inorganic N from soil organic matter (SOM) by soil microorganisms (Chapin III et al., 2011; Liu et al., 2017a), therefore, any modification that influences N mineralization will directly affect N availability and primary productivity in drylands (Schimel and Bennett, 2004; Schlesinger and Bernhardt, 2013), and thus impact ecosystem functioning and long-term resilience

(Heitkamp et al., 2008; Chen et al., 2009; Schlesinger and Bernhardt, 2013).

Covering about one-third of the Earth's land surface, arid and semi-arid regions serve as the largest biome type in the world (Reynolds et al., 2007; Delgado-Baquerizo et al., 2014). However, most of these regions have undergone degradation and desertification due to climate change and improper land use and management (Nosetto et al., 2006; Li et al., 2016). Ecological restoration through afforestation is a common and effective method to combat desertification in many arid regions of the world (Lal, 2004; Li et al., 2007; Li et al., 2016). Globally, this restoration practice has been found to increase vegetation cover, primary productivity and SOM accumulation in drylands (Guo and

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<https://doi.org/10.1016/j.catena.2018.05.026>

Received 21 November 2017; Received in revised form 20 April 2018; Accepted 19 May 2018

Available online 24 May 2018

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Soil Respiration of Biologically-Crusted Soils in Response to Simulated Precipitation Pulses in the Tengger Desert, Northern China

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(Received July 25, 2016; revised January 15, 2018)

ABSTRACT

Soil respiration (SR) is a major process of carbon loss from dryland soils, and it is closely linked to precipitation which often occurs as a discrete episodic event. However, knowledge on the dynamic patterns of SR of biologically-crusted soils in response to precipitation pulses remains limited. In this study, we investigated CO₂ emissions from a moss-crusted soil (MCS) and a cyanobacteria-lichen-crusted soil (CLCS) after 2, 4, 8, 16, and 32 mm precipitation during the dry season in the Tengger Desert, northern China. Results showed that 2 h after precipitation, the SR rates of both MCS and CLCS increased up to 18-fold compared with those before rewetting, and then gradually declined to background levels; the decrease was faster at lower precipitation amount and slower at higher precipitation amount. The peak and average SR rates over the first 2 h in MCS increased with increasing precipitation amount, but did not vary in CLCS. Total CO₂ emission during the experiment (72 h) ranged from 1.35 to 5.67 g C m⁻² in MCS, and from 1.11 to 3.19 g C m⁻² in CLCS. Peak and average SR rates, as well as total carbon loss, were greater in MCS than in CLCS. Soil respiration rates of both MCS and CLCS were logarithmically correlated with gravimetric soil water content. Comparisons of SR among different precipitation events, together with the analysis of long-term precipitation data, suggest that small-size precipitation events have the potential for large short-term carbon losses, and that biological soil crusts might significantly contribute to soil CO₂ emission in the water-limited desert ecosystem.

Key Words: biological soil crusts, C cycling, CO₂ emission, desert ecosystem, precipitation amount, soil water content

Citation: Li X J, Zhao Y, Yang H T, Zhang P, Gao Y P. 2018. Soil respiration of biologically-crusted soils in response to simulated precipitation pulses in the Tengger Desert, northern China. *Pedosphere*. 28(1): 103–113.

INTRODUCTION

Arid and semiarid ecosystems cover about 40% of the Earth's land surface (Reynolds *et al.*, 2007), and store 15.5% (equivalent to 232.5 Pg C) of the world's total soil organic carbon (SOC) (Lal, 2004). They have long been considered as carbon (C) sources in the terrestrial C cycle due to the low vegetation coverage (Schlesinger, 1990; Wang *et al.*, 1999; Conant *et al.*, 2000; Liu *et al.*, 2002). Soil respiration (SR) is a major process of C loss from dryland soils (Conant *et al.*, 2000), and changes in SR can slow or accelerate the increase of atmospheric CO₂ concentrations (Raich and Schlesinger, 1992; Trumbore *et al.*, 1996; Cox *et al.*, 2000; Raich *et al.*, 2002), and have a large impact on soil C storage and fertility, since these soils have relatively low organic C contents (West *et al.*, 1994; Castillo-Monroy *et al.*, 2011). Thus, quantifying likely responses of soil CO₂ emission to controlling factors is critical to our understanding of C budgets in dry ecosystems and their significance to global C cycling and

balance.

In arid and semiarid ecosystems, soil water availability, which is directly linked to precipitation, is the principle variable driving ecosystem processes (Noy-Meir, 1973), including C dynamics (Bowling *et al.*, 2011). Precipitation in these regions often occurs as a discrete episodic event. Dry soils are irregularly interrupted by precipitation pulses that elevate water availability for short periods and drive C effluxes (Sponseller, 2007; Munson *et al.*, 2010). Previous studies have reported that, after wetting, SR increases up to 30 times (Sponseller, 2007), and is several times greater than that of soil kept continually moist (Fierer and Schimel, 2003; Thomas and Hoon, 2010). This pulse-induced CO₂ emission may contribute a significant portion of the total annual CO₂ release from soil, since the soil in drylands often remains relatively dry for prolonged periods (Fierer and Schimel, 2003; Sponseller, 2007; Thomas *et al.*, 2008; Thomas and Hoon, 2010). Consequently, investigations on C cycling in drylands should focus on the implications of such even-

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Changes in surface soil organic carbon in semiarid degraded Horqin Grassland of northeastern China between the 1980s and the 2010s

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ARTICLE INFO

Keywords:

Soil carbon stock
Sandy grassland
Desertification
Horqin Sandy Land
Semiarid ecosystem

ABSTRACT

Soil organic carbon (SOC) plays an important role in the global carbon cycle and in mitigating climate change. The Horqin Grassland is one of the largest grasslands in China and has undergone serious aeolian desertification in recent decades. We conducted the largest field inventory to date, with the highest density of soil sampling, and explored changes in SOC in the region over the 30-year gap between the 1980s and the 2010s. Our results indicated that the mean SOC density to a depth of 20 cm decreased from 2.58 to 2.21 kg C m⁻², while the total SOC storage decreased from 311.11 to 266.70 Tg C, at an average of 12.29 g C m⁻² yr⁻¹. We ranked the SOC densities by ecosystem as woodland > grassland > cropland > sandy land. The decreased SOC storage in the Horqin Grassland can be ascribed to a combination of increasing temperature, decreasing precipitation, an expansion of the areas of extremely severely desertified land and cropland, and shrinkage of the grassland area. Our results provide an important updated regional baseline for quantifying how SOC storage will respond to future climate change and anthropogenic activities. Our results will also help policy makers determine how to achieve sustainable development of agriculture, forestry, and animal husbandry based on carbon sequestration.

1. Introduction

Soil is the largest reservoir of organic carbon in terrestrial ecosystems, as it holds about three times the amount stored in living vegetation (Lal, 2004a). It is therefore essential to understand changes in soil organic carbon (SOC) as well as its role in the global carbon cycle (Post and Kwon, 2000; Scharlemann et al., 2014). SOC accounts for approximately two-thirds of the carbon involved in active exchanges with the atmosphere in terrestrial ecosystems (Post et al., 1982). The amount of SOC represents the long-term net balance between photosynthesis and total respiration (Schlesinger, 1990). Many studies (Jobbágy and Jackson, 2000; Smith et al., 2008; Muñoz-Rojas et al., 2015; Valtera and Šamonil, 2018; Wang et al., 2018) have documented the link between SOC dynamics and the build-up of atmospheric carbon dioxide (CO₂), and the soil's potential to act as a carbon sink for mitigating climate change.

The SOC pool is highly dynamic, reactive, and sensitive to land use, climate change, and management. Deforestation, degradation of natural ecosystems, and conversion of natural ecosystems into cultivated fields

and grazing land have generally decreased SOC (Guo and Gifford, 2002; Smith et al., 2016), whereas afforestation and reforestation, re-establishing grasslands, and implementing conservation tillage can sequester SOC (FAO, 2004; Cantarello et al., 2011; Deng and Shangquan, 2017; Lu et al., 2018). Climate change can significantly affect the SOC level through the ability of changes in temperature, rainfall patterns, and CO₂ concentrations to influence carbon inputs and outputs from soils (Cao and Woodward, 1998; Soleimani et al., 2017).

Lal (2004b) reported that depletion of the global SOC pool, primarily due to land misuse and soil mismanagement, has contributed 78 ± 12 Pg of C to the atmosphere since the industrial revolution, versus global potential SOC sequestration that could reach 0.9 ± 0.3 Pg C yr⁻¹ if we adopted restorative land use practices and improved management practices. Kirschbaum (2000) created a model in which a decrease of just 10% in SOC storage would be equivalent to all the anthropogenic CO₂ emitted in the previous 30 years. Bellamy et al. (2005) and Yang et al. (2009) summarized numerous findings from small-scale laboratory incubations, field experiments, and modeling studies that suggested climate warming is likely to be inducing

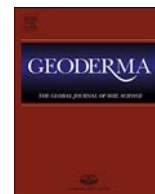
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<https://doi.org/10.1016/j.catena.2018.11.021>

Received 5 April 2018; Received in revised form 14 November 2018; Accepted 16 November 2018

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Spatial distribution of soil organic carbon in the ecologically fragile Horqin Grassland of northeastern China

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ARTICLE INFO

Handling Editor: Yvan Capowicz

Keywords:

Sandy grassland
Desertification
Carbon stock
Spatial pattern
Horqin Sandy Land

ABSTRACT

The spatial distribution of soil organic carbon (SOC) and its storage in the topmost 100 cm of the soil were investigated in the Horqin Grassland of northeastern China. Soil samples were collected at 1465 sites, covering $12.03 \times 10^4 \text{ km}^2$. The region had a mean SOC density of 6.84 kg C m^{-3} , which is lower than China's mean (9.60 kg C m^{-3}) and the world's mean ($10.40 \text{ kg C m}^{-3}$). The mean SOC density was much higher in the northern part of the study area (8.85 kg C m^{-3}) than in the southern part (4.84 kg C m^{-3}). The total SOC storage in the Horqin Grassland was 862.74 Tg . SOC storage decreased with increasing soil sampling depth. The SOC stored in the top 10, 20, 40, and 60 cm accounted for 17.7, 31.7, 53.8, and 71.3%, respectively, of the total amount in the top 100 cm. The region's extensive desertification appears to be one of the most important factors that led to the relatively low SOC content and the difference between the northern and southern parts of the Horqin Grassland. Our results provide an important baseline for evaluating past losses of SOC due to desertification, and for projecting the potential increase in SOC from the restoration of desertified land and how SOC will respond to climate change.

1. Introduction

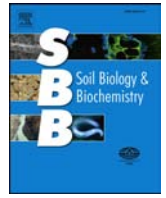
A large quantity of organic carbon is stored in the soil of the world's terrestrial ecosystems. The soil organic carbon (SOC) pool in the top 100 cm totals about 1550 Pg, which is about twice the size of the atmospheric pool and three times the size of the biotic pool (Lal, 2004a). Against the background of global warming, the relatively large size and long residence time of the SOC pool make it an important sink for carbon released into the atmosphere by anthropogenic activities (Post et al., 1982). Changes in SOC storage are now taken into account in international negotiations regarding climate change (Martín et al., 2011). SOC and its potential to mitigate the build-up of atmospheric carbon dioxide (CO_2) through soil carbon sequestration have attracted considerable scientific attention (Jobbágy and Jackson, 2000; Lal, 2004b; Smith et al., 2008; Schrumpf et al., 2011; Grüneberg et al., 2014; O'Rourke et al., 2015; Deng and Shangquan, 2017).

Accurate estimates of SOC storage and its changes are necessary to support improved carbon management and climate change mitigation, as well as to help parameterize the carbon cycle models that are being used to guide climate policy (Schrumpf et al., 2011; Scharlemann et al.,

2014). Many studies have estimated SOC storage at regional (Yang et al., 2009; Wiesmeier et al., 2015), national (Kern, 1994; Yu et al., 2007; Martín et al., 2011), and global (Post et al., 1982; Mitra et al., 2005; Scharlemann et al., 2014) scales. However, high uncertainty is associated with the estimates, especially for global SOC storage, because of inconsistent methods and limited data for many regions. Most studies have estimated global SOC at roughly 1500 Pg in the topmost 100 cm of the soil, but estimates range from 504 to 3000 Pg (Scharlemann et al., 2014). The estimates of SOC storage for the contiguous United States range from 62.1 to 99.3 Pg (Kern, 1994), whereas estimates for China's terrestrial ecosystems range from 50 to 180 Pg (Yu et al., 2007) and estimates for global wetlands range from 202 to 535 Pg (Mitra et al., 2005).

The inconsistencies among studies highlight the need for more detailed regional-level measurements of SOC storage and its spatial distribution through *in situ* sampling. SOC levels depend on local climatic conditions and other site-specific conditions, as well as on the type of land-use and land management (Yu et al., 2007). Thus, spatially explicit databases obtained from *in situ* measurements are important to help researchers establish the relationships between the geographical

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Changes in functional gene structure and metabolic potential of the microbial community in biological soil crusts along a revegetation chronosequence in the Tengger Desert

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ARTICLE INFO

Keywords:

Biological soil crusts (BSCs)
Microbial community composition
Microbial functional structure
Carbon and nitrogen cycles

ABSTRACT

Biological soil crusts (BSCs), the pioneers of restoration of degraded vegetation, act as an organizing principle in drylands largely through metabolic activities of microbial communities. However, little is known about the microbial functional potential involved in biogeochemical processes during BSC succession in desert ecosystems. Here, we utilized a functional gene array (GeoChip 5.0) in conjunction with determinants of microbial community compositions of BSCs along a revegetation chronosequence in the Tengger Desert, to address the following: (a) how the functional structure of the microbial community changes with BSC age in different soils and (b) how genes involved in carbon (C)- and nitrogen (N)-cycling change and whether they promoted an increased microbial metabolic potential during BSC succession in desert revegetation. The results showed that the relative abundance of functional genes was determined by the microbial community compositions in the BSC development process, and the significant differences in microbial functional genes were detected in 61-year-old BSCs from other aged BSCs. Redundancy analysis indicated that the abundance of fungi and moss and soil physico-chemical properties were the important factors determining differences in microbial functional structures. Functional genes associated with C degradation and N denitrification were the major components involved in C and N cycles, which were closely related to the increased fungal abundance during succession. The increased gene abundance of 61-year-old BSCs in both C and N cycles promoted microbial metabolic potential. These results indicated that fungi might be the key microbial mediators in C and N cycling in the later development of BSCs, and microbial functional structure could be a potential indicator of revegetation sustainability in desert ecosystems.

1. Introduction

In arid and semiarid areas, desertification is the main cause of land degradation (Tang et al., 2018), and ecological restoration is regarded as a global priority in the recovery of degraded ecosystems (Aronson and Alexander, 2013). Biological soil crusts (BSCs), pioneers of restoration in degraded vegetation, act as an organizing principle in drylands (Weber et al., 2016). BSCs are prominent surface features composed of desiccation-tolerant biological mats of cyanobacteria, lichens, mosses, and other microorganisms that cement surface soil particles in drylands (Weber et al., 2016). Formation of BSCs is a gradually successional process often involving stages that vary from

cyanobacteria-to lichen- or moss-dominated crusts associated with increased soil nutrient, varied topsoil texture, and enriched microbial communities (Liu et al., 2017a; Yair and Verrecchia, 2002). Principal functions of BSCs include soil surface stability (Chamizo et al., 2017), carbon (C) and nitrogen (N) fixation (Sancho et al., 2016), as well as complex interactions with vascular plants (Li et al., 2005).

It is well known that BSCs contribute to soil fertility by increasing nutrient availability via higher decomposition rates, such as by adding newly fixed atmospheric C and N to underlying soils (Belnap, 2002, 2003a), or by harboring greater microbial and microfaunal populations (Housman et al., 2007). Additionally, BSCs can significantly increase biodiversity in dryland ecosystems, especially a rich flora of lichens and

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<https://doi.org/10.1016/j.soilbio.2018.08.012>

Received 12 April 2018; Received in revised form 8 August 2018; Accepted 12 August 2018

Available online 13 August 2018

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Effects of extreme drought on plant nutrient uptake and resorption in rhizomatous vs bunchgrass-dominated grasslands

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Received: 16 October 2017 / Accepted: 18 July 2018
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Abstract

Both the dominance and the mass ratio hypotheses predict that plant internal nutrient cycling in ecosystems is determined by the dominant species within plant communities. We tested this hypothesis under conditions of extreme drought by assessing plant nutrient (N, P and K) uptake and resorption in response to experimentally imposed precipitation reductions in two semiarid grasslands of northern China. These two communities shared similar environmental conditions, but had different dominant species—one was dominated by a rhizomatous grass (*Leymus chinensis*) and the other by a bunchgrass (*Stipa grandis*). Results showed that responses of N to drought differed between the two communities with drought decreasing green leaf N concentration and resorption in the community dominated by the rhizomatous grass, but not in the bunchgrass-dominated community. In contrast, negative effects of drought on green leaf P and K concentrations and their resorption efficiencies were consistent across the two communities. Additionally, in each community, the effects of extreme drought on soil N, P and K supply did not change synchronously with that on green leaf N, P and K concentrations, and senesced leaf N, P and K concentrations showed no response to extreme drought. Consistent with the dominance/mass ratio hypothesis, our findings suggest that differences in dominant species and their growth form (i.e., rhizomatous vs bunch grass) play an important nutrient-specific role in mediating plant internal nutrient cycling across communities within a single region.

Keywords Dominance/mass ratio hypothesis · Dominant species · Extreme drought · Nutrient cycling

Communicated by Mercedes Bustamante.

Electronic supplementary material The online version of this article (<https://doi.org/10.1007/s00442-018-4232-1>) contains supplementary material, which is available to authorized users.

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Differential responses of canopy nutrients to experimental drought along a natural aridity gradient

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Abstract. The allocation and stoichiometry of plant nutrients in leaves reflect fundamental ecosystem processes, biotic interactions, and environmental drivers such as water availability. Climate change will lead to increases in drought severity and frequency, but how canopy nutrients will respond to drought, and how these responses may vary with community composition along aridity gradients is poorly understood. We experimentally addressed this issue by reducing precipitation amounts by 66% during two consecutive growing seasons at three sites located along a natural aridity gradient. This allowed us to assess drought effects on canopy nitrogen (N) and phosphorus (P) concentrations in arid and semiarid grasslands of northern China. Along the aridity gradient, canopy nutrient concentrations were positively related to aridity, with this pattern was driven primarily by species turnover (i.e., an increase in the relative biomass of N- and P-rich species with increasing aridity). In contrast, drought imposed experimentally increased N but decreased P concentrations in plant canopies. These changes were driven by the combined effects of species turnover and intraspecific variation in leaf nutrient concentrations. In addition, the sensitivity of canopy N and P concentrations to drought varied across the three sites. Canopy nutrient concentrations were less affected by drought at drier than wetter sites, because of the opposing effects of species turnover and intraspecific variation, as well as greater drought tolerance for nutrient-rich species. These contrasting effects of long-term aridity vs. short-term drought on canopy nutrient concentrations, as well as differing sensitivities among sites in the same grassland biome, highlight the challenge of predicting ecosystem responses to future climate change.

Key words: intraspecific variation; long-term aridity; manipulative experiment; nutritional response; sensitivity; short-term drought; species turnover.

INTRODUCTION

Droughts are projected to increase in magnitude and frequency in terrestrial ecosystems due to climate change (IPCC, 2013). Because nitrogen (N) and phosphorus (P) are essential nutrients for plant growth, maintenance, and reproduction (Reich and Oleksyn 2004, Li et al. 2017, Sardans et al. 2017), understanding the effects of increasing drought on the biogeochemistry of N and P is needed (Sardans and Peñuelas 2012). Patterns of plant nutrient allocation and stoichiometry reflect the use of N and P to sustain plant metabolism and growth (He et al. 2006, Yuan and Chen 2015). However, biogeochemical processes affecting N and P availability can be constrained by low soil water (Farooq et al. 2009), and in particular, the impact of drought on

plant N and P concentrations (hereafter [N] and [P]) remains unclear (Hartley et al. 2007, He and Dijkstra 2014).

During drought, low soil moisture and reduced microbial activity are known to retard decomposition and mineralization of organic matter, which in turn reduces the amount of N and P readily available for plant uptake (Hartley et al. 2007, He and Dijkstra 2014). Drought suppression of nutrient diffusion in soils, nutrient uptake by roots and nutrient transport in plant tissues have also been well-studied (Hartley et al. 2007, He and Dijkstra 2014). Plant N and P are tightly linked to many essential plant processes (e.g., photosynthesis, signal transduction, energy storage, Elser et al. 2007). However, the movement of P in soils is more sensitive to drought stress than that of N (Lambers et al. 2008, Benap 2011). Hence, shifts in plant [N] and [P] in response to drought stress may differ in magnitude and direction.


To date, much research has focused on assessing nutritional responses of individual species to drought, while such studies at the plant canopy scale are less common. However,

Manuscript received 23 February 2018; revised 5 June 2018; accepted 18 June 2018. Corresponding Editor: Scott L. Collins.

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RESEARCH ARTICLE

Relationships between aboveground and belowground trait responses of a dominant plant species to alterations in watertable depth

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Funding information

National Key Research and Development Program of China, Grant/Award Number: 2017FY100200; One Hundred Person Project of the Chinese Academy of Sciences, Grant/Award Number: Y551821; National Natural Science Foundation of China, Grant/Award Numbers: 41671208 and 31270501; West Light Foundation of The Chinese Academy of Science, Grant/Award Number: Y529891001; China Postdoctoral Science Foundation, Grant/Award Number: 2014T70947

Abstract

Drought impacts to plant growth can be indicated by changes in key functional traits. However, previous research has focused on aboveground trait responses to precipitation deficits, with less emphasis on concomitant belowground impacts and deep soil drought from groundwater depletion. We assessed changes in a suite of aboveground and belowground traits of a dominant plant, *Phragmites communis*, in response to an experimental gradient of underground watertable depth. Our study occurred within the northeastern Inner Mongolia region, where changes to groundwater tables have been pervasive in recent years. In general, the results indicate that both aboveground and belowground traits responded positively, yet eventually negatively, to continual increases in watertable depth, indicative of reduced access to soil moisture as watertable depths increased. Key adjustments include changes to the ratio of coarse roots to fine roots, and the distribution of fine roots within the soil profile. These changes in belowground traits had strong correlations with changes in aboveground traits. In particular, specific root length of fine roots was positively correlated with leaf area, height, and aboveground biomass, whereas root biomass was linked to leaf area, specific root length of coarse roots, and root length density. Fine and coarse root production also had positive and negative relationships with aboveground biomass, respectively, suggestive of biomass allocation tradeoffs. We suggest that biomass production responses of this species to changes in watertable depths may largely be driven by interactions between the distribution of fine and coarse roots in the soil profile and changes to leaf area.

KEYWORDS

drought, fine roots, root traits, underground watertable

1 | INTRODUCTION

Plant functional traits are used to indicate the ability of plants to capture and retain essential resources (Kazakou et al., 2014; Kraft, Godoy, & Levine, 2015; Reich et al., 2003). However, much attention has historically focused on aboveground traits, leading to an increased recognition about the need to better understand the dynamics of

belowground traits (Laliberté, 2017). Theory predicts that plants with 'fast' traits such as high specific leaf area (SLA: the ratio of leaf area to leaf dry mass), photosynthetic rate, and leaf nitrogen content will rapidly acquire key resources, whereas plants with longer life span or in resource poor habitats may exhibit opposite patterns of 'slow' traits with more conservative resource use (Perez-Harguindeguy et al., 2013). It is uncertain whether root traits fall along the same ecological



Limiting similarity mediates plant community niche hypervolume across a desert-steppe ecotone of Inner Mongolia



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ARTICLE INFO

Keywords:

Desert steppe ecotone

Niche hypervolume

Functional group

Leaf traits

Functional divergence

ABSTRACT

Quantifying niche space occupation based on assessments of multiple resource utilization traits can improve an understanding of plant species coexistence within communities of varying resource availability. We used an ‘occupied functional niche space (OFS)’ method based on multiple leaf traits to examine how plant communities accommodate changes in water availability within a desert-steppe ecotone spanning a limited geographic region. Our study area (western Inner Mongolia) spanned a range of conditions from highly water-limited (desert, D) to less water-limited (desert steppe, S), with two areas capturing the ecotonal boundary between these two vegetation types – partial desert (pD) and partial desert steppe (pS). We tested whether environmental filtering, heterogeneity, or limiting similarity drove trait convergence versus divergence of OFS across a desert-steppe ecotone. We quantified changes in plant community weighted means of both functional (specific leaf area and leaf dry matter content) and stoichiometric (leaf nitrogen content and leaf carbon concentration) leaf traits. OFS in the ecotonal areas (pS and pD) had larger volumes than the most mesic (S) subregion. However, divergence in the centroid of OFS was apparent for the driest (D) subregion, relative to the other three sub-regions. Underlying changes to OFS were changes in plant functional types, with more functional groups found in D and the fewest in S. For community-weighted leaf traits, SLA was highest in the ecotone area (pD and pS), while lowest in D. Further, community weighted means based on leaf dry matter content in D was the highest of all sub-regions, while both community weighted means based on leaf nitrogen content and community weighted means based on leaf dry matter content decreased as precipitation decreased, consistent with expectations. Our results suggest that communities alter both the volume and the centroid of functional trait space to adjust to decreasing water resource availability. We posit that limiting similarity (i.e. competitive exclusion) in water-resource use traits among species, supported by changes in life histories, led to OFS divergence in the ecotonal areas (pS and pD) and D, while environmental filtering may have led to convergence of OFS within the most mesic region (S) as water-stress lessens. In total, our results contribute knowledge as to how plant communities alter trait space in resource acquisition across climatic gradients, and underscores the utility of multi-trait approaches in understanding patterns of species coexistence in response to climatic changes.

1. Introduction

Trait-based approaches are now widely used to quantify plant functional diversity (FD), and to elucidate rules governing the assembly of ecological communities (Díaz et al., 2007; Mouchet et al., 2010; Pérez-Harguindeguy et al., 2013; Villéger et al., 2008). Ecologists also often use null models based on samples from a metacommunity species pool to infer whether functional trait dispersion is convergent or divergent within the same habitat (Coyle et al., 2014; Díaz et al., 2016).

Functional trait *convergence* may arise in harsh habitats primarily as a result of environmental filtering (Lhotsky et al., 2016), as only highly specific traits (e.g. CAM photosynthetic pathway) may allow individual survival and population persistence under certain conditions (Cornwell and Ackerly, 2009). By contrast, the principle of limiting similarity (MacArthur and Levins, 1967; Schellenberger Costa et al., 2017; Travis and S.J., 2009) suggests that coexisting species develop different functional strategies to minimize fitness differences and avoid interspecific competition, leading to functional trait *divergence* within a

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<https://doi.org/10.1016/j.envexpbot.2018.06.011>

Received 21 March 2018; Received in revised form 8 June 2018; Accepted 11 June 2018

Available online 15 June 2018

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Community structure of grassland ground-dwelling arthropods along increasing soil salinities

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Received: 3 June 2017 / Accepted: 11 December 2017 / Published online: 27 December 2017
© Springer-Verlag GmbH Germany, part of Springer Nature 2017

Abstract

Ground-dwelling arthropod communities are influenced by numerous biotic and abiotic factors. Little is known, however, about the relative importance of vegetation structure and abiotic environmental factors on the patterns of ground-dwelling arthropod community across a wide range of soil salinities. Here, a field survey was conducted to assess the driving forces controlling ground-dwelling arthropod community in the salinized grasslands in the Hexi Corridor, Gansu Province, China. The data were analyzed by variance partitioning with canonical correspondence analysis (CCA). We found that vegetation structure and edaphic factors were at least of similar importance to the pattern of the whole ground-dwelling arthropod community. However, when all collected ground-dwelling arthropods were categorized into three trophic guilds (predators, herbivores, and decomposers), as these groups use different food sources, their populations were controlled by different driving forces. Predators and decomposers were mainly determined by biotic factors such as vegetation cover and aboveground plant biomass and herbivores by plant density and vegetation cover. Abiotic factors were also major determinants for the variation occurring in these guilds, with predators strongly affected by soil electrical conductivity (EC) and the content of fine particles (silt + clay, CS), herbivores by soil N:P, EC, and CS, and decomposers by soil EC and organic matter content (SOM). Since plant cover, density, and aboveground biomass can indicate resource availability, which are mainly constrained by soil N:P, EC, CS, and SOM, we consider that the ground-dwelling arthropod community in the salinized grasslands was mainly influenced by resource availability.

Keywords China · Grassland · Pitfall trap · Ground-dwelling arthropod trophic guilds · Variance partitioning

Introduction

Ground-dwelling arthropods regulate key processes that control nutrient and energy flows in the food chain (Crawford 1986; Greenslade 1992; Cheli et al. 2010). The forces that

drive the patterns of ground-dwelling arthropod community are formed by a wide range of factors. For example, the patterns of ground-dwelling arthropod community are influenced by soil nutrient status (Liu et al. 2009; Tizado and Núñez 2016), texture (Shapiro et al. 2000; Alekseev et al. 2006), moisture (Mackay et al. 1986; Alekseev et al. 2006), and temperature (Lessard et al. 2011), and by abiotic stresses such as soil salinity (Desender and Maelfait 1999; Mckenzie et al. 2003; Owojori et al. 2009; Pétilion et al. 2008). Ground-dwelling arthropod community composition also depends on plant diversity (Siemann 1998; Perner et al. 2005; Padmavathy and Poyyamoli 2011), productivity (Siemann 1998; Perner et al. 2005), and density (Yamamura 1999). Factors influencing the patterns of ground-dwelling arthropod community are usually achieved through combining vegetation and environmental variables into single data set. However, many of these variables interact with each other making it difficult to identify the dominant drivers of ground-dwelling arthropod community structure into explicit measurable variables. Moreover, this combination hides

Responsible editor: Philippe Garrigues

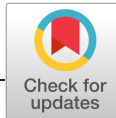
Electronic supplementary material The online version of this article (<https://doi.org/10.1007/s11356-017-1011-1>) contains supplementary material, which is available to authorized users.

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RESEARCH ARTICLE

WILEY

Dew formation characteristics at annual and daily scale in xerophyte shrub plantations at Southeast margin of Tengger desert, Northern China

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Funding information

National Key Research and Development Program of China, Grant/Award Number: (2016YFE0203400); the Chinese National Natural Sciences Foundation, Grant/Award Numbers: 41530750 and 41771101

Abstract

Being a potential water source in arid and semiarid regions, it is important to quantify the amount of dew. The objective of this study was to determine the annual formation characteristics of dew and the influence of vegetation reconstruction on dew formation in a revegetated desert area. Effects of condensing surface types associated with different plant microhabitats were investigated. We found soil dew mainly depended on air water vapour near soil surface, and primarily formed at 0–3 cm soil layer. Dew formed on 128 days during a 1-year experiment period could be divided into 2 different periods; the monthly dew yield and the number of dew formation days were highest from May to October, and the cumulative dew yield of July and August accounted for nearly 50% of the annual dew yield. Biological soil crusts facilitated dew formation, with annual dew accumulation of 15.3, 11.9, and 9.6 mm on moss crust, mixed crust, and dune sand, respectively. A longer daily dew production period was found on moss crusts than mixed crusts and dune sand. Plant microhabitats also influenced dew formation characteristics, less dew condense under plant canopies than on dune sand, but the daily dew production period was longer under plant canopies. The findings from this study will provide important and fundamental information to support accurate assessment of the relative importance of dew and rainfall in research on the hydrological cycle of this region, which will be a significant foundation for vegetation protection and ecological restoration in drought environments.

KEYWORDS

formation characteristics, substrate surface, vegetation community, water vapour source

1 | INTRODUCTION

Water is the main factor limiting plant and animal life in arid and semi-arid regions, however, desert plants and animals widespread persist even after long periods without rainfall, therefore, alternative water sources must be available to the desert biome during extended dry periods. A large number of studies have verified the importance of dew as a supplement water source in arid and semiarid areas (Pan, Wang, & Zhang, 2010; Temina & Kidron, 2011). Dew is usually attached to the leaves of plants and the soil's surface or into shallow soil and is the result of water condensing from air- (dewfall) or soil-

based atmospheric humidity (Garratt & Segal, 1988) on a radiatively cooled substrate (Beysens et al., 2007). Atmospheric water vapour includes water vapour within the air near the ground surface and from plant transpiration and respiration. Soil water vapour is found within pores below the soil surface. The two streams of water vapour exchange occur in opposite directions. Condensation processes remove water vapour from the atmosphere and result in a negative (downward) water vapour flux, whereas soil evaporation and transpiration by the lower canopy result in a positive (upward) flux. The net water vapour flux generally observed was a balance of these two opposing fluxes (Wen et al., 2012).

Research Article

Phylogenetics and dispersal patterns of Brassicaceae around the Qinghai–Tibet Plateau

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Received 29 September 2016; Accepted 13 March 2018; Article first published online 3 May 2018

Abstract Brassicaceae, one of the most diverse and economically valuable plant families, is distributed all over the world. Previous studies have suggested that Brassicaceae originated and diversified in the Old World. In this study, the phylogenetic relationships of 17 tribes of Brassicaceae from the Qinghai–Tibet Plateau (QTP) and adjacent areas were investigated using nuclear ribosomal internal transcribed spacer (nrITS) and chloroplast DNA sequence data (*rbcl* and *petB-petD*) with maximum likelihood, maximum parsimony, and Bayesian methods. As suggested by both the nrITS and chloroplast DNA trees, *Cardaria pubescens* (C.A.Mey.) Jarm. (Lepidieae) and *Draba lanceolata* Royle (Arabideae) should be classified in the Eutremeae and Cardamineae, respectively. Based on over 700 newly sequenced and published nrITS sequences of Brassicaceae, an up-to-date comprehensive phylogeny of the family was reconstructed using the maximum likelihood method. In the phylogenetic tree, 10 monophyletic tribes were detected. They were used to clarify the lineage diversification and dispersal patterns of the 10 tribes. The results showed that most of the monophyletic tribes may have originated in different regions of the world, and then dispersed into other regions surrounding the QTP. Rapid lineage diversification rate shifts were detected in several tribes, such as Anastaticae, which experienced a rapid shift event ~1.38 Mya, corresponding to the rapid uplift of the QTP, indicating that the recent uplift of the QTP could have promoted diversification in Brassicaceae across and adjacent to the QTP.

Key words: Brassicaceae, dispersal pattern, eastern Asia, phylogenetic relationship, Qinghai-Tibet Plateau (QTP).

1 Introduction

The Brassicaceae comprise ~3700 species assigned to 321 genera in 51 tribes, including 22 species in 15 genera that have not yet been classified into any tribe (Al-Shehbaz et al., 2006, 2014; German et al., 2014; Kiefer et al., 2014). In addition to its species richness, the family is also of special interest for its high economic and scientific value, including many important vegetable crops (e.g., *Brassica* and *Raphanus*), sources of industrial oils and spices (e.g., *Brassica*, *Armoracia*, and *Sinapis*), several medicinal herbs (e.g., *Rorippa* and *Erysimum*), and the model plant *Arabidopsis thaliana* (L.) Heynh. The phylogenetic relationships in the family have been the focus of interest of numerous scholars. Starting in the early 1990s, with the advancement of molecular technology and the use of additional markers for classification, some genera that were originally based on morphology were suggested to be non-monophyletic (Al-Shehbaz et al., 2006). Furthermore, molecular markers have also suggested discordant phylogenetic relationships within the Brassicaceae (Couvreur et al., 2010; Liu et al., 2011; Huang et al., 2016). For example, the tribe

Alyseae was classified in Lineage I based on *PISTILLATA* first intron sequences, but it was placed in a different lineage (Lineage III) based on *trnS_(CCU)-trnG_(UUC)* sequences (Liu et al., 2011). Due to frequent interspecific and intergeneric hybridization within Brassicaceae, whole-genome duplications, and rapid adaptive radiation events in their early evolutionary history (Al-Shehbaz et al., 2006; Koch et al., 2007; Franzke et al., 2009; Couvreur et al., 2010; Tsuda et al., 2014; Huang et al., 2016), a clear understanding of the phylogenetic relationships within the family has not been achieved.

Previous studies (Lysak & Koch, 2011) have documented that crucifers are widely distributed in mountainous and alpine regions worldwide, except in Antarctica. Based on species diversity, it is speculated that the Brassicaceae originated in the Irano-Turanian region, which is one of the major diversification centers, with approximately 900 species in approximately 150 genera (Franzke et al., 2009). The level of diversification is also high in the Mediterranean region of Europe, central and western Asia, and western North America (Al-Shehbaz, 2011). As a major biodiversity hotspot, with approximately 180 species of Brassicaceae in 76 genera, the



Transcriptomes Divergence of *Ricotia lunaria* Between the Two Micro-Climatic Divergent Slopes at “Evolution Canyon” I, Israel

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OPEN ACCESS

Edited by:

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Reviewed by:

Jing Wang,
Norwegian University of Life Sciences,
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Dongshi Wan,
Lanzhou University, China

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Specialty section:

This article was submitted to
Evolutionary and Population Genetics,
a section of the journal
Frontiers in Genetics

Received: 27 June 2018

Accepted: 08 October 2018

Published: 14 November 2018

Citation:

Qian C, Yan X, Yin H, Fan X, Yin X, Sun P, Li Z, Nevo E and Ma X-F (2018) Transcriptomes Divergence of *Ricotia lunaria* Between the Two Micro-Climatic Divergent Slopes at “Evolution Canyon” I, Israel. *Front. Genet.* 9:506. doi: 10.3389/fgene.2018.00506

As one of the hotspot regions for sympatric speciation studies, Evolution Canyon (EC) became an ideal place for its high level of microclimatic divergence interslopes. In this study, to highlight the genetic mechanisms of sympatric speciation, phenotypic variation on flowering time and transcriptomic divergence were investigated between two ecotypes of *Ricotia lunaria*, which inhabit the opposite temperate and tropical slopes of EC I (Lower Nahal Oren, Mount Carmel, Israel) separated by 100 m at the bottom of the slopes. Growth chamber results showed that flowering time of the ecotype from south-facing slope population # 3 (SFS 3) was significantly 3 months ahead of the north-facing slope population # 5 (NFS 5). At the same floral development stage, transcriptome analysis showed that 1,064 unigenes were differentially expressed between the two ecotypes, which enriched in the four main pathways involved in abiotic and/or biotic stresses responses, including flavonoid biosynthesis, α -linolenic acid metabolism, plant–pathogen interaction and linoleic acid metabolism. Furthermore, based on *Ka/Ks* analysis, nine genes were suggested to be involved in the ecological divergence between the two ecotypes, whose homologs functioned in RNA editing, ABA signaling, photoprotective response, chloroplasts protein-conducting channel, and carbohydrate metabolism in *Arabidopsis thaliana*. Among them, four genes, namely, *SPDS1*, *FCLY*, *Tic21* and *BGLU25*, also showed adaptive divergence between *R. lunaria* and *A. thaliana*, suggesting that these genes could play an important role in plant speciation, at least in Brassicaceae. Based on results of both the phenotype of flowering time and comparative transcriptome, we hypothesize that, after long-time local adaptations to their interslope microclimatic environments, the molecular functions of these nine genes could have been diverged between the two ecotypes. They might differentially regulate the expression of the downstream genes and pathways that are

Impact of Long-Term Gravel Mulching on Soil Bacterial and Fungal Communities in the Semi-Arid Loess Plateau of Northwestern China

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Gravel mulching is a traditional method of water conservation in the semi-arid regions of China. In this study, we investigated the soil microbial community in a field in China's Gaolan County which has been gravel mulching for over a period of 18 yr. Compared with the non-mulch control, total organic nitrogen (TON), microbial biomass carbon (MBC), and microbial biomass nitrogen (MBN) were all significantly increased in the field with gravel mulching for over 13 yr. Moreover, after 18 yr, the soil bulk density and sand content increased significantly, thus degrading the soil microenvironment. Gravel mulch significantly altered the bacterial community structure and composition, increased the abundance of Acidobacteria, Gemmatimonadetes, Bacteroidetes, and Firmicutes, and decreased the abundance of Actinobacteria compared with the control. Gravel mulch also significantly changed the fungal community structure and composition; the soils were found to have a greater abundance of Basidiomycota and Zygomycota and reduced abundance of Ascomycota and Glomeromycota compared with the control soils after long-term gravel mulching. Redundancy analysis (RDA) revealed that the bacterial genera after 18 yr of mulching were dominated by *Incertae_Sedis*, *Blastocatella*, *Desulfovibrio*, *Bacteroides*, *Gemmatimonas*, *Parabacteroides* and *Alloprevotella*, and that the composition of the bacterial community was related to soil pH, bulk density, MBC and MBN. However, significant decreases in the diversity indices of Chao1, abundance-based coverage estimator (Ace) and Shannon after 18 yr of mulching demonstrated negative effects on the complexity of the soil microbial community.

Key Words: bacterial genera, fungal community, gravel mulching, soil bulk density, soil microbial community

Abbreviations: ACE – abundance-based coverage estimator, BD – bulk density, MBC – microbial biomass carbon, MBN – microbial biomass nitrogen, OTU – operational taxonomic unit, PCoA – principal coordinate analysis, QIIME – Quantitative

INTRODUCTION

Gravel mulch is a traditional method of water conservation that has been used for hundreds of years in the Loess region of northwestern China, which lies in the transitional zone between the arid and semi-arid regions. In the Loess region, the mean annual precipitation is between 250 and 350 mm, of which nearly 70% occurs between June and September (Li and Gong 2002). The annual pan evaporation ranges from 1500 to 2000 mm. The gravel mulch used in the Loess region is a porous layer of gravel that is approximately 10 cm thick that lies on the soil surface. Mulch reduces the risk of crop failure, which frequently occurs due to a combination of low precipitation and high evaporation that creates severe deficits in soil moisture. This mulching technique has been promoted and widely adopted due to the lack of sufficient water and high cost of irrigation in the Gansu province. In the 1990s, 118 000 ha of mulched watermelon

fields were established in Gansu Province (Li 2003).

Gravel mulch effectively reduces water evaporation and runoff, increases the soil temperature in crop fields, retains soil moisture and affects the microenvironment (Li 2003; Wang et al. 2008; Ma and Li 2011). The efficiency of mulching varies widely, depending on the characteristics (position, thickness, particle size, coverage degree and roughness) of the gravel mulch (Yuan et al. 2009; Xie et al. 2006, 2010). Yuan et al. (2009) reported that gravel mulches reduced evaporation by 49.1–83.6% compared with the bare soil. In a study conducted in the semi-arid Loess region of northwestern China, the soil temperature at a depth of 10 cm was 0.5–4.5 °C warmer than that at a comparable depth below bare topsoil when the topsoil was covered with gravel mulch (Li 2003). In addition, Ma and Li (2011) found that gravel-sand mulches conserved soil water compared with the bare soil and that the soil water content increased with increasing mulch thickness.

Influence of Gravel Mulch on Rainfall Interception under Simulated Rainfall

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Abstract

Qiu Y., Xie Z., Wang Y. (2018): Influence of gravel mulch on rainfall interception under simulated rainfall. *Soil & Water Res.*

To understand the hydrological outcomes of interception by gravel mulches, rainfall simulation experiments were conducted in the loess regions of northwestern China. The rainfall interception decreased with gravel size but increased with the thickness of the gravel mulch layer, following two exponential functions. Interception was 15.1% of the gross rainfall at 1 cm thickness, followed by 17.2, 20.9, 30.5 and 45.6 % at 3, 5, 7 and 10 cm thickness, respectively. For the equivalent gravel grain size of 3.43 mm, relative interception was 45.6%, which was about 1.1, 1.2, 1.4 and 2.3 times higher than that for the equivalent grain size of 11.01, 19.31, 32.8 and 43.72 mm, respectively.

Keywords: gravel; interception; loess plateau; rainfall simulation

Rainfall intercepted, stored and subsequently evaporated from gravel mulch can be termed as interception of gravel mulch (LI *et al.* 2000). Gravel mulch is a traditional water-conservation technique that has been used for over 300 years in the Loess Plateau region of northwestern China. Many studies showed a gravel mulch to be effective in reducing evaporation and increasing soil temperature (LIGHTFOOT & EDDY 1994; YUAN *et al.* 2009; XIE *et al.* 2010; MA & LI 2011; QIU *et al.* 2014). YUAN *et al.* (2009) reported that gravel mulches reduced evaporation by 49.1 to 83.6% compared with the bare soil. However, little work has been carried out on rainfall interception loss by a gravel mulch layer itself. A field study of rainfall interception during naturally occurring rainfall events revealed that rainfall interception by a gravel mulch accounts for 14–36% of rainfall (LI *et al.* 2005). This highlights the importance of estimates of interception losses by gravel mulches. However, the interception losses by gravel mulches are difficult to measure precisely in the field during naturally occurring rainfall events, because the ignored

evaporation during the natural rainfall events would bring deviation and the rainfall intensity effects were not considered. The objective of this research is to quantify the interception losses by gravel mulches in response to varying gravel size, thickness and rainfall intensity under simulated rainfall.

MATERIAL AND METHODS

This study was conducted at the Gaolan Research Station of Ecology and Agriculture, Chinese Academy of Sciences (36°13'N, 103°47'E). Measurements of rainfall interception by gravel mulches were done according to methods proposed by LI *et al.* (2000). The gravel-mulch storage capacity was determined by the method of LEYTON *et al.* (1967). A 2 × 3 m steel tank with its longer sides parallel to the slope (15 %) was used to measure runoff. In our study, we used equivalent grain size (d_i) to describe the gravel samples, assuming the gravels are all spheroid, and the d_i is the diameter of the corresponding equivalent sphere.



RESEARCH ARTICLE

WILEY

The effect of biological soil crusts on soil moisture dynamics under different rainfall conditions in the Tengger Desert, China

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Funding information

National Natural Science Foundation of China, Grant/Award Number: 41530750 and 41771101; National Key Research and Development Plan of China, Grant/Award Number: 2016YFE0203400

Abstract

Rainfall is considered as the dominant water replenishment in desert ecosystems, and the conversion of rainfall into soil water availability plays a central role in sustaining the ecosystem function. In this study, the role of biological soil crusts (BSCs), typically formed in the revegetated desert ecosystem in the Tengger Desert of China, in converting rainfall into soil water, especially for the underlying soil moisture dynamics, was clarified by taking into account the synthetic effects of BSCs, rainfall characteristics, and antecedent soil water content on natural rainfall conditions at point scale. Our results showed that BSCs retard the infiltration process due to its higher water holding capacity during the initial stage of infiltration, such negative effect could be offset by the initial wet condition of BSCs. The influence of BSCs on infiltration amount was dependent on rainfall regime and soil depth. BSCs promoted a higher infiltration through the way of prolonged water containing duration in the ground surface and exhibited a lower infiltration at deep soil layer, which were much more obvious under small and medium rainfall events for the BSCs area compared with the sand area. Generally, the higher infiltration at top soil layer only increased soil moisture at 0.03 m depth; in consequence, there was no water recharge for the deep soil, and thus, BSCs had a negative effect on soil water effectiveness, which may be a potential challenge for the sustainability of the local deep-rooted vegetation under the site specific rainfall conditions in northwestern China.

KEYWORDS

biological soil crusts, infiltration dynamics, natural rainfall, soil moisture, soil water effectiveness

1 | INTRODUCTION

Soil moisture is a fundamental hydrological state variable that controls various critical zone processes including plant transpiration and photosynthesis, energy balance, and nutrient cycling (Austin et al., 2004; Seneviratne et al., 2010; Q. Zhu, Nie, et al., 2014). Desert ecosystem is characterized as a water-limited ecosystem with low water input (Noy-Meir, 1973). In desert ecosystems, soil moisture, especially soil water availability, is of critical importance in sustaining ecological processes and vegetation dynamics (Loik, Breshears, Lauenroth, & Belnap, 2004; Ratzmann, Gangkofner, Tietjen, & Fensholt, 2016;

Zhang, Zhao, Liu, Fang, & Feng, 2016). Therefore, the reasonable management of limited rainfall into soil water has always been the central issue in arid desert areas.

Biological soil crusts (BSCs), composed of associations of cyanobacteria, microfungi, lichens and mosses with soil particles, cover the first millimetres of topsoil (Lichner et al., 2013) and are ubiquitous cover types in desert ecosystems (Aguilar, Huber-Sannwald, Belnap, Smart, & Moreno, 2009). The existence of BSCs significantly change the surface soil characteristics, such as increasing C and N stocks, changing soil texture and aggregate stability, which contribute to enhancement in soil stability and improvement in soil fertility



RESEARCH PAPER

Integrated regulation triggered by a cryophyte ω -3 desaturase gene confers multiple-stress tolerance in tobacco

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Received 24 November 2017; Editorial decision 1 February 2018; Accepted 2 February 2018

Editor: Greg Rebetzke, CSIRO Agriculture and Food, Australia

Abstract

ω -3 fatty acid desaturases (FADs) are thought to contribute to plant stress tolerance mainly through linolenic acid (C18:3)-induced membrane stabilization, but a comprehensive analysis of their roles in stress adaptation is lacking. Here, we isolated a microsomal ω -3 FAD gene (*CbFAD3*) from a cryophyte (*Chorispora bungeana*) and elucidated its functions in stress tolerance. *CbFAD3*, exhibiting a high identity to *Arabidopsis AtFAD3*, was up-regulated by abiotic stresses. Its functionality was verified by heterologous expression in yeast. Overexpression of *CbFAD3* in tobacco constitutively increased C18:3 in both leaves and roots, which maintained the membrane fluidity, and enhanced plant tolerance to cold, drought, and salt stresses. Notably, the constitutively increased C18:3 induced a sustained activation of plasma membrane Ca^{2+} -ATPase, thereby, changing the stress-induced Ca^{2+} signaling. The reactive oxygen species (ROS) scavenging system, which was positively correlated with the level of C18:3, was also activated in the transgenic lines. Microarray analysis showed that *CbFAD3*-overexpressing plants increased the expression of stress-responsive genes, most of which are affected by C18:3, Ca^{2+} , or ROS. Together, *CbFAD3* confers tolerance to multiple stresses in tobacco through the C18:3-induced integrated regulation of membrane, Ca^{2+} , ROS, and stress-responsive genes. This is in contrast with previous observations that simply attribute stress tolerance to membrane stabilization.

Keywords: ω -3 FAD gene, Ca^{2+} signaling, *Chorispora bungeana*, multiple-stress tolerance, ROS, stress-responsive gene.


Introduction

Environmental stresses, such as low temperature, drought, and salinity, severely limit plant growth and productivity. To withstand these abiotic stresses, plants have evolved both constitutive and inducible mechanisms that prevent or reduce adverse effects. As the outer boundary of plant cells, the cell membrane is the primary sensor of environmental stresses, and its stabilization is required for the survival of the plant (Zhang *et al.*, 2005; Shi *et al.*, 2008). Membrane stabilization, especially the maintenance of its integrity and function, is affected by lipid

composition and the degree of fatty acid desaturation (Mikami and Murata, 2003; Shi *et al.*, 2008). Therefore, fatty acid desaturation caused by fatty acid desaturases (FADs), represented mainly by an increase in linolenic acid (C18:3), is considered as one of the factors involved in the tolerance of plants to many environmental stresses (Zhang *et al.*, 2005; Upchurch, 2008).

Three ω -3 FADs that catalyse the conversion of linoleic acid (C18:2) to C18:3 have been identified in *Arabidopsis*: two are plastidial desaturases, FAD7 and FAD8, and one is

Dominant plant species shape soil bacterial community in semiarid sandy land of northern China

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Funding information

National Nature Science Foundation of China, Grant/Award Number: 41401620, 41571106 and 41501572; China National Key Research and Development Plan, Grant/Award Number: 2016YFC0500506


Abstract

Plant species affect soil bacterial diversity and compositions. However, little is known about the role of dominant plant species in shaping the soil bacterial community during the restoration of sandy grasslands in Horqin Sandy Land, northern China. We established a mesocosm pots experiment to investigate short-term responses of soil bacterial diversity and composition, and the related soil properties in degraded soils without vegetation (bare sand as the control, CK) to restoration with five plant species that dominate across restoration stages: *Agriophyllum squarrosum* (AS), *Artemisia halodendron* (AH), *Setaria viridis* (SV), *Chenopodium acuminatum* (CA), and *Corispermum macrocarpum* (CM). We used redundancy analysis (RDA) to analyze the association between soil bacterial composition and soil properties in different plant species. Our results indicated that soil bacterial diversity was significantly lower in vegetated soils independent of plant species than in the CK. Specifically, soil bacterial species richness and diversity were lower under the shrub AH and the herbaceous plants AS, SV, and CA, and soil bacterial abundance was lower under AH compared with the CK. A field investigation confirmed the same trends where soil bacteria diversity was lower under AS and AH than in bare sand. The high-sequence annotation analysis showed that *Proteobacteria*, *Actinobacteria*, and *Bacteroidetes* were the most common phyla in sandy land irrespective of soil plant cover. The OTUs (operational taxonomic units) indicated that some bacterial species were specific to the host plants. Relative to bare sand (CK), soils with vegetative cover exhibited lower soil water content and temperature, and higher soil carbon and nitrogen contents. The RDA result indicated that, in addition to plant species, soil water and nitrogen contents were the most important factors shaping soil bacterial composition in semiarid sandy land. Our study from the pot and field investigations clearly demonstrated that planting dominant species in bare sand impacts bacterial diversity. In semiarid ecosystems, changes in the dominant plant species during vegetation restoration efforts can affect the soil bacterial diversity and composition through the direct effects of plants and the indirect effects of soil properties that are driven by plant species.

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SCIENTIFIC REPORTS



OPEN

Temporal and spatial variation of extreme temperatures in an agro-pastoral ecotone of northern China from 1960 to 2016

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The agro-pastoral ecotone of northern China is one of the areas most sensitive to global temperature change. To analyze the temporal and spatial trends of extreme temperature events in this area, we calculated the values of 16 extreme-temperature indices from 1960 to 2016 based on data from 45 national meteorological stations. We found that the coldest-temperature indices decreased significantly and the warmest-temperature indices increased significantly. The warming of night temperatures contributed more than warming of day temperatures to the overall warming trend. In addition, the warm-temperature indices appeared to be increasing since the late 1980s and early 1990s. Overall, though the four extremal indices showed an increasing trend, the rate of change in the minimum temperature was greater than that of the maximum temperature; thus, the minimum temperature contributed most strongly to the overall temperature increases. The growing season is being prolonged in higher-elevation areas, but vegetation maturation in lower-elevation areas has been accelerated by the high temperatures, potentially leading to a shorter growing season at low altitudes. However, the impacts of land-use changes caused by human activities on the temperature increases will require additional study.

Climate change and human land-use activities are interacting strongly, in unprecedented ways, with rapid changes in living conditions and in the structure and function of ecosystems¹. According to the third assessment report by IPCC, the global average temperature has risen by 0.6 ± 0.2 °C over the past 100 years, with the temperature in China rising slightly more (by 0.5 to 0.8 °C) than the global rate². Simultaneously, extreme climate events have become more and more frequent, with heat waves, storms, outbreaks of pests, and other disasters caused by extreme weather becoming commonplace in recent years³. These events have had huge impacts on the world's ecosystems and social systems. Therefore, researchers have increasingly focused on how to deal with the impacts of climate change, and especially extreme climate events, on ecosystems and human livelihoods, with the goal of promoting sustainable development of society and ecosystems^{4–10}.

In China, both the frequency and the intensity of extreme climate events have changed significantly since the 1960s, but the trends have differed among regions¹¹. Since the northern agro-pastoral ecotone, a key area for China's food security, is situated in a transition zone between areas with semi-arid and arid climates, this region is very sensitive to climate change. The transition zone includes lands that have undergone erratic but often unsustainable land use due to decades of alternations and upheavals caused by agriculture and animal husbandry. Owing to climate warming, regional drying, and increasing population pressure, the cultivated area has gradually expanded and the pastoral areas have shrunk. Variations of land use patterns and the intensity of the land uses would change the hydrologic and thermal balances of the land in this region¹². For example, land-use changes are primary driving forces for changes in the near-surface climate¹³. In addition, these changes will profoundly affect disease incidence, such as the spread of malaria in tropical Africa, beginning well before 2050¹⁴. In developed countries such as the United States,

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RESEARCH ARTICLE

Spatial pattern of soil organic carbon and total nitrogen, and analysis of related factors in an agro-pastoral zone in Northern China

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OPEN ACCESS

Citation: Wang X, Li Y, Chen Y, Lian J, Luo Y, Niu Y, et al. (2018) Spatial pattern of soil organic carbon and total nitrogen, and analysis of related factors in an agro-pastoral zone in Northern China. PLoS ONE 13(5): e0197451. <https://doi.org/10.1371/journal.pone.0197451>

Editor: Xiujun Wang, Beijing Normal University, CHINA

Received: June 24, 2017

Accepted: May 2, 2018

Published: May 17, 2018

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Data Availability Statement: All relevant data are within the paper and its Supporting Information files.

Funding: This research was supported by the National Key Research and Development Program of China (2016YFC0500901), One Hundred Person Project of the Chinese Academy of Sciences (Y551821), and the National Natural Science Foundation of China (grants 31640012, 31560161, and 31260089). All co-authors assisted with manuscript writing. Xuyang Wang, Yuqiang Li and

Abstract

The spatial pattern of soil organic carbon (SOC) and total nitrogen (TN) densities plays a profound important role in estimating carbon and nitrogen budgets. Naiman Banner located in northern China was chosen as research site, a total of 332 soil samples were taken in a depth of 100 cm from the low hilly land in the southern part, sandy land in the middle part and an alluvial plain in the northern part of the county. The results showed that SOC and TN density initially decreased and then increased from the north to the south, The highest densities, were generally in the south, with the lowest generally in the middle part. The SOC and TN densities in cropland were significantly greater than those in woodland and grassland in the alluvial plains and for Naiman as a whole. The woodland SOC and TN density were higher than those of grassland in the low hilly land, and higher densities of SOC and TN in grassland than woodland in the sandy land and low hilly land. There were significant differences in SOC and TN densities among the five soil types of Cambisols, Arenosols, Gleysols, Argosols, and Kastanozems. In addition, SOC and TN contents generally decreased with increasing soil depth, but increased below a depth of 40 cm in the Cambisols and became roughly constant at this depth in the Kastanozems. There is considerable potential to sequester carbon and nitrogen in the soil via the conversion of degraded sandy land into woodland and grassland in alluvial plain, and more grassland should be established in sandy land and low hilly land.

Introduction

Soil is a huge C pool and plays an important role in global warming due to greenhouse gas emission and mutual impact on nitrogen cycle. For example, soil emission of carbon dioxide into the atmosphere is estimated to be six times the amount derived from fossil fuels [1, 2]. The global soil carbon pool (2500 Gt) is three times the size of the atmospheric carbon pool (760 Gt), 4.5 times of the biotic pool (560 Gt) [3]. In addition, restored SOC and TN are

ORIGINAL ARTICLE

Dormancy and germination strategies of a desert winter annual *Echinops gmelini* Turcz. in a temperate desert of China

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Funding information

Creative Research Groups of China, Grant/Award Number: 41621001; National Natural Science Foundation of China, Grant/Award Numbers: 41530746, 41671210, 41501110, 31500370; Foundation for Excellent Youth Scholars of NIEER, CAS

Abstract

Echinops gmelini Turcz. is an annual Asteraceae species widely distributed in the desert habitats of northern China. However, little is known about how this species adapts to harsh desert habitats. In this study, *E. gmelini* germination behaviors were observed in a natural population at the southeastern edge of the Tengger Desert. In addition, the effects of temperature, light, hydration–dehydration (H–D) cycles and different storage conditions on seed germination were tested in the laboratory. *E. gmelini* behaves as a winter annual, and its seeds germinate during the summer and early autumn in the field. Fresh seeds have non-deep physiological dormancy (PD). A 15-day dry storage treatment under laboratory conditions was required to break PD. Non-dormant seeds can germinate rapidly and at a high rate in light at 30/20°C. Dry storage with seasonal temperature changes had little effect on seed germination and dormancy. However, under natural field conditions, greater and faster germination at a wide range of temperatures was observed after seeds were stored for 1–2 months, which allows seeds to germinate during short periods of moisture availability; seeds were induced into secondary dormancy after storage for 3 months which may prevent germination in autumn. Furthermore, seed germination was reduced and became faster after exposure to four or more H–D cycles. Our results suggest that precipitation is the key factor in determining *E. gmelini* seed germination time in natural habitats, and they provide information about the strategies that annual plants need to adapt to climatically unpredictable environments in temperate deserts.

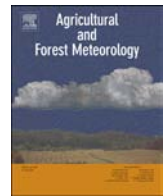
KEYWORDS

dormancy, *Echinops gmelini* Turcz., germination, temperate desert, winter annual

1 | INTRODUCTION

Seed dormancy and germination are critical elements of the plant life cycle, and the responses of these processes to environmental conditions are crucial for successful recruitment (Commander, Golos, Miller, & Merritt, 2017). This is particularly true for annual plants, for which seeds provide the only link to future years. Many species have mechanisms that allow seeds to remain dormant to overcome climate constraints (Baskin & Baskin, 2000). This strategy likely allows for dispersal of the germination risk over time and ensures that some seeds germinate when the conditions are favorable

for germination and seedling survival (Adonakis & Venable, 2004; Baskin & Baskin, 2000; Cohen, 1966; Venable, 2007). Thus, dormancy is crucial in the formation of soil seed banks, and long-lived seed banks maintained by annual desert plants are often regarded as evolutionary bet-hedging strategies against unpredictable environmental variations or harsh climatic regions (Gutiérrez & Meserve, 2003; Mott, 1974; Venable, 1985; Went, 1948). For instance, the available rainfall varies substantially among years in both amount and timing and acts as the primary limiting factor for seed germination in desert areas (Gutterman, 1993). The temperature is another environmental factor determining



Diverse responses of vegetation growth to meteorological drought across climate zones and land biomes in northern China from 1981 to 2014

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ARTICLE INFO

Keywords:

Climatic extremes
Dryland ecosystems
Landscape vulnerability
Functional diversity
Water balance

ABSTRACT

Improving our understanding of present and future impacts of drought on the vegetation in northern China is heightened by expectations that drought would increase its vulnerability and subsequently accelerate land degradation. The response of vegetation activity to drought and the underlying mechanisms are not well known. By using the third-generation Normalized Difference Vegetation Index (NDVI) and the Standardized Precipitation Evapotranspiration Index (SPEI), we investigated the relationship between NDVI and SPEI, across different climate regimes and land cover types, and determined the dominant time-scales at which different biome types respond to drought during the period of 1981–2014. Our results showed that biome response is coupled with drought trends in most regions of northern China. The highest correlation between monthly NDVI and SPEI at different time scales (1–48 months) assessed the impact of drought on vegetation, and the time scales resulting in the highest correlation were an effective indicator of drought resistance, which was related to the interactive roles of mean water balance and divergent drought survival traits and strategies. Diverse responses of vegetation to drought were critically dependent on characteristic drought time-scales and different growing environments. This study highlighted the most susceptible ecosystem types to drought occurrence under current climate, including temperate steppes, temperate desert steppes, warm shrubs and dry forests. Given that drought will be more frequent and severe under future climate scenarios, it may threaten the survival of mesic ecosystems, such as temperate meadows, alpine grasslands, dwarf shrubs, and moist forests not normally considered at drought risk. We propose that future research should be focused on arid and semi-arid ecosystems, where the strongest impact of drought on vegetation is occurring and the need for an early warning drought system is increasingly urgent.

1. Introduction

More frequent and severe drought has been forecast in the 21st century, particularly in the mid-latitudes (Sheffield and Wood, 2008). Increases in drought are driven primarily by decreased precipitation with increased evapotranspiration from higher temperatures (Trenberth et al., 2014). Drought is recognized as the world's most costly and pressing natural hazard that influences water resource systems, agricultural production and natural ecosystems (Mishra and Singh, 2010). Water availability acts as the main driver of vegetation distribution and productivity in arid and semi-arid regions (Neilson, 1995; Churkina and Running, 1998). Evidence is accumulating that semi-arid ecosystems dominate the trend and inter-annual variability in the land CO₂ sink, and are highly sensitive to drought trends (Zhao and Running, 2010;

Ahlström et al., 2015; Huang et al., 2016). Therefore, understanding the response of dryland ecosystems to drought is important for assessing vegetation vulnerability to climate extreme events (Smith et al., 2014) and has strong implications for enhancing drought mitigation and preparedness (Wilhite et al., 2007).

Northern China is located in the mid-latitude East Asia with arid, semi-arid and dry sub-humid regions accounting for approximately 34%, 27% and 16% of its total land area, respectively. The Taklimakan and Gobi Deserts constitute two major dust sources over East Asia (Tanaka and Chiba, 2006). The vegetation in northern China plays a pivotal role in the prevention and control of land degradation (Wang et al., 2015), which has a significant effect on the national ecological security (Miao et al., 2015). Soil water availability is a primary constraint on the survival of sand-binding vegetation (Li et al., 2013).

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<https://doi.org/10.1016/j.agrformet.2018.06.027>

Received 8 December 2017; Received in revised form 17 June 2018; Accepted 25 June 2018
Available online 28 June 2018

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Research article

A whole-transcriptome approach to evaluate reference genes for quantitative diurnal gene expression studies under natural field conditions in *Tamarix ramosissima* leavesXia Yan^{a,b}, Chaoju Qian^a, Xiaoyue Yin^a, Xingke Fan^a, Xueyong Zhao^{a,c}, Menghe Gu^d, Tao Wang^d, Xiao-Fei Ma^{a,*}^a Key Laboratory of Stress Physiology and Ecology in Cold and Arid Regions of Gansu Province, Cold and Arid Regions Environmental and Engineering Research, Chinese Academy of Sciences, Lanzhou 730000, China^b Key Laboratory of Inland River Ecohydrology, Cold and Arid Regions Environmental and Engineering Research, Chinese Academy of Sciences, Lanzhou 730000, China^c Naiman Desertification Research Station, Cold and Arid Regions Environmental and Engineering Research, Chinese Academy of Sciences, Lanzhou, 730000, China^d Key Laboratory of Desert and Desertification, Cold and Arid Regions Environmental and Engineering Research, Chinese Academy of Sciences, Lanzhou 730000, China

ARTICLE INFO

Article history:

Received 13 September 2017

Accepted 7 August 2018

Available online 24 August 2018

Keywords:

Desert plants

Desert restoration

Drought adaptation

Fragile ecosystem

Functional analysis

Gene expression

qPCR

Reference gene

RNA-seq

Tamarix ramosissima

Water transport

ABSTRACT

Background: *Tamarix ramosissima* is a desert forest tree species that is widely distributed in the drought-stricken areas to sustain the fragile ecosystem. Owing to its wide usage in the desert restoration of Asia, it can be used as an ecophysiological model plant. To obtain reliable and accurate results, a set of reference genes should be screened before gene expression. However, up to date, systematical evaluation of reference genes has not been conducted in *T. ramosissima*.**Results:** In this study, we used eigenvalues derived from principal component analysis to identify stable expressed genes from 72,035 unigenes from diurnal transcriptomes under natural field conditions. With combined criteria of read counts above 900 and CV of FPKM below 0.3, a total of 7385 unigenes could be qualified as candidate reference genes in *T. ramosissima*. By using three statistical algorithm packages, *geNorm*, *NormFinder*, and *BestKeeper*, the stabilities of these novel reference genes were further compared with a panel of traditional reference genes. The expression patterns of three aquaporins (AQPs) suggested that at least UBQ (high expression), EIF4A2 (low expression), and GAPDH (moderate expression) could be qualified as ideal reference genes in both RT-PCR and RNA-seq analysis of *T. ramosissima*.**Conclusions:** This work will not only facilitate future studies on gene expression and functional analysis of genetic resources of desert plants but also improve our understanding of the molecular regulation of water transport in this plant, which could provide a new clue to further investigate the drought adaptation mechanism of desert plant species under harsh environments.How to cite: Yan X, Qian C, Yin X, et al. A whole-transcriptome approach to evaluating reference genes for quantitative diurnal gene expression studies under natural field in *Tamarix ramosissima* leaves. *Electron J Biotechnol* 2018;35. <https://doi.org/10.1016/j.ejbt.2018.08.004>.© 2018 Pontificia Universidad Católica de Valparaíso. Production and hosting by Elsevier B.V. All rights reserved. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

1. Introduction

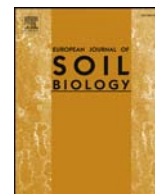
Gene expression analysis is increasingly important in many fields of biological research. Understanding gene expression patterns is expected to provide insights into complex regulatory networks and helps to identify genes that are relevant to new biological processes. Plants fluctuate diurnally for approximately 24 h under diurnal signals such as light–dark or temperature cycles with diverse biological

activities and physiological output [1,2]. Most transcripts were diurnally expressed following those signals in plants. In the dicot model *Arabidopsis thaliana*, this number amounts to approximately 80% [3,4,5,6]. In rice, poplar, maize, tomato, and soybean, similar results were observed [7,8,9,10]. In addition to rhythmic changes, complex and noise environmental signals also affect gene expression. Many studies have dissected these signals under artificial constant conditions to further investigate the contribution of environmental factors to the molecular mechanism in plants [2,11,12]. However, many results showed discrepancy with those obtained under natural field conditions, which is even more serious in transgenic crop plants [13,14,15,16]. Natural conditions are increasingly taken into

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Peer review under responsibility of Pontificia Universidad Católica de Valparaíso.



Impact of human trampling on biological soil crusts determined by soil microbial biomass, enzyme activities and nematode communities in a desert ecosystem



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ARTICLE INFO

Handling editor: Bryan Griffiths

Keywords:

Biocrusts

Human trampling

Trampling intensity

Soil nematodes

Soil microbial biomass

Soil enzyme activities

ABSTRACT

Human activities disturb Biological soil crusts (biocrusts) in desert areas throughout the world. To assess the effects of trampling on biocrusts and its consequence on sandy soil quality, soil beneath trampling to early-successional cyanobacteria–lichen crusts and late-successional moss crusts was served as the research object in vegetation areas of the Tengger Desert. Trampling intensity was divided into non-trampling, medium trampling and severe trampling of biocrusts. We analyzed changes in soil microbial biomass, enzyme activities and nematode communities one year after trampling biocrust. The results showed that trampling biocrusts reduced soil microbial biomass carbon (C) and nitrogen (N), lowered soil urease, invertase, catalase and dehydrogenase activity, as well as reduced soil nematode abundance, generic richness, Shannon–Weaver index (H') and Maturity index (MI) in the study areas, and severely-trampled biocrusts caused a strong decline in these parameters ($p < 0.05$). The declined soil available phosphorus (P), available N, total N and P may be the major factors that cause the observed reduction in soil microbial and nematode parameters. Impact was correlated with trampling intensity or successional stages of biocrusts. The studied soil microbial and nematode parameters were negatively correlated with trampling intensity. Furthermore, soil microbial biomass, the four enzyme activities, nematode abundance and generic richness were significantly greater underneath trampled/untrampled moss crusts than corresponding trampled/untrampled cyanobacteria–lichen crusts, indicating late-successional crusts have a higher tolerance to trampling disturbance compared to early-successional crusts. Overall, these results suggest that trampling biocrusts lead to a degradation of sandy soil quality in desert ecosystems.

1. Introduction

Biological soil crusts (biocrusts) are associations of soil organisms (mainly cyanobacteria, bryophytes, algae, lichens, microfungi and bacteria) and soil particles [1]. They are ubiquitous and extremely important in arid and semiarid areas, which occupy more than one-third of the earth's terrestrial surface [9,53]. Biocrusts constitute up to 70% of the living cover on arid soils [19] due to their ability to withstand high temperatures, strong radiation, low nutrient conditions, low water potential and to remain dormant for long dry periods in drylands [44]. Stabilizing soil and enhancing soil fertility are the most important ecological functions of biocrusts in many drylands [8,21]. However, soil

surface disturbance by footprints, hoof prints and vehicle tracks may cause significant damage to biocrust communities [25], which are highly susceptible to soil surface disturbances [9,14,54], leading to the degradation of biocrusts' ecosystem functions [13]. A number of studies have reported that trampling disturbance reduces biocrust biomass, coverage and species diversity, transforming late-successional crusts to early-successional crusts, which leads to accelerated soil erosion, reduced water infiltration, soil C and N loss, and alteration of soil temperature and aeration [3,6,7,9,17,19,22,23,26].

Soil microbes drive many ecological processes in soil, such as mineral weathering, organic matter decomposition and nutrient cycling, and so doing they can respond rapidly to environmental changes and

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<https://doi.org/10.1016/j.ejsobi.2018.05.005>

Received 20 October 2017; Received in revised form 5 May 2018; Accepted 16 May 2018

Available online 26 May 2018

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基于 UPLC-MS 的沙米代谢组学分析

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[摘要] 目的: 研究沙米地上部分不同组织的代谢物, 分析不同组织的差异标志代谢物, 挖掘其有效药用活性成分。方法: 采用基于 UPLC-MS 非靶向代谢组学技术对沙米地上组织的药用活性成分进行分析, 利用三重四级杆质谱的多反应监测模式(MRM)进行代谢物定量分析, 多元统计方法分析沙米地上不同组织差异代谢物。结果: 通过代谢组分析共检测到沙米地上组织中的 506 种代谢物, 其中具有药用活性的成分包括黄酮类、生物碱类、多酚类、维生素、萜类、氨基酸等, 大部分活性物质在沙米地上组织中含明显富集, 部分代谢物在叶、茎、穗中含量分布存在差异, 穗中氨基酸含量显著, 叶、茎中黄酮类、多酚类、生物碱类、维生素等次生代谢物含量显著。结论: 沙米具有潜在的抗氧化、抗肿瘤、抗炎、抗菌、降血压、降血脂和保护心脑血管等功能。该研究不仅支持利用沙米地上组织开发新药极具前景, 同时还为沙米作为新型中草药资源提供重要数据, 推动我国干旱区、半干旱区可持续生态农业和健康产业的发展。

[关键词] 沙米; 代谢组学; 不同组织; 差异代谢物; 药用活性成分; 氨基酸; 维生素

[中图分类号] R22; O657. 6; R969. 1; R284; R945; R282 **[文献标识码]** A

[doi] 10.13422/j.cnki.syfjx.20181503

[网络出版地址]

[网络出版时间]

Analysis of Metabolomics in *Agriophyllum squarrosum* Based on UPLC-MS

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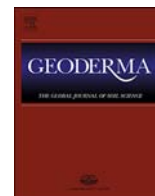
[Abstract] **Objective:** To evaluate the potential medicine usage, we aimed to verifying its medicinal active ingredients of *Agriophyllum squarrosum*. **Method:** We explored medicinal active ingredients in the above-ground tissues of *A. squarrosum* based on UPLC-MS non-targeted metabonomics analysis. Quantitative analysis of metabolites was carried out using a multi-reaction monitoring model (MRM) of triple quadrupole mass spectrometry. The multivariate statistical analysis was used to analyze the difference metabolites in the above-ground tissues of *A. squarrosum*. **Result:** With metabonomics analysis, a total of 506 metabolites were detected in the above-ground tissues of *A. squarrosum*, including flavonoids, alkaloids, polyphenols, vitamins, terpenes,

[收稿日期] 20171123(003)

[基金项目] 国家重点基础研究发展计划项目(2016YFC0500903); 国家自然科学基金项目(31500266); 甘肃省科技支撑计划项目(1604NKCA049)

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Fluxes of N₂O, CH₄ and soil respiration as affected by water and nitrogen addition in a temperate desert

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ARTICLE INFO

Handling Editor: Junhong Bai

Keywords:

Gurbantunggut desert
CH₄ sink
Precipitation
Nitrogen deposition
Interactive effects

ABSTRACT

An experiment was conducted to investigate the effect of precipitation and N deposition on N₂O and CH₄ fluxes and soil respiration (R_s) in the Gurbantunggut Desert from September 2014 to August 2015. The desert was a weak sink for CH₄ (−0.92 kg C ha^{−1} yr^{−1}) and a small source of N₂O (+0.13 kg N ha^{−1} yr^{−1}) and the annual rate of R_s was 874 kg C ha^{−1}. Our work confirmed a relatively strong sink for CH₄ in desert soils. Significant impacts on N₂O, CH₄ fluxes and R_s were found by increasing precipitation, with pulses of CH₄ uptake and R_s accounting for 79.1% and 33.2% of annual CH₄ uptake and R_s, respectively. N₂O and CH₄ fluxes were significantly enhanced by 7.8–109.6% by N addition, but it had no significant effect on R_s. Statistical significant interactions of precipitation and N addition on N₂O and CH₄ fluxes were found, and on R_s was lower than any single factor. Our results indicate that the Gurbantunggut Desert is a weak sink for CH₄ and a small source of N₂O, and is sensitive to elevated precipitation and N deposition.

Desert soils, as a net sink of greenhouse gases (GHGs) (Zhuang et al., 2013), are profoundly affected by precipitation patterns and nitrogen (N) deposition (Huang et al., 2015). However, the impacts of precipitation and N deposition on N₂O, CH₄ and soil respiration (R_s) are uncertain largely in desert soils. Previous studies (Zhang et al., 2008; Huang et al., 2015) investigating precipitation and N addition impacts on GHGs have primarily focused on the effect of single factor in grassland and forest, while the interaction effects in desert soils are very scarce.

Temperate desert, covering approximately one third of the global land area, is dynamically sensitive to precipitation and N deposition (Li et al., 2015). Climate change in Northwest China is for an increase in precipitation of 30%, with an increases of 3–5 mm yr^{−1} since 1979 (Li et al., 2015), and N deposition has increased significantly since 1980 to total deposition of 35.2 kg N ha^{−1} yr^{−1} (Song, 2015). These changes are important for soil biological processes because of the extreme limits of soil N and water in such deserts (Huang et al., 2015). However, information on the responses of N₂O, CH₄ fluxes and R_s to precipitation and N deposition in this ecosystem is scarce and merits research.

We therefore conducted an experiment from September 2014 to August 2015 in the Gurbantunggut Desert (44°26′–43°65′N,

84°31′–90°00′E). Weather and soil conditions are shown in Fig. 1(a, b). N addition rates were 0 (N0), 30 (N1) and 60 (N2) kg N ha^{−1} yr^{−1}. Precipitation was ‘natural’ (W0) and ‘natural’ plus 60 mm yr^{−1} (equivalent to 30% of annual precipitation) (W1). There were six treatments: W0N0 (the control), W0N1, W0N2, W1N0, W1N1 and W1N2. Four plots were established for each treatment, each plot 10 m × 10 m with a 5 m-wide buffer zone; a total of 24 plots. The enhanced precipitation was sprayed onto the plots as an extra 10% (i.e. 20 mm) in Autumn (September), Spring (April), and Summer (July) in four doses of 5 mm per week in September, April and July using a petrol-driven, single-nozzle spray. Nitrogen was applied as NH₄NO₃ directly (in W0N1 and W0N2) or just after the extra precipitation (in W1N1, W1N2) in all treatments.

N₂O, CH₄ fluxes and R_s were measured using static chambers in all 24 plots. Gas samples were collected from the headspace of each static chamber at 0, 10, 20 and 30 min after closing the chamber between 10:00 and 12:00 (GMT + 8). Gas samples were collected once or twice a week. Samples were measured using a gas chromatograph (GC; Agilent 7890A, Agilent Technologies, Santa Clara, CA). Fluxes were calculated according to Chen et al. (2013). Effects of precipitation and N deposition on R_s, N₂O and CH₄ fluxes were analyzed by two-way

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<https://doi.org/10.1016/j.geoderma.2018.10.020>

Received 1 June 2017; Received in revised form 8 October 2018; Accepted 12 October 2018

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Impact of elevated precipitation, nitrogen deposition and warming on soil respiration in a temperate desert

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Received: 31 October 2017 – Discussion started: 9 November 2017

Revised: 20 February 2018 – Accepted: 27 February 2018 – Published: 6 April 2018


Abstract. Soil respiration (R_s) is the most important source of carbon dioxide emissions from soil to atmosphere. However, it is unclear what the interactive response of R_s would be to environmental changes such as elevated precipitation, nitrogen (N) deposition and warming, especially in unique temperate desert ecosystems. To investigate this an in situ field experiment was conducted in the Gurbantunggut Desert, northwest China, from September 2014 to October 2016. The results showed that precipitation and N deposition significantly increased R_s , but warming decreased R_s , except in extreme precipitation events, which was mainly through its impact on the variation of soil moisture at 5 cm depth. In addition, the interactive response of R_s to combinations of the factors was much less than that of any single-factor, and the main response was a positive effect, except for the response from the interaction of increased precipitation and high N deposition ($60 \text{ kg N ha}^{-1} \text{ yr}^{-1}$). Although R_s was found to show a unimodal change pattern with the variation of soil moisture, soil temperature and soil NH_4^+ -N content, and it was significantly positively correlated to soil dissolved organic carbon (DOC) and pH, a structural equation model found that soil temperature was the most important controlling factor. Those results indicated that R_s was mainly interactively controlled by the soil multi-environmental factors and soil nutrients, and was very sensitive to elevated precipitation, N deposition and warming. However, the interactions of multiple factors largely reduced between-year variation of

R_s more than any single-factor, suggesting that the carbon cycle in temperate deserts could be profoundly influenced by positive carbon–climate feedback.

1 Introduction

Global climate warming, changes in precipitation patterns and increased atmospheric nitrogen (N) deposition have all occurred since the Industrial Revolution, especially in temperate regions (IPCC, 2013), which will be expected to significantly change soil respiration (R_s), the most important source of carbon dioxide (CO_2) from soil to atmosphere (Wu et al., 2011): the annual CO_2 flux from R_s was 10-fold that of fossil fuel emissions (Eswaran et al., 1993; Batjes, 1996; Gougoulias et al., 2014). Therefore, even a small change in R_s will profoundly affect greenhouse gas balance and climate (Heimann and Reichstein, 2008). Although a number of experiments of the effects of warming, precipitation and N deposition on R_s have been conducted in alpine grasslands, tundra regions, peatlands and temperate forests (Lafleur and Humphreys, 2008; Strong et al., 2017; Yang et al., 2017; Zhao et al., 2017), studies in temperate desert ecosystems are scarce, especially those on the impact of these changes' interactions on R_s . A field study of multi-factor interactive effects on R_s was therefore conducted in a temperate desert ecosystem to help in understanding the response of R_s to climate

The agronomic performance of sand rice (*Agriophyllum squarrosum*), a potential semi-arid crop species

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Received: 14 March 2018 / Accepted: 28 August 2018 / Published online: 25 September 2018
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Abstract *Agriophyllum squarrosum* (sand rice), a member of the Amaranthaceae family adapted to arid to semi-arid conditions in central Asia, produces highly nutritious seed. Three ecotypes collected from sand dunes in the western Chinese arid desert region (Linze, Minqin and Shapotou) and three from the semi-arid desert region (Duolun, Naiman, and Aerxiang) were grown in loess soil at an experimental station (Gaolan) to characterize their performance with respect to plant architecture and seed yield-

associated traits. The ecotypes originating from the more arid sites developed into taller, more strongly branching plants, formed thicker stems and a greater number of spikes. Those collected from the semi-arid sites developed larger seeds and were of shorter duration. The highest seed yields were obtained from the Aerxiang ecotype (129.55 g/m²). The same ecotype also exhibited both the highest emergence rate and the most favorable harvest index. The study represents the first assessment of the agronomic performance of sand rice and shows what needs to be done to domesticate and improve the species before it can be considered as a viable crop species.

Electronic supplementary material The online version of this article (<https://doi.org/10.1007/s10722-018-0689-3>) contains supplementary material, which is available to authorized users.

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Syntenly-based mapping of causal point mutations relevant to sand rice (*Agriophyllum squarrosum*) trichomeless1 mutant by RNA-sequencing

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ARTICLE INFO

Keywords:

Agriophyllum squarrosum
Trichome
Syntenly-based mapping
Allele frequencies
Bulked-segregant analysis
Potential crop

ABSTRACT

Sand rice (*Agriophyllum squarrosum*), a diploid Amaranthaceae species within the order Caryophyllales, has potential as a crop in response to concerns about ongoing climate change and future food security. Modifying the weedy traits, such as dense trichomes, is important for the domestication of sand rice. In this study, an ethyl methanesulfonate (EMS) induced *Agriophyllum squarrosum* trichomeless mutant (*astcl1*) was isolated and genetic analysis revealed that this mutant was controlled by a single recessive locus. RNA sequencing was employed to analyze sequence variations between the mutant and wild-type individuals based on allele frequencies. Syntenly-based mapping against two closely related and sequenced species finally delimited the causal mutations into an approximately 18.97 mega base pair (Mb) interval on the top portion of the chromosome 6 (*Bv6*) of sugar beet (*Beta vulgaris*) and two intervals (5.56 and 2.69 Mb) on the chromosomes 14 (*CqA14*) and 6 (*CqB06*) of quinoa (*Chenopodium quinoa*). These two quinoa intervals were located in the orthologous chromosomal regions against sugar beet *Bv6*. Differential expression analysis revealed that the *astcl1* mutation only affects the expression of a small subset of genes. Most significantly, 17 lipid transport and metabolism related genes, such as *GDSL esterases* and *very-long-chain 3-oxoacyl-CoA reductase 1*, and two R2R3 MYB genes, *MYB39* and *RAX3*, were down-regulated in *astcl1* mutants. These results imply that the *Astcl1* protein coordinately regulates trichome initiation and cuticle biosynthesis in sand rice.

1. Introduction

Trichomes, unicellular, or multicellular epidermal appendages, are found on the aerial tissues of nearly all land plants, and their structures are generally divided into two categories: secretory glandular or nonglandular (Hulskamp et al., 1998; Serna and Martin, 2006). One of the diverse functions of trichomes is as a biophysical barrier that can create a complex three-dimensional network to protect plants against abiotic damage and biotic challenges, including extreme temperature, UV irradiation, insects, pathogens, and herbivores (Hauser, 2014; Liu et al., 2017).

In *Arabidopsis thaliana*, a number of positive and negative regulators have been revealed to play a pivotal role in unicellular trichome formation (Hulskamp et al., 1994; Ishida et al., 2008; Pattanaik et al., 2014; Schellmann and Hulskamp, 2005). The core positive regulators consist of three protein classes: R2R3 MYB transcription factors (TFs)

encoded by *GLABRA1* (*GL1*), *MYB23*, and *MYB5* (Kirik et al., 2005, 2001; Li et al., 2009; Oppenheimer et al., 1991; Tominaga-Wada et al., 2012); basic helix-loop-helix (bHLH) proteins encoded by *GLABRA3* (*GL3*), *ENHANCER OF GLABRA3* (*EGL3*), *TRANSPARENT TESTA* (*TT8*), and *MYC1* (Payne et al., 2000; Zhang et al., 2003; Zhao et al., 2012); and the WD-repeat protein *TRANSPARENT TESTA GLABRA1* (*TTG1*) (Galway et al., 1994; Walker et al., 1999). These three groups of TFs form a MYB-bHLH-WD40 (MBW) complex to activate the expression of a homeodomain protein gene, *GLABRA2* (*GL2*), which, in turn, initiates trichome formation (Rerie et al., 1994). The negative regulators are single-repeat R3 MYB TFs encoded by a group of seven functionally redundant genes including *CAPRICE* (*CPC*; Wada et al., 1997), *TRIPTYCHON* (*TRY*; Schellmann et al., 2002; Schnittger et al., 1999), *ENHANCER OF TRY AND CPC1* (*ETC1*; Esch et al., 2004; Kirik et al., 2004a), *ETC2* (Kirik et al., 2004b), *ETC3* (Simon et al., 2007; Tominaga et al., 2008; Wang et al., 2008; Wester et al., 2009), *TRICHOMELESS1* (*TCL1*;

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Contents lists available at ScienceDirect

Science of the Total Environment

journal homepage: www.elsevier.com/locate/scitotenv

Meteorological influences on process-based spatial-temporal pattern of throughfall of a xerophytic shrub in arid lands of northern China

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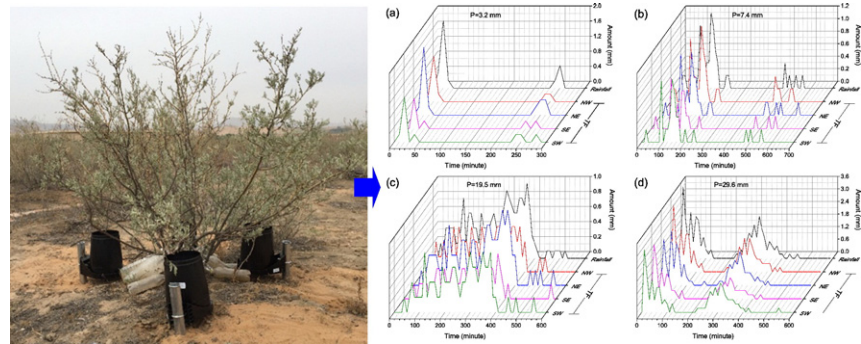
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HIGHLIGHTS

- Throughfall were monitored at 10-min intervals at different radial directions beneath shrub canopies.
- Temporal heterogeneity of rainfall clearly affected the timing of throughfall inputs.
- Throughfall differed markedly among different radial directions beneath shrub canopies.
- Principal Components Analysis was performed on meteorological variables.
- Three principal components were introduced into a multiple regression model to predict throughfall.

GRAPHICAL ABSTRACT



ARTICLE INFO

Article history:

Received 4 October 2017

Received in revised form 18 November 2017

Accepted 18 November 2017

Available online 29 November 2017

Editor: Ouyang Wei

Keywords:

Throughfall

Spatial-temporal variability

Meteorological variables

Principal components analysis

Caragana korshinskii

ABSTRACT

Numerous field experiments had demonstrated great spatial variability and temporal stability of throughfall under tree canopies within forested ecosystems. Nonetheless, no known studies have investigated the intrastorm spatial-temporal variability of throughfall beneath xerophytic shrub canopies within arid desert ecosystems where water is typically the principal limiting factor determining the structure and dynamics of ecosystems. Here we investigated the spatial-temporal pattern of throughfall at intrastorm scale, and systematically examined the effects of meteorological variables on throughfall based on the principal components analysis (PCA) and a multiple regression model. Throughfall was monitored at 10-min intervals by placing tipping-bucket rain gauges at different radial directions beneath 3 shrubs of *Caragana korshinskii* during the growing season of 2016 within a water-limited arid desert ecosystem of northern China. We found the temporal heterogeneity of rainfall clearly affected the timing of throughfall beneath shrub canopies within discrete rainfall events. Throughfall also differed markedly among different radial directions beneath shrub canopies, which was found to be well associated with wind directions during rainfall events. PCA on meteorological variables indicated that three principal components accounted for 84.2% of the total variance, and we found that the second principal component (loaded strongly on rainfall amount and maximum 10-min rainfall intensity) was the dominant component controlling throughfall and its spatial variability after introducing three principal components into a multiple linear regression model. Our findings highlight the spatial-temporal variability of throughfall at the intrastorm scale, and are expected to be helpful for an improved process-based characterization and modelling of throughfall in vast arid desert ecosystems.

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A study of viral coat protein accumulation in lily chloroplasts from mixed virus infections of *Lily mottle virus* and *Cucumber mosaic virus*

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Two viruses that frequently occur in many *Lilium* species are *Lily mottle virus* (LMoV) and *Cucumber mosaic virus* (CMV), which usually co-infect lilies causing severe disease symptoms. Recent reports have revealed that the viral coat protein (CP) affects chloroplast ultrastructure and symptom development. This study used western blot analysis to confirm that in leaves infected by mixed virus infections of LMoV and CMV, CPs of both viruses were accumulated in lily chloroplasts. Immunogold labelling further demonstrated that both the LMoV CP and CMV CP were localized in the stroma and the thylakoid membranes of the chloroplasts. In addition, it was found that CPs of both viruses were rapidly transported into isolated, intact chloroplasts (*in vitro*), and their transport efficiencies were positively related to CP concentrations. The lowest transmembrane concentration of CMV CP decreased from 38 $\mu\text{g mL}^{-1}$ recorded in the single CMV CP import system to 10 $\mu\text{g mL}^{-1}$ in the mixed import system of LMoV CP and CMV CP. CPs of both viruses exhibited species selection in their transmembrane transport into chloroplasts. This is the first report that the CPs from two viruses (LMoV and CMV) are simultaneously present in lily chloroplasts. Accumulation of high levels of LMoV CP and CMV CP inside the chloroplast appears to contribute to a synergistic interaction inducing the development of mosaic symptoms.

Keywords: chloroplast, coat protein, *Cucumber mosaic virus*, *Lilium* spp., *Lily mottle virus*, mixed virus infections

Introduction

Lily (*Lilium* spp.) is an important economic crop in the floricultural industry. Additional value is obtained from growing *Lilium davidii* var. *unicolor* bulbs, which are edible and have medicinal properties. Almost all lilies are propagated vegetatively, and virus-infected bulbs used for forcing may propagate diseases from one generation to the next. Viruses cause quantitative and qualitative yield reduction of lily worldwide. Two frequently occurring viruses in many *Lilium* species are *Lily mottle virus* (LMoV; genus *Potyvirus*, family *Potyviridae*) and *Cucumber mosaic virus* (CMV; genus *Cucumovirus*, family *Bromoviridae*). Generally, lilies infected with LMoV exhibit symptoms of leaf mottle, leaf mosaic, reddish-brown necrotic spots, vein clearing, chlorosis and yellow streaking, leaf curling and narrowing (Zhang *et al.*, 2016). Leaves infected with CMV initially display chlorotic, or yellow spotting, interveinal striping or vein-clearing, occasional leaf malformation, followed by the development of grey or brown necrotic spots (Ryu *et al.*, 2002). In the field, mixed infections of LMoV and CMV

have been confirmed in various lily species, resulting in more severe disease symptoms than those produced by single infections (Zhang *et al.*, 2014; Lim *et al.*, 2016).

Most plant viruses usually cause plants to exhibit mosaic symptoms. Studies have revealed that viral factors, especially the coat protein (CP), affect chloroplast ultrastructure and symptom development (Zhao *et al.*, 2016). Many hypotheses have been proposed about the pathogenesis of mosaic viruses, the most popular of which is that the interaction between the viral CP and chloroplasts is a major cause of the mottled symptoms of the host (Reinero & Beachy, 1989; Xu *et al.*, 2017). Earlier research confirmed that *Tobacco mosaic virus* (TMV) CP and CMV CP accumulate in the respective chloroplasts of systemically infected tobacco and cucumber leaves, and the severity of the symptoms is positively related to the amount of CPs in the host chloroplasts (Reinero & Beachy, 1989; Zhu & Francki, 1992). Subsequently, CPs of *Turnip mosaic virus* (TuMV), *Potato virus Y* (PVY), *Potato virus X* (PVX) and *Rice stripe virus* (RSV) were similarly found to accumulate in the chloroplasts of host plants (Fu *et al.*, 2004; Feki *et al.*, 2005; Qiao *et al.*, 2009; Cheng *et al.*, 2011).

Plants infected with LMoV and CMV exhibit symptoms of leaf mosaic. However, to date there is a lack of knowledge about the pathogenesis in the mixed

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Published online 26 October 2018



Short communication

The occurrence and distribution of viruses infecting Lanzhou lily in northwest, China



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ARTICLE INFO

Keywords:

Lanzhou lily
Lily symptomless virus
Cucumber mosaic virus
Lily mottle virus
Mixed infections

ABSTRACT

Field surveys were conducted during 2015–16 to document the occurrence of multiple virus infections and to record predominant viruses infecting Lanzhou lily (*Lilium davidii* var. *unicolor*) in the major area of cultivation, northwest China. Specimens were randomly collected from crops in eight different regions and tested for *Lily symptomless virus* (LSV), *Cucumber mosaic virus* (CMV) and *Lily mottle virus* (LMOV) using a quadruplex RT-PCR assay. Results indicated a high level of LSV (98.2%), a high level of CMV (42.5%), and a low level of LMOV (1.5%). In addition, a high level of mixed infections of LSV + CMV was confirmed in Lanzhou lily; in Huangyu, north Yuzhong and Yongjing, incidence of mixed infections of LSV + CMV occurred in over 50% of plants. Interestingly, 99% of CMV-infected plants were in combination with LSV. The sequence homology of LMOV isolate from this study (GenBank: MF781080) was similar to that previously reported in this region from *Lilium oriental*. Approaches to disease control using improved virus detection methods are also discussed.

1. Introduction

Lanzhou lily (*Lilium davidii* var. *unicolor*) is a popular edible vegetable bulb, as well as a traditional medicinal plant with a 150-year cultivation history. Lanzhou lily is mostly grown in the central area of Gansu province in north-western China, and it is mainly propagated via bulbs (Fig. 1). Nearly 25% of the cultivated area at elevations of 1800–2600 m has been planted with this crop (Wang et al., 2010). In recent years it has also been successfully introduced to Ningxia Hui Autonomous Region in the south, and Xinjiang Uyghur Autonomous Region in the north. Currently the area of Lanzhou lily cultivation is approximately 11,000 ha and its production is valued at RMB 2.5 billion (US\$ 375 M). The economic importance of Lanzhou lily bulb production has increased during the past decade because of a rapid increase in demand in both domestic and international markets. Currently Lanzhou lily bulbs are exported to Hong Kong, Japan, Southeast Asia, and Europe. A Lanzhou lily processing production chain has been established to the benefit of many farmers. Marketable Lanzhou lily bulbs are graded for size, weight and shape according to informal regional quality standards.

In recent years, virus infected plants exhibiting symptoms of plant stunting, have become a major problem. These infections have contributed to a deterioration in bulb quality and a reduction in yield of over 50% from 23,000 to 11,000 kg per hectare (Zhang et al., 2015a).

More than ten different viruses have been reported to infect lilies worldwide (Ryu et al., 2002). Among these lily-infecting viruses, *Lily symptomless virus* (LSV; Genus *Carlavirus*, family *Flexiviridae*), *Cucumber mosaic virus* (CMV; Genus *Cucumovirus*, family *Bromoviridae*), and *Lily mottle virus* (LMOV; Genus *Potyvirus*, family *Potyviridae*), are the most commonly recorded viruses in many cultivars of lily and in particular Lanzhou lily (Asjes, 2000; Wang et al., 2010; Lim et al., 2016). All three viruses may be transmitted vegetatively and mechanically, as well as by aphids. Few studies of viral diseases in Lanzhou lily have been undertaken, in particular those induced by multiple virus infections. In view of the recently increased area of Lanzhou lily, a preliminary survey was conducted to determine the occurrence of multiple infections and to record the predominant viruses infecting Lanzhou lily in China.

2. Materials and methods

2.1. Survey area and specimen collection

Surveys of Lanzhou lily were conducted during the growing seasons of 2015 and 2016 in northwest China over an area of approximately 2200 ha in eight major areas of cultivation in Gansu Province and Ningxia Hui Autonomous Region. These included the western zone (Yongjing), the central zone (Huangyu and Xiguoyuan), the southern zone (Lintao), and the eastern zone (south Yuzhong, and north

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<https://doi.org/10.1016/j.cropro.2018.02.028>

Received 18 September 2017; Received in revised form 27 February 2018; Accepted 28 February 2018
0261-2194/ © 2018 Published by Elsevier Ltd.



Research article

Transcriptional responses to phosphate starvation in *Brachypodium distachyon* rootsPengshan Zhao^{a,b,*}, Lirong Wang^a, Hengxia Yin^c^a Key Laboratory of Stress Physiology and Ecology in Cold and Arid Regions, Gansu Province, Northwest Institute of Eco-Environment and Resources, Chinese Academy of Sciences, Lanzhou, 730000, China^b Shapotou Desert Research & Experiment Station, Northwest Institute of Eco-Environment and Resources, Chinese Academy of Sciences, Lanzhou, 730000, China^c State Key Laboratory of Plateau Ecology and Agriculture, Qinghai University, Xining, 810016, China

ARTICLE INFO

Keywords:

Brachypodium distachyon
Low phosphate
Jasmonic acid
Inositol polyphosphates
Transcriptome responses

ABSTRACT

Brachypodium distachyon is a model plant that has recently emerged in grass research. Although the growth and photochemical efficiency of this species respond strongly to phosphate (Pi) availability, its Pi starvation response mechanism, which controls the Pi homeostasis, remains largely unknown. This study presents the transcriptomic response profiles of Pi-deficient roots at growth stages during which the plants were starved but obvious growth defects were absent. The results identify several phosphate transporters (i.e., *PHO1*), purple acid phosphatases, and SYG1/PHO81/XPR1 (SPX) domain-containing proteins out of a total of 1740 differentially expressed genes (DEGs). In particular, the transcription factor ethylene response factor (ERF), basic helix-loop-helix (bHLH), and WRKY family genes were the three most abundant DEG groups and the latter was significantly enriched. Comparative transcriptome analysis of *Brachypodium* versus *Arabidopsis* and rice revealed the presence of several common components in response to Pi fluctuations. Most significantly, jasmonic acid (JA) signaling-related genes were overrepresented in gene ontology (GO) enrichment tests. The presence of a possible link between low Pi response, inositol polyphosphates, and JA signaling is therefore discussed.

1. Introduction

Because phosphorus (P) is an essential macronutrient for plant lifecycles, the availability of inorganic phosphate (Pi) often limits growth, development, and yields in both natural and agricultural ecosystems (Zhang et al., 2014). As a result, plants have evolved a range of physiological and biochemical adaptations in order to cope with Pi deficiency, including the enhanced proliferation of lateral roots and the growth of root hairs, compromised shoot and primary root growth, and the secretion of protons, organic acids, phosphatases, and nucleases to enhance the acquisition of Pi from both inorganic and organic sources (Chiou and Lin, 2011; Plaxton and Tran, 2011). Advances in molecular biology in recent decades have revealed the central role of the PHOSPHATE STARVATION RESPONSE1 (PHR1) in transcriptional responses related to Pi deficiency as well as a number of other components involved in phosphorylation, dephosphorylation, and the SUMOylation of proteins. It is also understood that SYG1/PHO81/XPR1 (SPX) domain-

containing proteins are essential for plant Pi sensing and homeostasis (Chiou and Lin, 2011; Puga et al., 2014; Wang et al., 2014; Zhang et al., 2014; Wild et al., 2016). In addition, a number of microRNA-mediated modules, including miR399-PHOSPHATE2 (PHO2) and miR827-NITROGEN LIMITATION ADAPTATION (NLA), have also been shown to govern effective Pi transportation via ubiquitin-mediated protein degradation (Liu et al., 2014).

Throughout evolution, the expression of many thousands of genes have changed in a spatio-temporal manner in response to deficiencies in Pi, which in turn has fine-tuned the allocation and recycling of Pi (Zhang et al., 2014). Thus, in order to better understand these processes, numerous transcriptome analyses have been carried out on *Arabidopsis thaliana* (Misson et al., 2005; Morcuende et al., 2007; Woo et al., 2012) and on a range of crop plants, including rice (*Oryza sativa*; Secco et al., 2013a); and soybean (Zeng et al., 2016). These studies have led to significant improvements in our understanding of the sophisticated mechanisms underlying acclimation responses to Pi deficiencies

Abbreviations: bHLH, basic helix-loop-helix; CV, coefficient of variance; DEGs, differentially expressed genes; ERF, ethylene response factor; InsPs, inositol polyphosphates; JA, jasmonic acid; JAZs, jasmonate-zim-domain proteins; P, phosphorus; PAs, purple acid phosphatases; PHR1, phosphate starvation response1; Pi, phosphate; PP2C, protein phosphatase 2C family; PSRs, phosphate starvation responsive genes; RBH, reciprocal best hit; SPXs, SYG1/PHO81/XPR1 domain-containing proteins

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<https://doi.org/10.1016/j.plaphy.2017.11.010>

Received 17 July 2017; Received in revised form 16 November 2017; Accepted 16 November 2017

Available online 21 November 2017

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Effects of snowfall depth on soil physical–chemical properties and soil microbial biomass in moss–dominated crusts in the Gurbantunggut Desert, Northern China



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ARTICLE INFO

Keywords:

Biological soil crusts
Inorganic N
Snowfall
Soil water content
Soil nutrients

ABSTRACT

Winter snowfall is an important source of moisture that may influence the growth and development of biological soil crusts (BSCs) in temperate desert regions of China. Yet there is still limited empirical knowledge about the effect of snowfall on BSCs. In this study, moss crusts from the Gurbantunggut Desert were exposed to five snow depths to evaluate how snowfall affected the physical–chemical properties (pH; electric conductivity, EC; soil organic carbon, SOC; total nitrogen, TN; available nitrogen, AN; available phosphorus, AP; available potassium, AK) and microbial biomass (soil microbial biomass carbon, SMBC; soil microbial biomass nitrogen, SMBN; soil microbial biomass phosphorus, SMBP) of soil in the BSCs, before (in October 2016: representing three consecutive years of snow manipulation) and after winter (in April 2017). Results showed that the soil water content increased significantly as snowfall depth increased ($p < 0.05$) in October 2016 and April 2017. Most of the soil physical–chemical features (EC, SOC, TN, AN, AP, and AK) and microbial biomass (SMBC and SMBN) showed an increase with an increase of snowfall depth after three consecutive years of snow manipulation. Moreover, for most experimental treatments, after a winter of melting snow (in April 2017) most of the soil properties were significantly higher ($p < 0.05$) than found in October 2016. Together, these results showed that the dynamics of soil nutrients and microbial biomass in moss BSCs were affected by snowfall depth in Gurbantunggut Desert. Different snowfall depths can have different effects on the dynamics of soil nutrients and microbial biomass of moss crusts, an impact that may alter the future growth and development of BSCs. Thus, we suggest that the potential influence of snowfall depth on soil nutrients and microbial biomass dynamics in BSCs require consideration when discussing the effects of moisture on ecological functions of BSCs in arid and semi–arid regions.

1. Introduction

Biological soil crusts (BSCs) occur extensively in arid and semi–arid lands worldwide, where they play a large role in structuring desert ecosystems (Kidron and Vonshak, 2012; Li et al., 2005). BSCs are a complex association of soil particles and organisms found within the uppermost millimeters of the soil surface, which consist of cyanobacteria, bacteria, algae, fungi, lichens, liverworts, and mosses (Eldridge and Greene, 1994; Li, 2012). Development of BSCs can roughen the soil surface, improve soil stability and fertility, change soil

hydrological processes, influence the establishment and growth of vascular plants, and supply habitats for other microorganisms and protozoa (Liu et al., 2006; Li et al., 2011; Mendoza-Aguilar et al., 2014). However, poikilohydric organisms are especially resilient to changes in the abiotic conditions, especially those altering the availability of environmental water (Proctor et al., 2007).

It is widely believed that soil physical–chemical properties considerably affect the formation and development of BSCs, and that BSCs in turn affect soil physical–chemical properties—such as soil moisture and nutrient dynamics (Chamizo et al., 2012). Thus, BSCs may not only

Abbreviations: BSCs, biological soil crusts; EC, electric conductivity; SWC, soil water content; SOC, soil organic carbon; TN, total nitrogen; AN, available nitrogen; AP, available phosphorus; AK, available potassium; SMBC, soil microbial biomass carbon; SMBN, soil microbial biomass nitrogen; SMBP, soil microbial biomass phosphorus; ANOVA, analysis of variance

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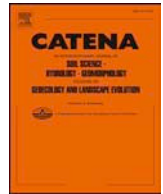
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<https://doi.org/10.1016/j.catena.2018.05.042>

Received 2 February 2018; Received in revised form 9 May 2018; Accepted 29 May 2018

Available online 02 June 2018

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Analysis of changes in characteristics of flood and sediment yield in typical basins of the Yellow River under extreme rainfall events

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ARTICLE INFO

Keywords:

Extreme rainfall
Middle reaches of the Yellow River
Flood waters
Sediment transport
Soil and water conservation

ABSTRACT

The future trend of water and sediment variation is closely related to the governance of the Yellow River. The increasingly frequent occurrence of extreme rainfall events has rendered the future water and sediment situation of the Yellow River uncertain. Understanding the characteristics of flood and sediment yield of the river basin under extreme rainfall conditions at different times is a prerequisite and foundation for accurate prediction of water and sediment situation in the Yellow River in the future period. We here used the July 26 extraordinary rainstorm event in 2017 in the Wuding River as a starting point for revealing the law of flood and sediment yields changes under extreme rainfall conditions around the year 2000. The results indicated that, during the period from 1960 to 2016, the average proportion of extreme rainfall depth in the middle Yellow River region over the total precipitation depth increased by 5.1%. Areas where extreme rainfall events frequently occur showed a trend of developing from localized regions in the Toudaoguai–Longmen reach to the majority of the middle reaches. There were obvious changes in the rainfall–flood and rainfall–sediment relations under extreme rainfall conditions. Compared with historical extreme rainfall events, the decline in flood and sediment yield in the river basin after 2000 under similar rainfall and intensity conditions was obvious. Among these results, flood decreased by 30.4–78.2%, sediment yield was decreased by 53.0–88.2% and sediment content in flood was decreased by > 47.2% on average when compared with the same rainfall conditions in the previous century. Comparative watershed studies showed that, during extreme rainfall events, areas under soil and water loss management programs suffer 57.2% and 75.7% less flood runoff modulus and sediment transport modulus, respectively, than non-managed areas. This indicates that soil and water loss management is the major driving factor for changes in rainfall–flood and rainfall–sediment relations under extreme rainfall conditions. This study highlights the importance of soil and water loss management in the flood control and sediment reduction. We concluded that, with the implementation of soil and water conservation measures, the probability of large flood and sediment events will greatly decrease and the amount of sediment entering the Yellow River under extreme rainfall will further decrease in the next 30 years.

1. Introduction

Global warming and the frequent occurrence of extreme meteorological and hydrological events caused by it results in great impact on society, economy, and ecosystems (Coskun et al., 2010). It has drawn a great deal of attention from various governments and international organizations (Ren et al., 2014; Jiang et al., 2016). This is particularly so for extreme rainfall events because their frequency and intensity

have increased, resulting in changes in flood runoff and serious damages to economic production and people's lives. Due to the severity of extreme rainfall events and the disaster chain it causes, research on its variation characteristics and effects has attracted widespread attention (Huang et al., 2014; Hibino et al., 2016).

The Yellow River being the second largest river in China is famous for its highest sediment content in the world and disastrous floods (Mu, 2010). It only accounts for 2% of the total water volume of China, but

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<https://doi.org/10.1016/j.catena.2019.02.001>

Received 20 June 2018; Received in revised form 22 January 2019; Accepted 3 February 2019

0341-8162/ © 2019 Published by Elsevier B.V.



Contents lists available at ScienceDirect

Animal Feed Science and Technology

journal homepage: www.elsevier.com/locate/anifeedsci

Effect of level of oat hay intake on apparent digestibility, rumen fermentation and urinary purine derivatives in Tibetan and fine-wool sheep

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ARTICLE INFO

Keywords:

Apparent digestibility
Rumen fermentation
Urinary purine derivatives
Tibetan sheep
The Qinghai-Tibetan Plateau

ABSTRACT

Tibetan sheep are indigenous to the Qinghai-Tibetan Plateau and are raised at an altitude between 3000–5000 m. In contrast, the crossbred fine-wool sheep were introduced to the plateau and are raised at an altitude between 2600 to 3500 m. Tibetan sheep graze grassland all year round while fine-wool sheep require feed supplements during the long cold season. Tibetan sheep were able to utilize dietary nutrients more efficiently than fine-wool sheep when offered adequate energy and protein diets. We questioned whether the responses would still favour Tibetan sheep with limited energy and protein intakes, as is often the case on the Qinghai-Tibetan Plateau. To answer this query, apparent nutrients digestibilities, rumen fermentation characteristics and urinary purine derivatives (PD) were compared between Tibetan and fine-wool sheep when fed oat hay at below maintenance levels: 0.3, 0.5, 0.7 and 0.9 voluntary intake. Five wethers of each breed of similar age and body weight (BW) were used in two concurrent 4 × 4 Latin square designs. Dry matter (DM), organic matter (OM) and neutral detergent fiber (NDF) digestibilities were higher in Tibetan than fine-wool sheep ($P < 0.05$), but were not affected by the level of oat hay intake ($P > 0.10$). As feed intake increased, ruminal pH decreased ($P < 0.01$) and total volatile fatty acid (VFA) concentration increased, both linearly ($P < 0.001$). Moreover, ruminal total VFA concentration ($P < 0.05$), ruminal soluble protein nitrogen (N) and saliva urea-N concentrations ($P < 0.01$) were higher in Tibetan than fine-wool sheep. Urinary total PD and its fractions increased linearly with feeding level ($P < 0.01$). Estimated microbial N synthesis was greater in Tibetan than fine-wool sheep ($P < 0.05$) and increased linearly with the level of oat hay intake ($P < 0.001$). It was concluded that both energy and protein metabolism were used more efficiently in Tibetan than in fine-wool sheep when offered below maintenance intakes, which would allow Tibetan sheep to cope better with the harsh, winter foraging conditions of the Qinghai-Tibetan Plateau.

Abbreviations: ADF, acid detergent fiber; ADG, average daily gain; BW, body weight; CP, crude protein; DE, digestible energy; DM, dry matter; N, nitrogen; NDF, neutral detergent fiber; OM, organic matter; PD, purine derivatives; VFA, volatile fatty acid; VI, voluntary intake

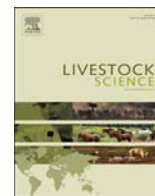
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<https://doi.org/10.1016/j.anifeedsci.2018.04.023>

Received 12 January 2018; Received in revised form 4 April 2018; Accepted 30 April 2018

0377-8401/© 2018 Published by Elsevier B.V.



Apparent digestibility, rumen fermentation, digestive enzymes and urinary purine derivatives in yaks and Qaidam cattle offered forage-concentrate diets differing in nitrogen concentration

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ARTICLE INFO

Keywords:

Apparent digestibility
Rumen fermentation
Urinary purine derivatives
Yak
Qaidam yellow cattle
The Qinghai-Tibetan Plateau

ABSTRACT

Yaks (*Bos grunniens*) and Qaidam yellow cattle (*Bos taurus*) are indigenous to the Qinghai-Tibetan Plateau and graze natural pasture all year. Yaks are raised at higher elevations than cattle and are not offered supplementary feed whereas cattle receive supplementary feed and are sheltered at night during winters. We hypothesized that the species differ in metabolism of energy and nitrogen (N) and predicted that the differences would favour yaks to the harsh conditions of the plateau. To test our prediction, we examined nutrient digestibility, rumen fermentation, digestive enzymes and urinary purine derivatives (PD) in yaks and cattle offered forage-concentrate diets differing in N concentration. Four castrated yaks and 4 castrated cattle of similar ages (2.5 years) and body weights (200 kg) were used in two concurrent 4 × 4 Latin square designs. There was no difference ($P > 0.05$) between yaks and cattle in apparent digestibilities of dietary nutrients, concentrations of ruminal N components and activities of digestive enzymes ($P > 0.05$). Crude protein and acid detergent fiber digestibilities increased linearly ($P < 0.001$) while neutral detergent fiber digestibility decreased linearly ($P < 0.05$) with increased dietary N intake for both species. Ruminal concentration of total VFA was greater in yaks than in cattle across diets ($P < 0.05$), but pH was similar between species ($P > 0.05$), and both variables were not affected by dietary N content ($P > 0.05$). As dietary N increased, ruminal concentrations of ammonia, urea and amino acids increased linearly (all $P < 0.001$), peptides tended to increase ($P < 0.10$), but soluble protein remained constant ($P > 0.10$) for both species. The activity of carboxymethylcellulase decreased linearly ($P < 0.01$) while activities of deaminase and urease increased linearly ($P < 0.001$) with increased dietary N. Urinary PD and components did not differ between species ($P > 0.10$); however, the PD nitrogen index (PNI) was greater in yaks than in cattle for the lowest N diets (linear dietary N × species, $P < 0.01$). With an increase in dietary N, urinary total PD, allantoin and uric acid increased linearly ($P < 0.001$), as did microbial N synthesis ($P < 0.001$), whereas PNI decreased linearly ($P < 0.001$). In addition, microbial N production was greater in yaks than in cattle ($P < 0.05$). We concluded that energy and nitrogen metabolism were more efficient in yaks than in Qaidam cattle, which enable yaks to better cope with the harsh foraging conditions of the Qinghai-Tibetan Plateau.

1. Introduction

The Qinghai-Tibetan Plateau, known as ‘the third pole’ of the earth, possesses the highest (average altitude > 4000 m), the largest (1.29 × 10⁸ ha) and the only year-round grazing alpine grassland in the world

(Long, 2007). Due to the extremely harsh environment, namely high altitude, severe cold, hypoxia, strong ultraviolet light and short forage growing season, feed availability is often deficient for herbivores during the long, cold period of the year (November - June), especially when raised under traditional grazing management (Weiner et al., 2003; Long

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<https://doi.org/10.1016/j.livsci.2017.11.020>

Received 19 April 2017; Received in revised form 21 September 2017; Accepted 28 November 2017

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Effects of lily/maize intercropping on rhizosphere microbial community and yield of *Lilium davidii* var. *unicolor*

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Funding information

Funds for Regional Cooperation of Lanzhou Branch, Chinese Academy of Sciences, Grant number: 2BY52B161; Key Program of Chinese Academy of Sciences, Grant number: KFZD-SW-104-4

Continuous cropping of lily (*Lilium davidii* var. *unicolor*) or any other crop seriously affects yield and quality. In this study, we compared continuous cropping with lily/maize intercropping. We also examined the lily rhizosphere microbes community in both sole lily cropping and lily/maize intercropping systems, by the Illumina Miseq platform. Here we refer to data of recent years field experimentation of a lily/maize intercrop system in different planting configurations in the Gaolan Ecological and Agricultural Research Station. Treatments included sole crops of lily and maize, an intercrop consisting of strips of four lily rows alternating with one maize rows. The land equivalent ratio (LER) of intercrops was 1.294. The results showed that compared to sole cropping, the yield of lily in the first year of planting increased when lily was intercropped with maize. The species annotation of the high-throughput sequencing experiment showed that there was no difference in the diversity of the lily rhizosphere soil microbes on phylum taxonomic level, but the relative abundance of some genus changed obviously. The relative abundance of harmful fungus *Fusarium* spp. and, *Funneliformis* spp., decreased, and the relative abundance of beneficial bacteria *Sphingomonas* spp. and, *Nitrospira* spp., increased. In addition, we found that *Lecanicillium* spp., appeared only in the intercropping lily rhizosphere soil and sole cropping maize rhizosphere soil. In conclusion, the findings indicated that lily/maize intercropping could change soil microenvironment, and affect the diversity and structure of microorganism community in lily rhizosphere, with further beneficial effect on the yield of lily.

KEYWORDS

intercrop, lily, microorganism, rhizosphere, yield

1 | INTRODUCTION

Lily (*Lilium davidii* var. *unicolor*) is the top grade, and the only sweet lily in China. It is renowned at home and abroad because of its large bulbs, white color, and delicate taste. It

has high value in edibility, medicine, health protection, and ornamental. *Lilium davidii* var. *unicolor* is a variant of *Lilium davidii* Duchartre, and is a perennial bulbs herbaceous plant, Its underground stems are stacked together with dozens of scales, its planting in Gansu province began in the Qing Dynasty, has been more than 130 years ago [1]. With the improvement of people's living standards, the increasing demand for edible lilies, especially *Lilium davidii* var.

Lijing Zhou and Yajun Wang contributed equally to this work.

Effects of elevated CO₂, increased nitrogen deposition, and plant diversity on aboveground litter and root decomposition

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Citation: Zuo, X., and J. M. H. Knops. 2018. Effects of elevated CO₂, increased nitrogen deposition, and plant diversity on aboveground litter and root decomposition. *Ecosphere* 9(2):e02111. 10.1002/ecs2.2111

Abstract. Global change-induced litter decomposition strongly affects the carbon (C) and nitrogen (N) dynamics in grassland ecosystems. However, few studies show the interactive effects of global change factors on litter and root decomposition. We conducted a four-year grassland field experiment to examine the quality and decomposition of litter and root in a three-factorial experiment with elevated CO₂, increased N deposition, and plant species richness. We found that elevated CO₂ decreased the litter N content and root lignin content. N addition increased the root N content and decreased the litter lignin content. Increasing plant richness decreased the N and lignin contents in litter and root. In contrast to the quality changes, elevated CO₂ had no effect on decomposition of litter and root. N addition increased the C loss of the litter by 4.8%, but did not affect C and N loss in root. Increasing plant richness affected the C and N loss in litter and root. ANCOVAs showed that tissue quality and root biomass affected the C and N loss in litter and root, and soil C and N affected the N loss of litter and root. However, changes in tissue quality, biomass, and soil as covariates did not significantly change the effects of CO₂, N, and plant richness on decomposition. The structural equation model showed that elevated CO₂ indirectly decreased litter N loss and increased root N loss, while N addition indirectly increased the C and N loss in litter and root, via their effects on tissue quality. Increasing plant richness increased litter C and N loss, but indirectly decreased root C and N loss. N deposition can accelerate litter and root decomposition, thus modifying the limitation of elevated CO₂ on soil N availability. Biodiversity loss greatly alters litter and root decomposition, potentially driving any changes in C and N cycling. Our study clearly demonstrates a relative certainty of a predicted increase in the C loss and N release in litter and root decomposition with increased N deposition, whereas the effects of elevated CO₂ and plant diversity changes on decomposition strongly differ between litter and root in grassland ecosystems.

Key words: biodiversity; decomposition rate; direct or indirect effect; global change; nitrogen addition; tissue quality.

Received 6 January 2018; accepted 10 January 2018. Corresponding Editor: Debra P. C. Peters.

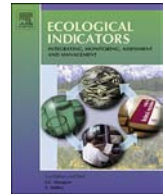
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INTRODUCTION

Litter decomposition may accelerate or decelerate global climate changes, because changes in litter quantity and quality can change both the cycling rates and the pools of carbon (C) and nutrients within an ecosystem (Dijkstra et al. 2004, Sierra et al. 2011, van Groenigen et al. 2014). Litter decomposition in terrestrial ecosystems is

mainly driven by the litter chemical components and climatic factors (Coûteaux et al. 1995, Garcia-Palacios et al. 2013a, 2017). Global climate changes can strongly affect litter decomposition due to the changes in physical decomposition environment induced by temperature or precipitation and the indirect roles through their effects on productivity and litter quality (Zhang et al. 2008, Boyero et al. 2011). Global changes, such as



Effects of plant functional diversity induced by grazing and soil properties on above- and belowground biomass in a semiarid grassland

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ARTICLE INFO

Keywords:

Ecosystem function
Functional trait
Grassland degradation
Structural equation modelling
Horqin grassland

ABSTRACT

The trait-based plant functional diversity is associated with ecosystem functioning. However, few studies show the effects of plant functional diversity induced by grazing disturbance and environmental changes on above-ground plant biomass (AGB) and belowground root biomass (BGB) in semiarid grasslands. We examined the effects of long-term grazing on plant functional diversity across four grassland types (meadow, steppe, scattered tree grassland and sandy grassland) in Horqin grassland, Northern China. The structural equation model (SEM) was used to evaluate the direct or indirect effects of long-term grazing, soil properties and functional diversity reflected by the single-trait (community-weighted mean) and multi-trait (functional dispersion, FDis) on AGB and BGB across four grassland types. We found that long-term grazing significantly decreased plant height and FDis, while the responses of leaf traits to grazing differed among four grassland types. The correlation analyses showed that AGB and BGB were negatively associated with grazing and positively associated with plant height, FDis, soil carbon (C) and nitrogen (N). The SEM results indicated that AGB was directly affected by grazing, soil N, plant height and perennial richness, and BGB was directly affected by grazing, soil N, soil water content and elevation. Grazing and soil N also indirectly affected AGB through their effects on plant height and FDis. Effect of plant height on aboveground plant biomass was direct rather than indirect, while FDis acted indirectly through its effect on perennial richness, thereby lending more support to the mass ratio hypothesis. Our results clearly highlight the critical role of plant functional diversity induced by grazing and soil properties in affecting AGB in a semiarid grassland ecosystem. So, we recommend considering the linkages of plant functional diversity with ecosystem function in assessing the effects of grazing and soil changes on grassland ecosystems.

1. Introduction

Grazing is one of the main drivers of plant community structure and ecosystem function in arid and semiarid grassland ecosystems (Zheng et al., 2010; Wu et al., 2015; Eldridge et al., 2016; Zhang et al., 2017a). Long-term grazing or overgrazing is thought to be an important cause for the grassland degradation (Bai et al., 2012; Li et al., 2011). Long-term grazing can affect plant community compositions by altering the plant functional traits (Niu et al., 2015). Long-term grazing can also result in the greater changes in soil properties (Medina-Roldan et al., 2012; Deng et al., 2017), and changes in soils are likely to induce the coordinate responses of different plant functional traits (Jager et al., 2015). A number of studies have revealed that the trait-based plant functional diversity has a strong effect on plant community assembly and ecosystem function (Lavorel, 2013; Milcu et al., 2016). So, it is

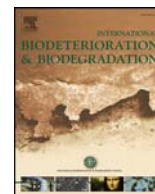
essential to explore the effects of plant functional diversity controlled by long-term grazing and related soil properties on ecosystem functioning, thus giving guidelines for the improvement of grassland management practices.

Numerous studies have reported that long-term grazing decreases the species richness and community biomass in semiarid grasslands (Bai et al., 2012; Zhang et al., 2004). Grazing-induced habitat changes affect plant community compositions by reducing plant diversity or altering dominant species (Kohyani et al., 2011), and changes in community compositions have the direct impacts on aboveground biomass (Eldridge et al., 2016; Milcu et al., 2016). Aboveground plant biomass (AGB) and belowground root biomass (BGB) responses to long-term grazing are very important for understanding the effects of grazing regime on ecosystem function (Zeng et al., 2015). In many grassland ecosystems, there is more biomass in belowground than aboveground

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<https://doi.org/10.1016/j.ecolind.2018.05.032>

Received 12 January 2018; Received in revised form 17 April 2018; Accepted 15 May 2018
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Differences of Microbial Community on the wall paintings preserved *in situ* and *ex situ* of the Tiantishan Grottoes, China

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ARTICLE INFO

Keywords:

Wall paintings
Tiantishan grottoes
Illumina MiSeq sequencing
In-situ & ex-situ conservation
Salvageable conservation

ABSTRACT

Tiantishan Grottoes, a famous site well known for its historical status in the spread of Buddhism art in ancient China, were selected for a comparison and analysis of microbial taxonomic characteristics on the wall paintings under different preservation conditions: *in situ* and *ex situ* conservation. A total of 12 samples were collected from three different cave wall paintings preserved *in situ* or *ex situ*. The 16/18S rRNA gene-based sequences revealed a high bacterial diversity and a relative low fungal abundance, including bacterial groups Firmicutes, Actinobacteria, Proteobacteria, Bacteroidetes, Cyanobacteria, Acidobacteria, Deinococcus-Thermus and Fusobacteria; and fungal groups Ascomycota and Basidiomycota. Among them, two bacterial genera of the *Promicromonospora* and *Planomicrobium* and fungal order of the Sordariales and the family of Trichocomaceae were dominant in the samples preserved *ex situ*. Some of them have been reported at other cultural heritage sites and associated with the biodeterioration of cultural relics. The over-growth of these microbes led to the abundant filaments formed visible on the surface of the *ex situ* wall paintings, which preserved under museum conditions. Application of preservation materials including animal glue and wet gypsum to take them off from grottoes and strengthen, and subsequent long-term preservation under poor conditions in museums were mainly responsible for the microbial outbreaks. To avoid similar problems in the future, reasonable intervention measures and strict micro-environmental control must be implemented to the *ex situ* preservation of wall paintings. Our results have profound significance for clarify the occurrence of microbial invasions and mechanisms on the wall paintings; it is helpful to development a reasonable artificial intervention measures for conservation work of the wall paintings in the future.

1. Introduction

Microorganisms, including bacteria, fungi, archaea and cyanobacteria, are capable of colonizing on surfaces of a wide range of materials and could result in the biodeterioration of the substratum materials, particularly for historical objects exposed to changing environmental conditions, such as temperature, relative humidity, pH and sun light (Miichaelsen et al., 2006). These organisms dwelling on wall paintings may induce aesthetic and structural damage such as pigment discoloration, contamination and biofilm formation on the painted surface leading to cracking and disintegration of paint layers

and degradation of binders resulting in detachment of the painted layer from the underlying support (Capodicasa et al., 2010; Ciferri, 1999; Felice et al., 2010; Pepe et al., 2010). Knowledge about microflora on the historical objects is of utmost importance to assessment and development of effective conservation strategies for management of microbial induced biodeterioration.

Conventionally, culture-dependent method was commonly utilized to isolate and identify the members in the microbial communities, but only less than 1% of the whole population can be detected by the techniques (Schloss and Handelsman, 2003). A vast majority of microorganisms ($\geq 99\%$) in environmental samples cannot be cultured

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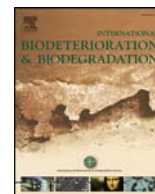
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<https://doi.org/10.1016/j.ibiod.2018.02.013>

Received 26 January 2018; Received in revised form 24 February 2018; Accepted 27 February 2018

Available online 07 April 2018

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Corrigendum

Corrigendum to "Differences of Microbial Community on the wall paintings preserved *in situ* and *ex situ* of the Tiantishan Grottoes, China" [Int. Biodeterior. Biodegrad. 2018 DOI: 10.1016/j.ibiod.2018.02.013]



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Figs. 3B and 4B appear identical in the online publication of this article. The corrected Fig. 4B is shown below.

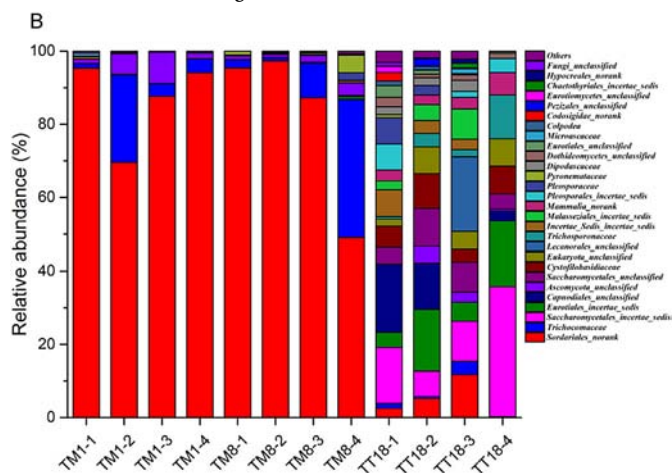


Fig. 4B. Relative abundance of fungal community at the family levels (non-fungal amplicons sequenced were also included).

Additional information for the 18S rDNA high throughput sequences that affiliated to non-fungal Eukaryota

In recent years, the use of high-throughput sequencing technologies with the 16S rRNA gene for characterization of bacterial or archaeal communities has become more popular. However, the adoption of such

techniques for eukaryotes has been relatively slow, despite their significance in both natural and engineered systems. This situation is primarily a result of the large variation in copy numbers of targeted genes among different species, and multiple hypervariable regions that are typically longer than early DNA sequencing platforms could handle (Bradley et al., 2016).

In the article "Differences of Microbial Community on the wall paintings preserved *in situ* and *ex situ* of the Tiantishan Grottoes, China" published on the journal of International Biodeterioration & Biodegradation, we employed a typical fungal primer SSU-0817F, 5'-TTAGCATGGAATAARRAAG-3', and SSU-1196R, 5'-TCTGGACCTG GTGAGTTTCC-3', targeting the V5-V7 regions of the 18S rRNA genes. These primers were chosen as they flank a conserved region of the 18S gene that differs among fungal families, but they are similar enough to be aligned in multiple sequence alignments. This 18S region is often considered to be more conserved than the ITS regions; the use of 18S region may lower diversity estimates and make the obtained data to be at the family level (Kivlin et al., 2014). Thus, the universal primers 817F/1196R for fungi was used for the amplification and then MiSeq sequencing of the PCR products in our research.

Of course, many reports show that it also has a slightly but inevitable weakness for successful detection of fungi. Our results show that the most of the reads belonged to the fungal phyla of Ascomycota (197,465, 90.45% for reads and relative abundance, respectively) and Basidiomycota (11,289, 5.17%). Meanwhile, very tiny fractions of reads were classified as non-fungal Eukaryota, but they are typically detected at relatively low abundances (ca. 2.73%); most of them were affiliated with the Vertebrata, Ciliophora, Arthropoda and Bicosoecida (Duan

DOI of original article: <https://doi.org/10.1016/j.ibiod.2018.02.013>

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<https://doi.org/10.1016/j.ibiod.2018.05.004>

Received 4 May 2018; Accepted 5 May 2018

Available online 08 August 2018

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Citation: Huang WD, Zhao XY, Li YL, *et al.*, 2018. Relationship between the haplotype distribution of *Artemisia halodendron* (Asteraceae) and hydrothermal regions in Horqin Sandy Land, northern China. *Sciences in Cold and Arid Regions*, 10(2): 0151–0158. DOI: 10.3724/SP.J.1226.2018.00151.

Relationship between the haplotype distribution of *Artemisia halodendron* (Asteraceae) and hydrothermal regions in Horqin Sandy Land, northern China

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Received: March 15, 2017 Accepted: July 29, 2017

ABSTRACT

The genetic diversity of *Artemisia halodendron* (Asteraceae), a constructive and dominant species in Horqin Sandy Land, was investigated to examine the genetic relationships with different hydrothermal regions in Horqin Sandy Land. We sequenced chloroplast DNA (cpDNA) fragments (*trnL-F*) of 243 plants from 10 populations across the Horqin Sandy Land. The analyses of cpDNA variation identified seven haplotypes. A low level of haplotype diversity ($H_d=0.706$) and nucleotide diversity ($\pi=0.0013$) was detected. Haplotypes clustered into two tentative clades. Low genetic differentiation among regions was consistently indicated by hierarchical analyses of molecular variance (AMOVA). Across the sampled populations, the haplotype distributions were differentiated with hydrothermal gradients.

Keywords: *Artemisia halodendron*; population genetics; chloroplast DNA; *trnL-F*; Horqin Sandy Land

1 Introduction

Artemisia halodendron Turcz. ex Bess. (Asteraceae, Anthemideae, Subgen. *Dracunculus*) is one of the most common semishrub species in the Horqin Sandy Land in Northeast China. It is important for vegetation rehabilitation in Horqin Sandy Land because of its high ecological value, including that (1) it is the key species of the plant communities and landscapes studies in Horqin Sandy Land (Li, 1991); (2) it plays a key role in the vegetation-restoration process due to

its high drought tolerance, anti-wind erosion properties, and sand-burial resistance (Dong *et al.*, 2000; Li *et al.*, 2002; Zhao *et al.*, 2006). Previous studies on *A. halodendron* focused on aspects of population-distribution patterns (Chao *et al.*, 1999; Cao *et al.*, 2008), biomass allocation (Li *et al.*, 2005), breeding distribution (Li *et al.*, 2005), morphological characteristics and physiological adaptations (Zhou *et al.*, 1999), root longevity (Huang *et al.*, 2009), genetic diversity (Huang *et al.*, 2011, 2014), and establishment (Li *et al.*, 2002) in Horqin Sandy Land. However, systemat-



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Sciences in Cold and Arid Regions

Volume 10, Issue 2, April, 2018



Citation: Hua CP, Wang YJ, Xie ZK, *et al.*, 2018. Effects of intercropping on rhizosphere soil microorganisms and root exudates of Lanzhou lily (*Lilium davidii* var. *unicolor*). *Sciences in Cold and Arid Regions*, 10(2): 0159–0168. DOI: 10.3724/SP.J.1226.2018.00159.

Effects of intercropping on rhizosphere soil microorganisms and root exudates of Lanzhou lily (*Lilium davidii* var. *unicolor*)

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Received: May 8, 2017 Accepted: July 21, 2017

ABSTRACT

Both yield and quality of Lanzhou lily (*Lilium davidii* var. *unicolor*) are seriously affected by continuous cropping. We attempted to understand the effects of intercropping on the obstacles associated with continuous cropping of Lanzhou lily (*Lilium davidii* var. *unicolor*). The changes of rhizosphere microbial biomass and diversity in interplanting and monoculturing systems were studied by using the Illumina HiSeq sequencing technique. The contents and composition of lily root exudates were measured by gas chromatography–mass spectrometer (GC–MS). The intercropping results of Lanzhou lily showed: (1) There was no difference in the composition of the rhizosphere soil microbes at the phylum level, but the relative abundance of the microbes decreased; and the relative abundance of harmful fungi such as *Fusarium sp.* increased. The relative abundance of *Pleosporales sp.* and other beneficial bacteria were reduced. After OTU (operational taxonomic unit) clustering, there were some beneficial bacteria, such as *Chaetomium sp.*, in the lily rhizosphere soil in the interplanting system that had not existed in the single-cropping system. We did not find harmful bacteria that had existed in the single-cropping system in the rhizosphere soil of interplanting system. The above results indicated that the changes of relative abundance of soil fungi and bacteria in lily rhizosphere soil was not conducive to improving the ecological structure of rhizosphere soil microbes. At the same time, the microbial composition change is very complex—beneficial and yet inadequate at the same time. (2) Root exudates provide a matrix for the growth of microorganisms. Combined with the detection of root exudates, the decrease in the composition of the root exudates of the lily was probably the reason for the decrease of the relative abundance of microbes after intercropping. At the same time, the decrease of the relative content of phenolic compounds, which inhibit the growth of microorganisms, did not increase the relative content of rhizosphere soil microorganisms. Changes in amino acids and total sugars may be responsible for the growth of *Fusarium sp.*. The results showed that the intercropping pattern did not noticeably alleviate the obstacle to continuous cropping of Lanzhou lily, and the change of microbial biomass and diversity was even unfavorable. However, the emergence of some beneficial bacteria, the disappearance of harmful fungi, and other changes with intercropping are in favor of alleviation of obstacles to continuous cropping of Lanzhou lily.

Keywords: continuous cropping obstacle; Lanzhou lily (*Lilium davidii* var. *unicolor*); rhizosphere microbial

1 Introduction

The soil-related obstacles to continuous cropping

of economic crops have a negative impact on the yield and quality of crops. Lanzhou lily is a variant of *Lilium davidii* Duchartre, a perennial herbaceous bulb plant.



Plant diversity enhances productivity and soil carbon storage

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Edited by Susan E. Trumbore, Max Planck Institute for Biogeochemistry, Jena, Germany, and approved September 20, 2017 (received for review February 15, 2017)

Despite evidence from experimental grasslands that plant diversity increases biomass production and soil organic carbon (SOC) storage, it remains unclear whether this is true in natural ecosystems, especially under climatic variations and human disturbances. Based on field observations from 6,098 forest, shrubland, and grassland sites across China and predictions from an integrative model combining multiple theories, we systematically examined the direct effects of climate, soils, and human impacts on SOC storage versus the indirect effects mediated by species richness (SR), aboveground net primary productivity (ANPP), and belowground biomass (BB). We found that favorable climates (high temperature and precipitation) had a consistent negative effect on SOC storage in forests and shrublands, but not in grasslands. Climate favorability, particularly high precipitation, was associated with both higher SR and higher BB, which had consistent positive effects on SOC storage, thus offsetting the direct negative effect of favorable climate on SOC. The indirect effects of climate on SOC storage depended on the relationships of SR with ANPP and BB, which were consistently positive in all biome types. In addition, human disturbance and soil pH had both direct and indirect effects on SOC storage, with the indirect effects mediated by changes in SR, ANPP, and BB. High soil pH had a consistently negative effect on SOC storage. Our findings have important implications for improving global carbon cycling models and ecosystem management: Maintaining high levels of diversity can enhance soil carbon sequestration and help sustain the benefits of plant diversity and productivity.

soil carbon storage | species richness | aboveground net primary productivity | belowground biomass | human disturbance

Soils represent the largest carbon stocks in Earth's terrestrial ecosystems, and compelling evidence indicates that large amounts of soil carbon in natural ecosystems have been lost in recent decades because of the effects of climate change and human disturbance (1–3). Therefore, soil carbon sequestration plays an important role in mitigating the positive feedback between terrestrial carbon and climate (2, 4). A central issue to understanding the mechanisms controlling soil carbon sequestration and a much-debated subject is how plant diversity and productivity are related to soil carbon storage (5, 6). Soil organic carbon (SOC) storage, in general, represents the balance of two main processes: carbon inputs (e.g., net carbon gain by plants) and losses (e.g., microbial decomposition) (2, 5, 7). Theoretical and experimental studies suggest

that biodiversity has the potential to influence ecosystem carbon sequestration by modifying both processes (7–9). Recent experimental studies at small spatial scales have shown that high plant diversity increases SOC storage by elevating carbon inputs (particularly belowground carbon inputs) and increasing soil microbial community diversity and activity, and/or by suppressing carbon losses from decomposition (6, 10). However, many studies at large spatial scales have reported that the patterns of SOC storage are controlled by climate, vegetation, and soil conditions (11–13). Thus, it remains unclear whether plant diversity has important positive effects on

Significance

Soil carbon sequestration plays an important role in mitigating anthropogenic increases in atmospheric CO₂ concentrations. Recent studies have shown that biodiversity increases soil organic carbon (SOC) storage in experimental grasslands. However, the effects of species diversity on SOC storage in natural ecosystems have rarely been studied, and the potential mechanisms are yet to be understood. The results presented here show that favorable climate conditions, particularly high precipitation, tend to increase both species richness and belowground biomass, which had a consistent positive effect on SOC storage in forests, shrublands, and grasslands. Nitrogen deposition and soil pH generally have a direct negative effect on SOC storage. Ecosystem management that maintains high levels of plant diversity can enhance SOC storage and other ecosystem services that depend on plant diversity.

Author contributions: Y.B. designed research; Y.B. served as principal investigator (PI) of the grassland ecosystem carbon project; S.C., Yang Wang, H.W., D.Z., Z.S., J.H., J.-S.H., Yanfen Wang, J.S., L.T., X.L., M.D., and Yan Wu contributed data collection for grassland ecosystems; G.Z. served as PI of the forest ecosystem carbon project, and provided data collection for forest ecosystems; Z.X. and Z.T. served as PIs of the shrubland ecosystem carbon project, and provided data collection for shrubland ecosystems; S.C., W.W., W.X., Yang Wang, H.W., D.C., Z.W., and Y.B. analyzed data; and S.C., J.W., F.S.C., and Y.B. wrote the paper.

The authors declare no conflict of interest.

This article is a PNAS Direct Submission.

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¹S.C., W.W., W.X., Yang Wang, and H.W. contributed equally to this work.


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This article contains supporting information online at www.pnas.org/lookup/suppl/doi:10.1073/pnas.1700298114/-DCSupplemental.

Published online April 16, 2018.

LETTER

Shifts in the dynamics of productivity signal ecosystem state transitions at the biome-scale

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 Alan K. Knapp,⁵ Philippe Ciais,⁶
 Xinrong Li⁷ and Guirui Yu^{2,3}

Abstract

Understanding ecosystem dynamics and predicting directional changes in ecosystem in response to global changes are ongoing challenges in ecology. Here we present a framework that links productivity dynamics and ecosystem state transitions based on a spatially continuous dataset of above-ground net primary productivity (ANPP) from the temperate grassland of China. Across a regional precipitation gradient, we quantified spatial patterns in ANPP dynamics (variability, asymmetry and sensitivity to rainfall) and related these to transitions from desert to semi-arid to mesic steppe. We show that these three indices of ANPP dynamics displayed distinct spatial patterns, with peaks signalling transitions between grassland types. Thus, monitoring shifts in ANPP dynamics has the potential for predicting ecosystem state transitions in the future. Current ecosystem models fail to capture these dynamics, highlighting the need to incorporate more nuanced ecological controls of productivity in models to forecast future ecosystem shifts.

Keywords

Climate change, grassland, resilience, state transition, tipping point, variability.

Ecology Letters (2018)

INTRODUCTION

With rapidly increasing global environmental changes, ecosystems are at risk of shifts in structural and functional states (Lenton 2011; IPCC 2014). Such changes may negatively impact ecosystem services and thus, human well-being (Costanza *et al.* 1998). System dynamics theory predicts that as an ecosystem approaches an alternative state (or tipping point), recovery from perturbations require more time (van Nes & Scheffer 2007). This phenomenon, known as a critical slowing down (CSD), leads to increased temporal autocorrelation, skewness and variability in state and functional variables prior to the system undergoing a regime shift (Scheffer *et al.* 2009). These statistical indicators have been argued to be useful proxies of system resilience and thus can serve as early warning signals of transitions (Scheffer *et al.* 2009; Dakos *et al.* 2012). Examples of these indicators predicting regime shifts have been documented for lake eutrophication (Dakos *et al.* 2010; Donangelo *et al.* 2010; Wang *et al.* 2012), reductions in marine fish populations (Litzow *et al.* 2008; Carpenter *et al.* 2011; Batt *et al.* 2013; Cline *et al.* 2014) and the collapse of coral reef ecosystems (Fung *et al.* 2013; Hughes *et al.* 2013; van Woesik 2013). However, with the exceptions of a few

studies in deserts (Rietkerk *et al.* 2004; Kefi *et al.* 2007), studies that link these CSD-based indicators to state transitions in terrestrial ecosystems are rare (e.g. Eby *et al.* 2017).

Net primary productivity (NPP), as a core ecosystem function, determines energy flow and mediates biogeochemical cycles within ecosystems (McNaughton *et al.* 1989; Chase *et al.* 2000). Furthermore, understanding determinants of the dynamics of NPP [e.g. interannual variability (IAV), climatic sensitivity, asymmetric response to climate fluctuations] has been a longstanding goal of ecosystem ecology. These indices of NPP dynamics have also been used as indicators of ecosystem stability and more broadly of resilience, reflecting the vulnerability of ecosystems to global change drivers (Isbell *et al.* 2009; Seddon *et al.* 2016; Smith *et al.* 2017). For example IAV of productivity has been studied at regional and global scales to quantify ecosystem responses to climatic variability (Knapp *et al.* 2002; Zscheischler *et al.* 2014; Gherardi & Sala 2015; Xia *et al.* 2015; Niu *et al.* 2017). Similarly, asymmetry in responses of NPP to precipitation variability and shifts in the sensitivity of NPP to climate, have been used to investigate ecosystem responses to changes in precipitation regimes (Knapp & Smith 2001; Huxman *et al.* 2004; Wang *et al.* 2014; Seddon *et al.* 2016; Haverd *et al.* 2017; Knapp *et al.* 2017;

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基于无人机可见光波段对荒漠植被覆盖度提取的研究——以沙坡头地区为例

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摘要: 以腾格里沙漠东南缘沙坡头地区为研究区域, 采用无人机(Phantom 3A)拍摄获取指定范围可见光影像, 通过ENVI软件分析照片的红、绿、蓝信息进行植被指数的提取和植被覆盖度的计算, 主要分析了可见光波段差异植被指数、归一化绿化差异指数、归一化绿蓝差异指数、过绿指数、红绿比值指数与研究区荒漠植被覆盖度回归模型, 探究最优反演模型, 目的是验证在相同区域、相同时间拍摄的无人机影像的植被覆盖度. 计算出来的植被覆盖度和无人机航片的处理方法进行比对, 验证反演模型的正确性. 结果表明: 通过无人机可见光波段提取的植被指数结果中可见光波段差异植被指数的提取精度最好, 能很好的将植被与非植被区分, 为荒漠植被覆盖度和植被指数的反演模型的验证提供了依据, 节约了实地测量带来的时间和人力成本. 对比研究植被指数和荒漠植被覆盖度的线性、对数、三次、乘幂、增长及指数的回归模型结果, 最优的荒漠植被覆盖度的反演模型是可见光波段差异植被指数的三次模型, 为 $y = -200.06x^3 + 706.763x^2 - 430.779x + 17.916$, 能很好地监测荒漠植被覆盖度的动态变化, 为今后荒漠生态系统的防护和管理提供较好的技术支持.

关键词: 无人机; 荒漠生态系统; 植被指数; 植被覆盖度; 反演模型

中图分类号: TP722.4; Q151.94 **文献标识码:** A **文章编号:** 0455-2059(2018)06-0001-06

DOI: 10.13885/j.issn.0455-2059.2018.06.001

Extraction of desert vegetation coverage based on visible light band information of unmanned aerial vehicle: a case study of Shapotou region

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Abstract: On the edge of the southeast Tengger Desert, visible-light images were collected by using unmanned aerial vehicle (Phantom 3 advanced). Based on ENVI software, red, green, and blue band infor-

收稿日期: 2017-09-11 **修回日期:** 2017-11-23

基金项目: 国家自然科学基金项目(41671103)

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沙质草地生长季土壤 CO₂ 排放特征及水热因子分析

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摘要: 草地土壤 CO₂ 排放是陆地生态系统碳循环的关键生态学过程之一, 研究其通量特征可以定量评估和预测区域 CO₂ 排放状况, 服务于全球气候变化下的区域碳管理。应用 LI-8150 土壤碳通量测定系统, 定位观测并分析科尔沁沙地沙质草地生长季(6—9月)土壤 CO₂ 通量特征, 探究水热因子(降水、土壤温度和土壤含水量)对碳排放的影响机制。结果表明, (1) 在日动态变化尺度上, 晴天和雨天土壤 CO₂ 通量呈现不对称“单峰型”曲线, 最高值出现在 11:00—16:00, 最低值在 04:00—06:00。(2) 在生长季动态变化尺度上, 土壤 CO₂ 日平均通量呈现明显的多峰和季节变化, 土壤 CO₂ 月平均日通量分别在 7 月和 9 月出现高峰值和低峰值; 2016 年 6 月 1 日—9 月 30 日日平均排放通量最小值(0.35 μmol·m⁻²·s⁻¹) 出现在晴天(6 月 8 日), 最大值(2.68 μmol·m⁻²·s⁻¹) 出现在雨天(7 月 23 日), 生长季平均排放通量为 1.26 μmol·m⁻²·s⁻¹。(3) 土壤 CO₂ 通量表现为雨天高于晴天, 降水事件是扰动土壤 CO₂ 排放的关键因子。(4) 土壤 CO₂ 通量与土壤温度和土壤含水量分别表现出不同的时间尺度效应。在日尺度上, 无论晴天还是雨天, 7 月土壤 CO₂ 月平均日通量与表层(5 cm)土壤温度和含水量均呈正相关关系, 且相关系数高于其他月份; 晴天和雨天土壤含水量和温度的协同作用分别可解释土壤 CO₂ 排放的 95.0% 和 85.5%。在生长季尺度上, 晴天的土壤含水量和雨天的土壤温度分别能够解释土壤 CO₂ 排放的 63.6% 和 48.0%; 当土壤含水量低于 4.87%、土壤温度低于 25.94 °C 时, 土壤 CO₂ 排放量随含水量、温度的增加而增加; 晴天和雨天土壤含水量和温度的协同作用分别可解释土壤 CO₂ 排放的 61.6% 和 43.7%。

关键词: 沙质草地; 生长季; 土壤 CO₂ 通量; 土壤含水量; 土壤温度

DOI: 10.16258/j.cnki.1674-5906.2018.04.006

中图分类号: S153; X144; S812.2

文献标志码: A

文章编号: 1674-5906(2018)04-0634-09

引用格式: 龚相文, 李玉强, 王旭洋, 牛亚毅, 连杰, 罗永清. 2018. 沙质草地生长季土壤 CO₂ 排放特征及水热因子分析[J]. 生态环境学报, 27(4): 634-642.

GONG Xiangwen, LI Yuqiang, WANG Xuyang, NIU Yayi, LIAN Jie, LUO Yongqing. 2018. Characteristics of soil CO₂ emission in relation to hydrothermal factors during the growing season in Horqin sandy Land [J]. Ecology and Environmental Sciences, 27(4): 634-642.

土壤向大气排放 CO₂ 的过程, 是土壤将植物固定的碳释放回大气的主要途径 (Schlesinger et al., 2000; Ma et al., 2017)。土壤每年产生的碳 (C) 排放约 50~75 Pg (Wang et al., 2009), 超过全球陆地生态系统净初级生产力和化石燃料等燃烧排放 CO₂ 的量, 其变化可能对全球碳平衡和气候变化方面等产生重要的影响 (周萍等, 2009)。因此, 土壤 CO₂ 排放过程已被用于表征陆地生态系统过程和研究全球气候变化的关键生态过程 (王新源等, 2012)。草地生态系统是地球上广泛分布的全球陆地生态系统之一, 在全球碳循环中至关重要 (李学斌等, 2014; Wang et al., 2016)。目前, 国际上有关草地生态系统土壤 CO₂ 排放的研究主要集中在北美温带草原 (Frank, 2002; Huxman et al., 2004;

Peri et al., 2015) 和澳大利亚热带草原等 (Hunt et al., 2002; Fan et al., 2015)。虽然中国学者在研究草地碳库及其动态变化方面已有大量的工作, 但仍然缺乏对草地碳库动态特征的全面认识 (方精云等, 2010)。中国草地土壤 CO₂ 排放研究主要集中在青藏高原的高寒草甸生态系统 (吴琴等, 2005; 白炜等, 2011; 黄晓宇等, 2016; 柴曦等, 2017)、祁连山高山草甸生态系统 (常宗强等, 2007; 魏巍等, 2015; 解欢欢等, 2016)、贝加尔针茅草原 (张盼弟等, 2014)、内蒙古典型草原 (齐玉春等, 2005) 和内蒙古锡林河流域草地 (李明峰等, 2003; 王风玉等, 2003; 齐玉春等, 2010) 等生态系统, 而针对沙质草地土壤 CO₂ 排放的研究相对较少 (于占源等, 2006; 韩春雪等, 2017)。精确量

基金项目: 中国科学院“百人计划”项目 (Y551821); 国家重点研发计划项目 (2016YFC0500901); 国家自然科学基金项目 (31640012; 31560161; 31500369)

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收稿日期: 2017-11-09

DOI:10.11829/j.issn.1001-0629.2018-0272

龚相文,李玉强,王旭洋,牛亚毅,连杰,罗永清,余沛东.科尔沁地区植被净初级生产力时空动态特征.草业科学,2018,35(10):2306-2317.

GONG X W, LI Y Q, WANG X Y, NIU Y Y, LIAN J, LUO Y Q, YU P D. Temporal-spatial dynamic changes of net primary productivity in Horqin region, China. Pratacultural Science, 2018, 35(10): 2306-2317.



科尔沁地区植被净初级生产力 时空动态特征

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摘要:植被净初级生产力(NPP)是碳收支平衡和气候变化的核心内容之一。本研究基于 NPP、气象(气温和降水)和植被类型数据,采用趋势分析、偏相关和回归分析法对 2000—2010 年科尔沁地区 NPP 时空格局演变及其气象因子进行分析。结果表明,2000—2010 年科尔沁地区植被 NPP 年均值为 $121.32 \text{ g} \cdot (\text{m}^2 \cdot \text{a})^{-1}$,增加速率为 $0.53 \text{ g} \cdot (\text{m}^2 \cdot \text{a})^{-1}$,呈增加趋势的面积占总区域的 48.77%,其中 NPP 增加的区域主要集中在科尔沁区 [$7.46 \text{ g} \cdot (\text{m}^2 \cdot \text{a})^{-1}$]、库伦旗 [$5.09 \text{ g} \cdot (\text{m}^2 \cdot \text{a})^{-1}$]等地,减少区域主要集中在巴林左旗 [$-4.64 \text{ g} \cdot (\text{m}^2 \cdot \text{a})^{-1}$]、巴林右旗 [$-3.53 \text{ g} \cdot (\text{m}^2 \cdot \text{a})^{-1}$]等县域。不同植被的固碳能力存在差异,其中阔叶林最强,栽培植被次之,灌丛最弱。植被 NPP 受降水量的影响高于气温,降水和气温协同作用的解释率高于单一因子,分别可解释草甸、阔叶林、草原、栽培植被和灌丛的 94.70%、87.50%、85.80%、85.30%和 76.30%。因此,降水和气温的协同作用对 NPP 变化的影响不容忽视。

关键词:净初级生产力;时空特征;趋势分析;偏相关分析;降水;气温;科尔沁地区

中图分类号:S181.1;F323.6 文献标志码:A 文章编号:1001-0629(2018)10-2306-12*

Temporal-spatial dynamic changes of net primary productivity in Horqin region, China

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Abstract: Net primary productivity (NPP) is one of the key areas in research on regional carbon budget and climate change. Based on NPP, vegetation type maps and meteorological data (air temperature and precipitation), evolution of spatio-temporal patterns of NPP, and driving factors in Horqin region from 2000 to 2010 were analyzed using trend analysis, partial correlation analysis, and regression analysis. The results showed that the average annual NPP of Horqin region from 2000 to 2010 was $121.32 \text{ g} \cdot (\text{m}^2 \cdot \text{a})^{-1}$, and increased at a rate of $0.53 \text{ g} \cdot (\text{m}^2 \cdot \text{a})^{-1}$ in an area covering 48.77% of the region. The areas in which NPP increased were mainly located in Horqin district [$7.46 \text{ g} \cdot (\text{m}^2 \cdot \text{a})^{-1}$] and Kulun [$5.09 \text{ g} \cdot (\text{m}^2 \cdot \text{a})^{-1}$], and areas with decreasing NPP

* 收稿日期:2018-05-02 接受日期:2018-07-27

基金项目:中国科学院百人计划项目(Y551821);国家重点研发计划(2016YFC0500901);国家自然科学基金(31560161,31500369)

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黄土高原不同种植年限苜蓿地土壤酶活性的季节性变化研究

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摘要:研究黄土高原长期种植紫花苜蓿地的土壤酶活性季节性变化,同时测定紫花苜蓿种植1、2、4、11和16年土壤中的脲酶、碱性磷酸酶、蔗糖酶和过氧化氢酶的活性。结果表明:土壤脲酶、碱性磷酸酶、过氧化氢酶和蔗糖酶的活性受到紫花苜蓿的种植年限、季节和土层深度的影响。不同种植年限紫花苜蓿地土壤酶活性与季节呈显著相关,土壤脲酶和碱性磷酸酶的活性表现为6月较高,蔗糖酶活性3月较高,而过氧化氢酶活性差异不显著。紫花苜蓿地土壤酶活性具表层富集性,在0~5 cm土层中脲酶、蔗糖酶和磷酸酶活性高于5~10 cm土层的1~3倍,而过氧化氢酶活性在土层之间差异不显著。种植4年紫花苜蓿地土壤酶活性较高,种植11、16年的土壤酶活性显著下降。可见,种植紫花苜蓿达10年以上土壤酶活性下降明显,需加强人工牧草地管理。

关键词:紫花苜蓿;土壤酶活性;种植年限;季节变化;土层深度

中图分类号:S 154.2;S 541 文献标志码:A 文章编号:1009-5500(2018)05-0059-06

DOI:10.13817/j.cnki.cyyep.2018.05.010

紫花苜蓿(*Medicago sativa*)是一种高产、生存力极强的多年生豆科牧草。长期种植苜蓿可改善土壤结构、增强土壤肥力,尤其是对黄土高原的生态修复以及畜牧业发展具有重要意义^[1]。土壤酶作为土壤中最活跃的成分之一,是土壤有机体的代谢动力,在土壤生态系统的物质循环和能量流动方面扮演着重要的角色^[2-4]。土壤酶主要来源于土壤中动植物残体分解、植物根系分泌以及土壤微生物的释放,土壤酶活性是评价土壤肥力和土壤质量的重要生物学指标^[5-7]。黄土高原是水土流失最严重和生态环境最脆弱的地区之一,也是我国畜牧业生产、生态安全保障的重点区域。虽已开展了盐碱草地^[8]、退耕草地^[9]、荒漠盐生植被和

丘陵坡地植被^[10-11]的土壤酶活性变化研究,但黄土高原牧草地土壤酶活性变化的研究较少^[12],因此,研究黄土高原长期种植紫花苜蓿地的土壤酶活性变化,可为黄土高原科学种植紫花苜蓿提供参考。

1 材料和方法

1.1 试验区概况

试验地设在农业部兰州黄土高原生态环境重点野外科学观测试验站,位于N 36°01', E 103°45',海拔1 750 m。年均降水量324 mm,主要集中在6~9月,年均蒸发量1 450 mm,日照时间2 750 h,年均气温9.4℃,≥0℃的活动积温为3 700℃。试验站种植有苜蓿、柠条等多种优质牧草,已成为我国草业、畜牧等综合性试验基地。该试验区属黄土高原半干旱丘陵沟壑区,土壤为灰钙土,试验地土壤基本养分见表1。

1.2 试验处理

在2016年3、6、9和12月选取试验站内种植1、2、4、11和16年的紫花苜蓿地作为试验处理,分0~5 cm和5~10 cm土层进行土壤样品的采集。每层土样均按“S”形采集5个点的混合样,将土样带回实验室4℃

收稿日期:2018-03-02; 修回日期:2018-05-21

基金项目:甘肃农业大学科技创新基金(GSAUXKJS-2018209);国家自然科学基金(41671103)资助

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甘肃河西干旱区温室葡萄对地表覆盖的响应

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摘要: 试验了温室葡萄超氧化物歧化酶(SOD)活性、过氧化氢酶(CAT)活性、游离脯氨酸(Pro)含量、丙二醛(MDA)含量和果粒生长对地表覆盖的响应。结果表明:整个生育期内,砂土覆盖、秸秆覆盖、秸秆+白地膜覆盖及秸秆+黑地膜覆盖都对0~40 cm 土层土壤有显著的保水作用,其中秸秆+黑地膜保水性能最强(土壤含水量比无覆盖的提高14.53%, $P < 0.05$),且各覆盖方式的保水能力随着土层的加深而增强。秸秆+白地膜覆盖下葡萄细胞的抗氧化酶活性最高。砂土覆盖极显著($P < 0.01$)提高果粒内Pro含量(约增加42.40%)。砂土覆盖后葡萄果粒粒径最大,秸秆+地膜覆盖、秸秆覆盖下的果粒粒径均小于无覆盖的粒径。秸秆覆盖能够提高土壤水分含量,抑制果粒的增长。砂土覆盖可以作为温室葡萄适宜覆盖方式。

关键词: 葡萄; 地表覆盖; 生理指标; 保水性; 抗逆性

文章编号: 1000-694X(2018)05-1049-10

DOI: 10.7522/j.issn.1000-694X.2017.00055

中图分类号: Q945.79

文献标志码: A

0 引言

西北干旱地区土壤水分相对缺乏,是影响经济植物生长及产量形成的关键环境因素^[1-2]。地表覆盖技术能显著改善土壤水热效应,创造有利于植物生长的环境条件^[3-4],明显提高植物抗旱性能,被广泛使用。当前主要推广的有地膜、秸秆及砂土覆盖等^[5-8]。单一地表覆盖(地膜、秸秆、砂土覆盖)及双重覆盖(地膜+秸秆覆盖)均能在一定程度上起到保墒、保温、保肥、增产功效^[9-13]。有关地表覆盖研究的报道,多在影响土壤水分^[14]、土壤肥力^[15]、土壤温度^[16]、生长与产量效应^[17]等方面。土壤水分活跃层主要在0~40 cm^[18],地表覆盖能够提高0~40 cm 内的土壤水分含量和土壤日最低温度,降低土壤日最高温度和日平均温度^[19],增加土壤中的速效磷及速效钾含量,保持土壤的湿度,从而促进土壤理化性质的改变,改善土壤的质量和生产力^[20]。地表覆盖通过对土壤水分、温度和土壤理化性状的影响,显著促进了植物的生长发育^[21-22],最终提升了植物的产量^[23]。地表覆盖的效果会受到覆盖时间的影响,在土地休闲期进行地膜覆盖后,土壤蓄水量比播种前30 d 覆盖的和播

种时覆盖的分别提高了87%和28%^[24],更加有利于保墒和植物的生长。地膜覆盖中,地膜的颜色更是不可忽视的因素。与黑色和白色地膜相比,红色地膜覆盖更能显著促进植物的生殖生长,提高植物质量^[25]。

超氧化物歧化酶(SOD)和过氧化氢酶(CAT)是植物体内关键抗氧化酶。SOD通过歧化反应将超氧自由基转化为 H_2O_2 来保护细胞质膜免受活性氧自由基的伤害^[26-27]。CAT通过清除过量 H_2O_2 来保护细胞质膜系统的分解酶^[28-29]。植物遭受干旱胁迫时体内SOD、CAT活性提高^[30-31]。抗旱性强的品种,保护酶活性也较高^[32-33]。游离脯氨酸(Pro)的累积,有利于维持细胞较高的渗透势,增强细胞吸水能力,保证植物的抗逆性,也可以作为碳源和氮源,为处于逆境胁迫中的植物在压力解除后的细胞恢复提供一定的能量^[34-36]。但是,Pro在降解过程中也会产生有毒物质^[37]。逆境胁迫程度较低时,植物叶片内的保护酶活性高,能够将体内的自由基清除。但是当胁迫程度超过保护酶系统的有限防御能力时,植物体内抗氧化酶活性不再维持较高水平,膜脂过氧化作用加强,细胞质膜受损,导致丙二醛(MDA)增多^[38]。因此,对于上述生理指标的研

收稿日期:2017-02-05; 改回日期:2017-06-05

资助项目:中国科学院战略性先导科技专项(XDA0505201-04-01); 国家自然科学基金项目(41371053)

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红砂(*Reaumuria soongorica*)、珍珠(*Salsola passerina*)蒸腾耗水规律的尺度整合

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摘要: 利用 LI-6400XT 便携式光合仪和大型称重式蒸渗仪研究红砂(*Reaumuria soongorica*)、珍珠(*Salsola passerina*)灌丛在干旱和湿润条件下的蒸腾耗水特征,并探讨从叶片到灌丛尺度转换中,在非破损状态下植物叶面积的可靠测定方法。结果表明:用图像法获得非破损状态下植物叶面积是可行的,基于植物叶面积通过尺度转换得到灌丛尺度的蒸腾量与蒸渗仪测定的蒸腾量具有较高一致性($r=0.9752, P<0.01$)。干旱条件下,红砂蒸腾速率的日变化呈单峰曲线,主要影响因素为气孔导度($P<0.01$);湿润条件下,红砂和珍珠蒸腾速率的日变化均呈单峰曲线,主要的影响因素为气孔导度、空气相对湿度、饱和蒸汽压亏缺和光合有效辐射($P<0.01$)。珍珠水分利用效率和气孔限制值均高于红砂。此外,干旱条件下红砂的水分利用效率和气孔限制均高于湿润条件。通过尺度转换得到的灌丛尺度的蒸腾量和蒸渗仪测定的蒸腾量的结果均表明,红砂的蒸腾量始终大于珍珠,且随土壤湿润状况的改善而增大。红砂灌丛蒸腾量与蒸散量之比在干旱条件下($T/ET=21\%$)较湿润条件下高(约 2%)。同时,红砂灌丛 T/ET 高于珍珠灌丛。因此,基于图像法获得的叶面积参数可用于从叶片(便携式光合仪法)到植株及灌丛水平(称重式蒸渗仪法)的植物蒸腾耗水尺度转换研究。

关键词: 红砂(*Reaumuria soongorica*); 珍珠(*Salsola passerina*); 蒸腾

文章编号: 1000-694X(2018)02-0286-08

DOI: 10.7522/j.issn.1000-694X.2017.00071

中图分类号: Q945.79

文献标志码: A

0 引言

蒸散是全球水循环的重要组成部分,陆地生态系统的年蒸散量约为 672 mm^[1]。在 85% 的陆地地区,蒸腾量占地表蒸散量的 2/3 以上,蒸腾主导陆地生态系统蒸散过程。从水资源预测的角度来看,基于生物过程的蒸腾研究比基于物理过程的蒸发研究更重要^[2]。目前,国内外在森林植被、草地植被、荒漠植被不同尺度的蒸腾耗水特征和研究方法方面已取得了较多进展^[3-5]。荒漠地区因水分限制极为明显,植被斑块分布、下垫面不均一使得准确估算荒漠植被的蒸腾耗水在方法上有局限性,影响因子主要包括环境因子和植物生理特性^[6-7]。当前蒸渗仪(Lysimeter)法被认为是研究干旱沙漠地区实际蒸散的可靠研究方法^[8]。蒸渗仪测得的蒸散量常被视为实际测量蒸散的标准,可为其他测量技术的开发、校准和验证提供基准信息^[9-10]。LI-6400XT 便携式光合仪法是通过短时间内较精确地测定植物叶片

实际蒸腾速率、进而在时空尺度上扩展研究植物蒸腾量的主要方法之一^[11]。已有研究表明,定量研究优势植物的蒸腾量及其主要影响因素是准确研究区域蒸散状况和生态需水的基础,对预测水分受限的荒漠地区的水分平衡和气候响应尤为重要^[12]。

红砂(*Reaumuria soongorica*)为柽柳科(Tamaricaceae)多年生小灌木,是荒漠灌丛植被的主要优势种和建群种,生境为荒漠和半荒漠的山麓淤积平原、山地丘陵、山前砂砾质和砾质洪积扇、剥蚀残丘、戈壁等^[13]。珍珠(*Salsola passerina*)为藜科(Chenopodiaceae)猪毛菜属半灌木,常生长在山坡或砾质滩地^[14]。两种植物的光合强度和蒸腾强度低,属于超旱生植物^[15-16]。红砂和珍珠群落是腾格里沙漠东南缘草原化荒漠的气候性顶级群落^[17-18]。但目前对草原化荒漠优势灌木种红砂和珍珠生态耗水研究较少,且多数研究仅针对植物水分参数的描述和比较,无法揭示荒漠灌丛蒸腾耗水规律^[19-21]。因此,本研究以红砂和珍珠为对象,测定红砂和珍珠叶片

收稿日期:2017-04-19; 改回日期:2017-08-28

资助项目:国家自然科学基金项目(41530750,41371101)

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DOI: 10.11686/cyxb2017141

http://cyxb.lzu.edu.cn

罗永清, 岳祥飞, 李玉强, 等. 降水格局对科尔沁沙地三种草本植物凋落物分解的影响. 草业学报, 2018, 27(2): 206—212.

Luo Y Q, Yue X F, Li Y Q, et al. Effect of precipitation patterns on litter decomposition in three annual herb species in the Horqin Sandy Land. Acta Prataculturae Sinica, 2018, 27(2): 206—212.

降水格局对科尔沁沙地三种草本植物凋落物分解的影响

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摘要: 基于研究区多年降水特征, 设置高频低量、中频中量和低频高量 3 种降水格局, 采用凋落物分解袋法, 对科尔沁沙地 3 种常见一年生草本植物一个生长季地上和地下凋落物分解特征进行了研究。结果表明, 降水格局和凋落物埋深均是影响分解率的关键因素。其中地表凋落物的分解率显著低于地下凋落物, 随埋深增加地下凋落物的分解率有增加的趋势, 10~20 cm 层狗尾草地下凋落物分解率显著高于 0~10 cm 层 ($P < 0.01$)。低频高量降水状况下地上凋落物的分解率显著降低 ($P < 0.01$)。降水格局与凋落物埋深存在显著的耦合关系 ($F = 3.60$, $P = 0.008$), 随土壤深度增加, 降水格局对凋落物分解率的影响减少, 且物种间存在差异性, 不同降水格局下狗尾草和黄蒿地上凋落物和 0~10 cm 埋深地下凋落物分解率均存在显著差异性 ($P < 0.05$), 而尖头叶藜仅地上凋落物在不同降水格局下的分解率表现出显著差异性 ($F = 48.42$, $P < 0.001$)。

关键词: 降水格局; 凋落物; 分解率; 科尔沁沙地

Effect of precipitation patterns on litter decomposition in three annual herb species in the Horqin Sandy Land

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Abstract: The effect of precipitation patterns on both aboveground and belowground litter decomposition in three annual herb species in the Horqin Sandy Land was investigated by the litter-bag method. Precipitation patterns, which were designed according to historical precipitation characteristics, included high-, medium-, and low-frequency precipitation, but the total amount was the same in each treatment. The results showed that precipitation patterns and depth of litter burial were the two main factors affecting the litter decomposition rate. The aboveground litter decomposition rate was significantly slower than the belowground litter decomposition rate. The belowground litter decomposition rate was faster at deeper depths than at shallower depths, especially for *Setaria viridis*. The decomposition rate of *S. viridis* litter belowground was significantly ($P < 0.01$) faster at the 10—20 cm depth than at the 0—10 cm depth. The aboveground litter decomposition rate

收稿日期: 2017-03-28; 改回日期: 2017-05-22

基金项目: 国家自然科学基金项目(31500369), 中国科学院“百人计划”项目(Y551821001), 国家科技基础资源调查专项(2017FY100200), 国家重点研发计划课题(2016YFC0500907, 2017YFA0604803)和西北院青年人才基金(Y651K21001)资助。

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科尔沁沙地封育过程中植被特征的动态变化

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摘要 为研究沙地退化植被封育恢复过程中植被特征的动态变化规律, 分别于 2011 年、2013 年和 2015 年 8 月中旬在流动、半固定、固定沙丘和沙质草地上开展了 3 次植被特征调查。结果表明: 2011—2015 年, 流动沙丘优势植物沙米 (*Agriophyllum squarrosum*) 的优势度逐渐降低, 半固定沙丘优势植物差巴嘎蒿 (*Artemisia halodendrom*) 的优势度波动下降、一年生植物优势度有所增加; 固定沙丘和草地中一年生植物的优势度有所下降, 多年生植物所占比例逐渐增加; 随着退化植被封育恢复, 植被盖度、物种丰富度、凋落物量和地上-地下生物量明显增加; 2011—2015 年, 4 种生境上的平均凋落物量和半固定沙丘的植被盖度逐年增加, 而物种丰富度和地上生物量表现出波动变化趋势, 地下生物量年际间变化不显著; 沙地退化植被封育恢复过程中, 物种丰富度与植被盖度、地上生物量、凋落物量、地下生物量和总的植物生物量呈极显著线性正相关。沙地退化植被封育恢复过程中植物群落组成和优势种的动态变化, 反映了沙地植物群落的正向演替与群落结构复杂化的趋向; 沙地退化植被的封育恢复导致了物种多样性与生物量的线性正相关。

关键词 群落组成; 生物量; 恢复年限; 沙地; 生境类型

Temporal changes of vegetation characteristics during the long-term grazing exclusion in Horqin Sandy Land. LV Peng^{1,2,3}, ZUO Xiao-an^{1,2,*}, YUE Xi-yuan^{1,2,3}, ZHANG Jing^{1,2,3}, ZHAO Sheng-long^{1,2,3}, CHENG Qing-ping^{1,2,3} (¹Urat Desert-grassland Research Station, Northwest Institute of Eco-Environment and Resources, Chinese Academy of Sciences, Lanzhou 730000, China; ²Naiman Desertification Research Station, Northwest Institute of Eco-Environment and Resources, Chinese Academy of Sciences, Lanzhou 730000, China; ³University of Chinese Academy of Sciences, Beijing 100049, China).

Abstract: To reveal the variation of vegetation characteristics during the enclosure restoration of degraded vegetation in Horqin Sandy Land, we investigated the vegetation characteristics in mobile dune, semi-fixed dune, fixed dune, and sandy grassland after grazing exclusion, in mid-August of 2011, 2013 and 2015. The results showed that during 2011–2015, the dominance of dominant species *Agriophyllum squarrosum* in mobile dunes was gradually decreased, while that of the dominant species *Artemisia halodendrom* in semi-fixed dunes undulately decreased and that of therophytes increased. The dominance of therophytes was decreased and the perennials increased in fixed dunes and grasslands. Along with enclosure restoration, vegetation cover, species richness, litter biomass, aboveground biomass and belowground biomass were significantly increased. During 2011–2015, the mean litter biomass in the four habitats and the vegetation coverage in semi-fixed dunes were significantly increased, while species richness and aboveground biomass were changed undulately and there was no significant difference in the belowground biomass among the three years. Vegetaion coverage, aboveground biomass, litter biomass, belowground biomass and total plant biomass were positively related to species richness during the enclosure restoration. Changes of plant community composition and dominant species

国家自然科学基金项目(41571106 和 41622103)和国家重点研发计划重点专项课题(2016YFC0500506)资助。

收稿日期: 2018-01-10 接受日期: 2018-06-20

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DOI: 10.11686/cyxb2017231

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牛亚毅, 李玉强, 王旭洋, 等. 干旱年份沙质草地生态系统净 CO₂ 通量年变化特征. 草业学报, 2018, 27(1): 215—221.

Niu Y Y, Li Y Q, Wang X Y, *et al.* Characteristics of annual variation in net carbon dioxide flux in a sandy grassland ecosystem during dry years. *Acta Prataculturae Sinica*, 2018, 27(1): 215—221.

干旱年份沙质草地生态系统净 CO₂ 通量年变化特征

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摘要:草地生态系统是干旱半干旱区生态系统类型的重要组成部分,在区域生态系统碳平衡中起着极为重要的作用。采用涡度相关法对科尔沁沙质草地生态系统进行连续两年(2015 和 2016 年)的碳通量观测,此两年恰逢研究区的相对干旱之年,年降水量约为历史平均值的 60%。研究结果表明:1)年最大日均 CO₂ 吸收速率分别为 -6.68 和 -9.58 g·m⁻²·d⁻¹,年最大日均释放速率分别为 5.69 和 5.21 g·m⁻²·d⁻¹。2)生长季(5—9 月)碳吸收量分别为 -120.54 和 -139.83 g·m⁻²,非生长季碳释放量分别为 230.33 和 212.82 g·m⁻²。3)全年尺度上沙质草地生态系统表现为碳源,2015 年净碳释放量(109.79 g·m⁻²·年⁻¹)稍高于 2016 年(72.99 g·m⁻²·年⁻¹)。4)生态系统净 CO₂ 交换量(NEE)与空气温度、土壤温度及土壤湿度存在显著相关关系,但不同年份同期 NEE 对环境温度和湿度的响应程度不尽一致。

关键词:沙质草地;年变化;生态系统净 CO₂ 通量;科尔沁沙地

*Characteristics of annual variation in net carbon dioxide flux in a sandy grassland ecosystem during dry years

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Abstract: Grassland ecosystems are a major component of terrestrial ecosystems in arid and semi-arid regions and play an important role in regional carbon balances. Continuous observation (from 2015 to 2016) of carbon dioxide flux was conducted using the eddy covariance technique in the ‘Horqin Sandy Land’ grassland ecosystem. The study period coincided with the drought in the study area and the annual rainfall during the study was 60% of the historical average. Key results were: 1) The maximum daily absorption rates were -6.68 and -9.58 g·m⁻²·d⁻¹, respectively, in 2015 and 2016, while the release rate was 5.69 and 5.21 g·m⁻²·d⁻¹. 2) The amount of CO₂ absorption was -120.54 and -139.83 g·m⁻² during growing season and the emission was 230.33 and 212.82 g·m⁻² during the non-growing season. 3) The Horqin sandy grassland ecosystem was a carbon source when considered from an annual perspective. The net carbon release in 2015 (109.79 g·m⁻²·yr⁻¹) was slightly greater than that in 2016 (72.99 g·m⁻²·yr⁻¹). 4) There were significant correlations between net ecosystem exchange (NEE) and air temperature, soil temperature, and soil moisture. However, the

* 收稿日期:2017-05-08;改回日期:2017-09-11

基金项目:国家重点研发计划(2016YFC0500901),中国科学院百人计划项目(Y551821)和国家自然科学基金项目(31640012,31560161)资助。

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降雪对荒漠生物土壤结皮光合生理特性的影响

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摘要: 生物土壤结皮(BSC)广泛分布在干旱、半干旱区,对荒漠生态系统的稳定、平衡等具有重要意义。初步探讨了降雪量对腾格里沙漠东南缘藻类、地衣和藓类结皮叶绿素荧光参数、光合色素、丙二醛(MDA)及可溶性蛋白含量的影响。结果表明:结皮光合生理特性对降雪量的响应有显著差异。适量降雪激发3种结皮PSII反应中心,引起光合色素、可溶性蛋白合成升高,MDA含量降低;过量降雪导致藻类和地衣结皮光合电子传递受阻,光合色素、可溶性蛋白合成减少,MDA含量升高,产生光抑制现象。适量冬季降雪对结皮具有一定的促进作用,而藓类结皮更能适应极端降雪环境,但相关分子机制还需深入研究。

关键词: 水分; 生物土壤结皮; 降雪; 叶绿素荧光; 光合色素

文章编号: 1000-694X(2018)03-0560-08

DOI: 10.7522/j.issn.1000-694X.2017.00013

中图分类号: Q944.52

文献标志码: A

0 引言

光合作用是植物有机物积累的基础,也是机体内一切生命活动的基础,对植物的生长发育至关重要^[1]。水分是影响植物光合生理特性的重要因子,水分胁迫使植物的光合能力明显下降^[2]。大多数荒漠生态系统受非生物因子的调控和胁迫,尤其是水分因子的限制,地表不能支撑连续且相对均一的维管束植物群落的分布,斑块状分布为生物土壤结皮(BSC)的拓殖发育提供了空间和适宜的生态位^[3]。BSC是由不同种类的蓝藻、荒漠藻、地衣、藓类和土壤中微生物,以及相关的其他生物体通过菌丝体、假根和分泌物等与土壤表层颗粒胶结形成的复合体^[4-5],它是土壤拓殖演替中的重要结构,具有防止土壤侵蚀、调节降水分配、改变荒漠生境中生物多样性的生态作用^[6]。BSC属于“变水植物”(poikilohydric plants),体内水分含量随环境水分状况而变动^[7]。生物土壤结皮仅在湿润条件下才能进行新陈代谢,因此其光合生理特性与降水量密切相关^[8]。为适应环境中水分变化,不同类型BSC在组成结构上会表现出一定的适应特性^[9-10]。目前已有不少学者做了水分变化对BSC生理特性的影响。在模拟降雨条件下,随降雨量的增加藓类结皮植株含水量增加,进而光合色素含量有所增加,光合生理活性

较强^[11]。藓类结皮在脱水后,随着其植株体内含水量的逐渐减少,光合色素含量表现出先升后降的趋势,在含水量适中情况下光合速率最大^[12]。实验室条件下,藻类结皮CO₂的变化速率随模拟降水量的增加呈单峰变化,表明BSC在最适水分条件下表现出最大光合速率^[13];同时对藻类结皮在浇水后光合值的测定发现其能够对水分改变迅速做出响应,并在约5mm模拟降水条件下维持这一活性^[14]。

随着冬季变暖的加剧,中国冬季降水呈现出增加的趋势。中国冬季气温每升高1℃,冬季降水增加9.7%^[15]。降水的主要形式除了降雨之外,还有降雪、雾、冰雹等。降雪是荒漠地区冬季水分的重要来源,降雪融化能增加土壤含水量,为BSC提供水分,起到湿润作用^[16],同时积累的降雪具有较高的绝热能力,在很大程度上阻隔了结皮土壤热量的散失,对土壤温度有很好的保温作用^[17]。Su等^[18]发现,初冬和早春的积雪融化能延长BSC光合活性时间,增加结皮的碳截获量。尹本丰等^[19]研究表明,降雪降低了齿肋赤藓的水分胁迫程度,改善并促进了生理活性和光合作用。

丝状蓝藻和土生对齿藓作为BSC的主要组成成分,广泛分布于干旱半干旱荒漠环境中。研究不同降雪量处理下藻类、地衣和藓类结皮的光合生理特性,为进一步研究它们在BSC中对降雪的响应差

收稿日期:2016-12-06; 改回日期:2017-03-07

资助项目:国家自然科学基金项目(41701104,41771105);中国科学院“西部之光”博士项目

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DOI: 10.5846/stxb201703290549

孙岩,何明珠,王立.降水控制对荒漠植物群落物种多样性和生物量的影响.生态学报,2018,38(7): - .

Sun Y, He M Z, Wang L.Effects of precipitation control on plant diversity and biomass in a desert region.Acta Ecologica Sinica,2018,38(7): - .

降水控制对荒漠植物群落物种多样性和生物量的影响

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摘要:在全球气候变化背景下,干旱和极端降水事件将对荒漠区植物群落物种多样性和生产力产生深远影响,研究植物群落应对降水变化的响应机制对于荒漠生态系统的科学管理具有重要意义。通过人工增减雨措施利用遮雨棚和滴灌技术对研究区的降水量进行人为调控,探究极端干旱、干旱和降水增加等条件对荒漠植物群落物种多样性和生物量的影响。结果表明:经过一年的降水控制处理,发现灌木和草本层片物种多样性指数在极端干旱、干旱和降水增加等试验处理中差异不显著;灌木的生物量对不同降水控制条件的响应也不显著,而草本层片地上生物量对降水变化的响应最为明显,并随着降水量的增加呈线性增长趋势,极端干旱处理(D1)条件下草本生物量为(10.54±2.36)g/m²,当降水增加50%(W1)后,草本生物量可达到(105.69±28.60)g/m²;草本地表生物量与土壤浅表层(40cm)的含水量之间显著相关($P<0.05$),草本层片生物量与短期(一年)降水波动显著相关。本研究将通过定位控制试验进一步探究长时间序列降水变化如何作用于荒漠植物群落特征,研究结果将对全球气候变化背景下荒漠生态系统响应机制方面的研究提供数据和理论支撑。

关键词:降水控制;极端干旱;荒漠植被;物种多样性;生物量

Effects of precipitation control on plant diversity and biomass in a desert region

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Abstract: In the context of global climate change, drought and extreme precipitation events will have far-reaching influences on species diversity and productivity of desert plant communities. Studying response mechanisms of plant communities to precipitation fluctuations is of great significance for the scientific management of desert ecosystems. By using rain shelters and drip irrigation systems to control precipitation input, this study evaluated the effects of extreme drought (decreasing precipitation by 50%, D1 treatment), drought (decreasing precipitation by 25%, D2 treatment) and increasing precipitation (increasing precipitation by 50%, W1 treatment; increasing precipitation by 25%, W2 treatment) on species diversity and biomass of desert plant communities. After one-year precipitation control experiments, we found that there was no significant difference in shrub and grass diversity indices, nor shrub biomass, under D1, D2, W1 and W2 treatments. The above-ground biomass of grass layers was sensitive to the precipitation changes. Grass biomass was (10.54±2.36) g/m² under D1 treatment, in contrast, grass biomass reached (105.69±28.60) g/m² with 50% precipitation enhancement (W1 treatment). Grass biomass showed a linear increasing trend with precipitation enhancement and was significantly correlated with soil water content of the shallow layer (40cm depth, $P<0.05$). Therefore, biomass of grass layers were closely related to short-term (one year) precipitation fluctuations. Based on long-term location experiments, this

基金项目:国家自然科学基金(41671103);宁夏交通建设管理局项目(WMKY1)

收稿日期:2017-03-29; 网络出版日期:2017-00-00

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科尔沁沙地优势固沙灌木的生物量预测模型

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摘要: 灌木生物量预测模型对于快速估算固沙灌木林生产力具有重要作用。以科尔沁沙地3种常见的固沙灌木小叶锦鸡儿(*Caragana microphylla*)、差不嘎蒿(*Artemisia halodendron*)、黄柳(*Salix gordejvii*)为对象, 基于对灌木地上、根系和整株生物量及高度、冠幅等的测定, 建立3种灌木地上、根系和总生物量的估算模型, 通过决定系数(R^2)、估计值的标准误(SEE)和回归检验显著水平($P < 0.05$)筛选最优的生物量预测模型。结果表明: 小叶锦鸡儿和黄柳生物量的最佳估算变量为冠幅体积, 而差不嘎蒿的最佳预测变量为冠幅面积。幂函数回归模型具有最大的 R^2 和较小的 SEE , 说明相对生长方程是估算小叶锦鸡儿、黄柳、差不嘎蒿灌木生物量较理想的模型。通过实测值检验, 3种灌木幂函数模型预测生物量的预估精度在93%以上, 具有较好的预测精度。

关键词: 固沙灌木林; 生物量; 预测模型; 预估精度; 科尔沁沙地

文章编号: 1000-694X(2018)03-0553-07

DOI: 10.7522/j.issn.1000-694X.2018.00033

中图分类号: Q948.1

文献标志码: A

0 引言

灌木植物地上多分枝的茎与近地的树冠具有很强的防风固沙和保持水土能力, 地下根系分布深而且具有很强的抗旱能力^[1], 成为生态建设和退化生态系统修复中广泛采用的植物种。灌木林在防风固沙、保持水土、改善土壤、维持生态系统平衡等方面发挥着重要功能, 特别是在年降水量400 mm以下的干旱半干旱风沙区, 灌木林营造面积已占总造林面积的70%以上^[2]。

灌木生物量作为灌木群落和生态系统研究的重要指标, 不仅反映灌木与其他物种如草本植物的资源竞争能力, 而且在一定程度上体现了灌丛生态系统对周围环境的适应^[3-4]。灌木根系往往较深且根幅较大, 挖掘根系不仅费时费力, 并且会造成灌木林地的较大破坏, 因此实际生产中大多采用直接收割法测定灌木地上部生物量, 地下根系生物量的观测往往被忽略。在干旱半干旱风沙区, 固沙灌木林承载着防风固沙、保持土壤的重要功能, 即使采用直接收割法也会引发强烈的土壤风蚀, 造成一定程度的破坏^[5]。因此通过数理方法建立灌木生物量与易测因子之间对应的模型, 有助于迅速、准确无破坏性地

预测固沙灌木林的生物量, 也是目前实际生产中经常采用的方法。生物量预测模型通常主要应用于高大乔木植物的生产力估算^[6], 关于灌木植物的生物量预测模型较多集中在林下灌木层^[7], 对固沙灌木生物量的预测模型虽有零星报道^[8-9], 但大多仅是对地上生物量的预测。地区之间自然环境条件的差异, 不同气候区灌木植物的地上分枝结构、地下根系分布深度等存在较大差异, 很多灌木生物量预测模型存在较大局限性^[1,10]。因此针对不同生态系统类型、气候区及生产目的等构建各自的灌木生物量预测模型, 对于准确估算生态系统生产力并指导实际生产具有重要意义。

科尔沁沙地是中国土地沙漠化最严重的区域之一, 沙漠化土地一度达到总面积的40%以上^[11]。为了有效地遏制土地沙漠化, 国家及地方政府在该区域重点实施了三北防护林体系、退耕还林还草等重大生态工程, 建植防风固沙灌木林是该区域生态治理的重要措施^[12]。差不嘎蒿(*Artemisia halodendron*)、小叶锦鸡儿(*Caragana microphylla*)和黄柳(*Salix gordejvii*)是科尔沁沙地固沙灌木林主要建群种^[13-14], 但相关的生物量预测模型尚不完善。本研究以灌木地上冠幅和株高为复合因子, 通过野外大范围采样, 使用数理统计方法建立3种优势固

收稿日期: 2018-03-12; 改回日期: 2018-04-10

资助项目: 国家重点研发计划项目(2016YFC0500907); 国家自然科学基金项目(41471083)

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DOI: 10.5846/stxb201703060365

王新源,陈翔舜,丁乾平,赵学勇,王小军,马仲武,连杰.不同荒漠化阶段植被生态特征对土壤环境因子的响应——以民勤荒漠绿洲过渡带为例.生态学报,2018,38(5):1569-1580.

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不同荒漠化阶段植被生态特征对土壤环境因子的响应 ——以民勤荒漠绿洲过渡带为例

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摘要:荒漠绿洲过渡带是荒漠化和绿洲化两种地理过程共同影响的生态交错区,是恢复生态学重点关注的区域。利用第五次全国荒漠化和沙化监测数据,采用方差分析和冗余分析,研究了民勤荒漠绿洲过渡带 4 种不同荒漠化发展阶段的植被生态特征和土壤环境因子的变化规律与相互关系。结果表明:(1)随着荒漠化的发展,土壤环境因子中,除有效土层厚度逐渐变浅外,风蚀痕迹占地率、表土砾石含量、盐碱斑占地率和坡度均呈现增加的动态趋势;植被因子中,除优势种盖度与植被总盖度的比值逐步增加,物种丰富度、优势种多度等其他指标均表现出明显的下降特征;(2)土壤环境因子中,有效土层厚度在 4 种荒漠化阶段对植被生态特征的影响程度达显著水平($P<0.05$),风蚀痕迹占地率在轻度、中度和重度阶段是植被生态特征变化的主导驱动因子。其他因子在多数荒漠化阶段与植被生态特征相关性不显著;(3)相比其他荒漠化阶段,中度阶段中植被生态特征对土壤环境因子的响应更加敏感,应是荒漠化防治重点关注的阶段。

关键词:荒漠绿洲过渡带;荒漠化发展阶段;植被因子;土壤环境因子;冗余分析

Vegetation and soil environmental factor characteristics, and their relationship at different desertification stages: a case study in the Minqin desert-oasis ecotone

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Abstract: The desert oasis ecotone is a ecological zone influenced by desertification and oasisization, and is a major research focus for restoration ecology. Based on the fifth national desertification monitoring, our research used variance analysis and redundancy analysis to study the relationships between vegetation ecological characteristics and soil environmental factors at four different desertification developmental stages in the Minqin Desert Oasis Transition Zone. The results showed that (1) with the development of desertification, all the soil environmental factors, such as occupancy rate of wind erosion, topsoil gravel content, and saline-alkali spots, showed an increased dynamic trend, while the effective soil thickness showed a decreased dynamic trend. Among the vegetation factors, species richness, total vegetation coverage, shrub coverage, herb coverage, dominant species coverage, plant height, and abundance decreased significantly, whereas the ratio of dominant species coverage to total vegetation coverage increased gradually; (2) among the soil environmental

基金项目:国家重点研发计划(2016YFC0500907);中国科学院率先行动“百人计划”(Y551821002);国家自然科学基金(41471083, 41501572);中国科学院战略性先导科技专项专题(XDA05050406-4);国家财政专项“第五次全国荒漠化和沙化监测”

收稿日期:2017-03-06; 网络出版日期:2017-11-21

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科尔沁沙地不同生境植被凋落物年际及年内动态

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摘要 凋落物是植被土壤系统之间重要的物质和能量通道之一,在生态脆弱区植被和土壤修复过程中发挥着特殊的功能和作用.以科尔沁沙地流动沙丘、固定沙丘和草地为对象,通过连续测定9个生长季凋落物量,并结合气温与降水量数据,研究沙地生态系统不同生境的凋落物年际和年内动态及其调控因子.结果表明:不同生境植被年凋落物大小依次为:流动沙丘($9.01 \text{ g} \cdot \text{m}^{-2}$) < 固定沙丘($67.46 \text{ g} \cdot \text{m}^{-2}$) < 草地($119.55 \text{ g} \cdot \text{m}^{-2}$).凋落物总量年际动态波动明显,固定沙丘年际变化呈“双峰”曲线,草地年际变化呈“W”型曲线.凋落物量年内变化均表现为“U”型曲线,在4和9月出现高峰值.降水量和气温对固定沙丘和草地凋落物量月际动态影响显著,而对不同生境条件下凋落物量年际变化影响均不显著.气温是影响该沙地生态系统生长季(4—9月)凋落物量月动态的主要因素.

关键词 科尔沁沙地; 生境; 凋落物

Inter- and intra-annual dynamics of vegetation litter at different habitats in Horqin Sandy Land, China. WANG Xu-yang^{1,2}, LI Yu-qiang^{1*}, LUO Yong-qing¹, LIAN Jie¹, NIU Ya-yi^{1,2}, GONG Xiang-wen^{1,2}, YANG Huan¹ (¹Northwest Institute of Eco-Environment and Resources, Chinese Academy of Sciences, Lanzhou 730000, China; ²University of Chinese Academy of Sciences, Beijing 100049, China).

Abstract: As one of the important pathways of material and energy flow between plant and soil system, litterfall plays a key role in the process of vegetation and soil restoration in ecologically fragile region. To explore the inter- and intra-annual dynamics of litter production and related regulatory factors at different habitats in sandy land ecosystem, we investigated the litter production during nine continuous growing seasons, while the air temperature and precipitation were measured over mobile dune, fixed dune, and grassland in Horqin Sandy Land. The results showed that annual litter production at different habitats were in the order of mobile dune ($9.01 \text{ g} \cdot \text{m}^{-2}$) < fixed dune ($67.46 \text{ g} \cdot \text{m}^{-2}$) < grassland ($119.55 \text{ g} \cdot \text{m}^{-2}$). The inter-annual dynamics of litterfall fluctuated significantly, with a double-peak curve in fixed dune and “W” curve in grassland. The intra-annual variation of litterfall exhibited a “U” curve at all the three habitats, with peaks appearing in April and September, respectively. Precipitation and temperature had significant effects on the intra-annual dynamics of litterfall production in fixed sand dune and grassland, but had no significant effect on the inter-annual dynamics of litter production at three habitats. Temperature was the major factor affecting the dynamics of the litter fall during the growing season in Horqin Sandy Land.

Key words: Horqin Sandy Land; habitat; litter.

植物体通过凋落物的形式将所积累的营养物质返回地表,经过分配与分解,将营养物质归返土壤,

本文由中国科学院百人计划项目(Y551821)、国家自然科学基金项目(31500369, 31640012, 31560161)和国家重点研发计划项目(2016YFC0500901)资助 This work was supported by the Pioneer Hundred Talents Program of the Chinese Academy of Sciences (Y551821), the National Natural Science Foundation of China (31500369, 31640012, 31560161), and the National Key Research and Development Program of China (2016YFC0500901).

2017-11-12 Received, 2018-02-12 Accepted.

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从而实现生态系统的物质循环^[1].凋落物量作为生物量的重要组成部分,可以表征生态系统的初级生产力水平,是生态系统功能的体现^[2].同时,凋落物量的动态变化规律能反映外界环境对生态系统结构和功能的影响^[3].目前,国外主要在森林生态系统开展了凋落物及其分解动态的研究^[4-8],也进一步探究了植被群落结构和气候因子对凋落物量动态的影响机制^[9-10].国内对不同林种凋落物养分循环及归还也开展了大量研究^[11-16],但有关草地凋落物动态

不同生境下砂蓝刺头(*Echinops gmelini*) 形态结构及生物量分配特征

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摘要: 砂蓝刺头(*Echinops gmelini*)是沙区常见一年生草本,具有繁殖比例高、密度高和生长速度快等特征,是研究区春季和早夏季节植物群落组成中最重要的草本植物。沙区人工植被演替过程中,群落中砂蓝刺头个体构件形态和生物量分配特征及其对土壤生境恢复的指示意义是本研究目的。分析了不同植被恢复阶段的沙地中(2010年铺设草方格、始植花棒、始植油蒿和1989年始植柠条与油蒿的固沙区,分别为生境1、2、3和4)砂蓝刺头构件形态及生物量分配特征。结果表明:(1)人工植被建立早期,初步稳定的沙面条件有利于砂蓝刺头的生长,而随着人工植被建立时间的增长呈现出种群衰退的趋势。4个生境间砂蓝刺头在株高、基径、根长、花序数及各器官生物量方面均差异显著($P < 0.05$),其大小关系是生境 $2 > 3 > 1 > 4$ 。(2)不同生境地上-地下生物量间均为等速生长关系,且存在共同相关生长指数1.036,支持等速生长假说;地上-叶生物量间具有共同异速生长指数(0.874,异速生长关系);营养体-繁殖生物量间均表现出 $\alpha > 1$ 异速生长关系,即繁殖生长资源的积累速率快于营养体生长。(3)株高、花序数与地上部分生物量间具有显著或极显著的正相关关系,表现出较好的协同变化趋势。总之,不同生境间砂蓝刺头形态结构及生物量特征具有明显差异,而构件生物量间相关生长关系的一致规律性及较稳定的繁殖生物量分配,有利于其适应异质生境并完成生长发育。

关键词: 砂蓝刺头(*Echinops gmelini*); 一年生植物; 形态结构; 生物量分配; 人工固沙植被区

文章编号: 1000-694X(2018)04-0756-09

DOI: 10.7522/j.issn.1000-694X.2017.00043

中图分类号: Q948.11

文献标志码: A

0 引言

植物个体构件形态和生物量分配特征是植物和环境共同作用的结果,直接体现植物对环境变化的响应及生长发育规律^[1-2]。近年来,生态学家在植物对环境变化的适应策略方面已做了大量研究^[3]。例如在水分和养分条件贫瘠的干旱地区,植物会通过促进根系伸长生长,将生物量更多地分配给根系,增大根冠比,有利于植株对水分和养分资源的获取^[4];而在光照资源较缺乏的情况下,植物增加株高的生长能够提高光照的获取效率^[5-7],增强植株的竞争力和繁殖活力^[8]。因此,对不同生境条件下植物形态特征、生物量分配格局及二者相关性的研究,有助于理解全球变化背景下环境因子对植物生长发育、生活史进程、种群稳定性及分布的影响^[9]。

中国沙地生态系统包含从流动沙丘到生物土壤结皮覆盖的固定沙丘截然不同的生境类型^[10-11]。目前,在沙地恢复演替过程中植物对生境变化的适应策略研究还相对较少。包兰铁路沙坡头段的防护体系是中国乃至全球沙漠地区固沙植被建设的成功模式^[12-13]。经过60年的演变,沙坡头人工固沙植被系统发生变化的生物和非生物环境因子主要包括土壤养分、土壤水分、植被盖度和物种丰富度^[14]。研究表明,随着流动沙丘的固定,0~300 cm层土壤含水量明显降低,土壤养分状况得到改善,土壤结皮增厚;随着植被演替的进行,群落结构由单一的灌木组成演化为一年生草本层逐渐占优势的复杂结构^[15-16],一年生植物是维持沙面稳定、物种多样性及生态系统稳定性的重要贡献者^[17]。然而,随着沙地生境的恢复和植被的演变,群落中给定的一年生植物个体构件形态和生物量分配特征是否也会发生

收稿日期:2017-03-12; 改回日期:2017-04-24

资助项目:国家自然科学基金项目(41530746)

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干旱荒漠区土壤酶活性对降水调控的响应

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摘 要: 在野外控制试验平台通过设置遮雨棚和滴灌系统对降水进行调控, 设计了极端干旱处理(减少降水 50%)、干旱处理(减少降水 25%)、增雨处理 I (增加降水 50%)、增雨处理 II (增加降水 25%)、自然降雨和对照组. 通过人工控制降水量的增减, 研究土壤酶活性(蛋白酶、淀粉酶、过氧化氢酶、碱性磷酸酶、脲酶、纤维素酶和蔗糖酶)对季节、土壤深度变化规律及不同降水处理的响应. 结果表明: 对荒漠土壤进行人为的降水控制, 显著地改变了土壤酶活性, 除淀粉酶和过氧化氢酶活性受水分影响不显著之外, 其他土壤酶活性均随着水分的增加而逐渐升高; 土壤酶活性受土壤深度影响存在差异, 除蛋白酶和磷酸酶对土壤深度变化未表现出显著差异之外, 其他几种酶活性均达到了显著水平($P < 0.05$), 且表层 0~5 cm 土层酶活性最高, 随着土壤深度的增加土壤酶活性逐渐降低; 土壤酶活性受季节的影响也存在差异, 研究发现除蛋白酶和淀粉酶活性冬季明显高于其他季节, 其他几种土壤酶活性在春、夏季都明显高于秋、冬季. 土壤酶与土壤理化性质之间相关性不强, 土壤酶之间存在较强的相关性.

关键词: 降水控制; 季节; 土壤深度; 极端干旱; 土壤酶活性

中图分类号: S154.36 **文献标识码:** A **文章编号:** 0455-2059(2018)06-0001-08

DOI: 10.13885/j.issn.0455-2059.2018.06.001

Response of soil enzyme activities to precipitation regulation in arid desert areas

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Abstract: By using the rain-shelter and drip irrigation system to control precipitation input in the field experimental platform, precipitation gradients were designed in this study, including extreme drought treatment (-50%), drought treatment (-25%), precipitation increase I (+50%), precipitation increase II (+25%) and natural rainfall. Response of soil enzyme (proteinase, amylase, catalase, alk-phosphatase, urease, cellulase, invertase) activities to season, soil depth and different precipitation treatments were studied. Activities of proteinase, alk-phosphatase, urease, cellulase, and invertase were significantly

收稿日期: 2017-09-11 **修回日期:** 2017-11-20

基金项目: 国家自然科学基金项目(41671103); 宁夏公路建设管理局项目(WMKY1)

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降水量和短期极端干旱对典型草原植物群落及优势种羊草 (*Leymus chinensis*) 叶性状的影响

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摘要: 植物叶性状在植物响应环境变化中具有重要作用。在气候变化的背景下, 典型草原植物叶性状如何响应降水格局与短期极端干旱还不十分清楚。利用野外控制试验, 研究了降水量 (323 mm 和 236 mm) 和短期极端干旱 (生长季减雨 66% 和生长季干旱 60 d) 对典型草原植物群落及优势植物羊草 (*Leymus chinensis*) 叶性状的影响。结果表明: 降水格局显著影响着植物群落和羊草的叶性状 ($P < 0.05$), 短期极端干旱对典型草原群落和羊草叶面积具有显著影响 ($P < 0.05$)。随着降水量的减少, 群落和羊草的叶面积与叶干物质含量降低, 而比叶面积与叶片氮含量增加。降水格局与短期极端干旱交互作用显著影响着群落的叶面积与叶片氮含量 ($P < 0.05$), 323 mm 降水量下短期极端干旱显著降低了叶面积, 266 mm 降水量下生长季干旱 60 d 增加了叶片氮含量。降水格局与短期极端干旱交互作用也显著影响着羊草叶面积与比叶面积 ($P < 0.01$), 323 mm 降水量下短期极端干旱降低了叶面积, 266 mm 降水量下生长季干旱 60 d 显著增加了比叶面积。回归分析表明, 不同处理下羊草叶面积、叶干物质含量、叶片氮含量能较好地解释群落叶性状。典型草原植物群落通过优势植物的主要叶性状改变来适应降水格局变化, 而通过叶面积改变来适应短期极端干旱。

关键词: 叶性状; 短期极端干旱; 降水; 羊草 (*Leymus chinensis*); 典型草原

文章编号: 1000-694X(2018)05-1009-08

DOI: 10.7522/j.issn.1000-694X.2018.00031

中图分类号: Q948.11

文献标志码: A

0 引言

气候变化背景下, 极端气候事件发生的频次、强度、空间范围与持续时间等出现变化。一些极端气候事件发生的频率与量级呈现增加的趋势^[1], 对自然与人类社会均产生了不利的影响^[2]。20 世纪 80 年代后, 中国西北东部、华北和东北地区极端干旱发生频率明显增加^[3]。从中国内蒙古地区看, 随着草原区气候暖干化的加剧, 草原干旱呈现多发的趋势, 且影响范围越来越广, 干旱对国民经济造成的损失也越来越大^[4]。降水是制约干旱、半干旱区植被生长的关键因素, 也是生态系统生产力形成的重要驱动因子^[5]。草原生态系统是对降水最敏感的生态系统之一, 在全球气候变化的大背景下, 草原生态系统具有一定的指示作用^[6]。

植物功能性状能够响应生存环境的变化, 并对生态系统功能有一定影响^[7-8]。植物功能性状作为

联系植物与环境的桥梁, 对研究植物与环境的关系具有重要的作用。国内外在地形^[9-10]、放牧^[11-12]、温度与降水^[13-15]等对植物功能性状影响方面开展了广泛的研究, 较好地阐述了植物对环境的响应与适应^[16]。由于植物叶片性状易于观测, 并对气候变化敏感, 叶性状特征的变化将直接影响到植物的功能^[17]。越来越多的研究表明, 植物叶片功能性状在植物功能性状研究具有重要的地位。其中植物叶面积 (*LA*)、比叶面积 (*SLA*)、叶干物质含量 (*LDMC*) 与单位质量叶片氮含量 (*LNC*) 是植物功能性状研究中的常用指标^[18]。

内蒙古温带典型草原作为欧亚大陆草原的重要组成部分, 对气候变化响应敏感^[19]。羊草 (*Leymus chinensis*) 作为典型草原的多年生优势物种, 也是中国内蒙古地区优良牧草。在长期环境选择下, 羊草对不同生境表现出较强的适应能力, 具有耐盐碱、抗寒冷与干旱等特性^[20]。全球气候变化背景下, 羊草

收稿日期: 2017-04-21; 改回日期: 2018-04-09

资助项目: 国家自然科学基金项目 (41622103, 41320104002); 国家重点研发计划项目 (2016YFC0500506)

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· 专题论坛 ·

植物表皮毛研究进展

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摘要 表皮毛是大多数植物地上部分表皮组织所延伸出来的一种特化的毛状结构附属物。表皮毛在植物表皮层和环境间构筑了一道天然的物理屏障, 不但对植物的生长发育具有重要意义, 而且还具有非常高的应用价值和经济价值。近几年, 研究者从不同植物中不断克隆出新的表皮毛发育相关基因, 在揭示植物调控表皮毛生长发育的分子机制方面取得很大进展。该文综述了植物表皮毛的最新研究进展, 并展望了植物表皮毛的研究方向及应用开发价值。

关键词 表皮毛, 物理屏障, 发育, 基因, 分子机制

张继伟, 赵杰才, 周琴, 陈国雄 (2018). 植物表皮毛研究进展. 植物学报 53, 726–737.

植物表皮毛由表皮细胞发育而来, 是生长在植物表皮组织的一种特化结构(Balkunde et al., 2010; 高英等, 2011)。植物表皮毛形态多种多样, 因物种而异, 即便同一物种也可能同时存在几种不同类型, 常见的有星状、分枝状、头状、钩状和鳞片状等。表皮毛可以由1个细胞构成, 也可以由多个细胞构成; 有的有分枝, 有的无分枝; 有的有腺体, 有的则无腺体。植物表皮毛的大小和密度因其生长发育阶段和所处位置不同而异(卢阳和龙鸿, 2015; Redonda et al., 2016; Andrade et al., 2017)。这些差异不但为植物表皮毛生物学功能多样性研究提供了理论基础, 而且在植物的鉴定和分类中也具有重要的指示作用(Atalay et al., 2016)。

植物表皮毛不仅对其自身有重要的保护作用, 而且还具有很高的应用价值和经济价值。有些植物具有分泌作用的腺毛, 它们可以合成、储存和分泌多种代谢物, 包括有机酸、多糖、蛋白质、多酚类、生物碱和萜类化合物等(Schillmiller et al., 2010; Maes et al., 2011; Bryant et al., 2016; Wang et al., 2016a; Akhtar et al., 2017; Champagne and Boutry, 2017)。这些化合物赋予了植物一种独特的气味, 可提炼成为香料、药物、杀虫剂、食物添加剂、树脂和精油等, 具有巨大的商业价值。因此, 植物表皮毛被誉为生成高

价值天然产物的小型化工厂(Tiwari, 2016; Champagne and Boutry, 2017)。例如, 从黄花蒿(*Artemisia annua*)中提取的抗疟药物青蒿素, 由薄荷(*Mentha* spp.)表皮毛合成的薄荷醇和大麻(*Cannabis sativa*)的有效成分大麻素都是在表皮毛合成的, 这些物质往往都具有很高的经济价值和药用价值(Tiwari, 2016; Akhtar et al., 2017)。另外, 棉花(*Gossypium* spp.)种子的表皮毛是纺织工业中重要的天然原料棉纤维。Wang等(2013)和Guan等(2014)研究表明, 棉纤维品质和参与表皮毛调控的基因表达密切相关。Patel等(2015)研究表明, 棉花叶片和茎表皮毛缺失会导致农艺性状变劣, 影响衣分和纤维产量。Li等(2005)研究表明, 蕨类植物蜈蚣草(*Pteris vittata*)的表皮毛具有吸收和储存重金属砷的能力, 这也为治理土壤重金属污染提供了新的思路。

植物表皮毛的研究在其精细结构、生态学功能及次级代谢物的开发和利用方面均已取得了一些重要成果(Balkunde et al., 2010; Dai et al., 2010; Kang et al., 2010b; Ma et al., 2016)。由于表皮毛形态明显有别于周围的表皮细胞且易于观察, 使其已成为一种良好的模式系统来研究细胞分化调控(Yanagisawa et al., 2015; 杨淑华等, 2016; Zou et al., 2016)。近几年, 在植物表皮毛发育的分子调控机制方面也取得了

收稿日期: 2017-04-09; 接受日期: 2017-08-30

基金项目: 国家重点基础研究发展计划(No.2013CB429904)

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doi:10.13866/j.azr.2018.01.17

科尔沁沙地典型草地植物功能性状及其相互关系^①

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摘要:以科尔沁沙地长期封育草地的19种植物为对象,分别测定植物高度(Height)、比叶面积(SLA)、叶片干物质含量(LDMC)、碳含量(LNC)、氮含量(LNN)5个植物功能性状,比较不同生活型(一二年生植物、多年生植物)和功能型(C₃植物、C₄植物)植物功能性状的差异性,探讨沙地内典型草地不同植物功能性状的内在联系及其对环境的适应性。结果表明:多年生植物的LDMC极显著大于一二年生植物,且C₃植物的高度显著大于C₄植物;对于一二年生植物而言,C₃植物的LNC显著大于C₄植物;对于C₄植物而言,多年生植物的LDMC和LNC显著大于一二年生植物。植物功能性状相关分析表明,SLA与LDMC极显著负相关,LNC与LNN极显著正相关。科尔沁沙地长期封育草地植物不同生活型、功能型的功能性状存在明显差异,多年生C₄植物具有较强的生态适应能力。

关键词:草地植物;功能性状;生活型;光合途径;科尔沁沙地

植物功能性状被看成是植物适应环境变化与干扰的不同反映^[1],主要包括植物对生长环境的响应和适应,是将环境、植物个体和生态系统结构、过程与功能联系起来的重要指标^[2],植物周围的基础环境因子如水分、温度、光照、养分等都会影响其功能性状及生长发育。植物高度(Height)、比叶面积(SLA)及叶片干物质含量(LDMC)等,是植物长期适应外部环境过程中经遗传变异以及自然选择而形成的功能性状稳定指标,可以较好地反映植物碳收获最大化所采取的生存对策^[3],且这些功能性状易于观测,可以同时大量植物种类进行比较^[4]。植物高度会影响光来源、热量负荷、湿度和种子扩散^[5];比叶面积(SLA)是重要的植物功能性状之一,往往与植物的生长与生存对策有紧密的联系,能很好地反映植物对周围环境的适应特征,是植物比较生态学研究中的首选指标^[6-8],且SLA的变化并不是独立的,它与LDMC、叶片氮含量以及净光合速率呈一定的相关关系^[9];LDMC表征叶片组织密度、叶片物理抗性,从而体现植物的耐性和抗压能力,Willson等^[10]认为LDMC是在资源利用分类轴上定位植物种类的最佳变量;C和N作为植物生长的生命元素,其化学计量特征是分析C、N元素生物地球化学循环的基础^[11],C是植物生理及代谢过程中的

底物来源,而植物体内C的固定又需要大量酶(N库)的参与,且N素是构建植物光合器官必不可少的营养元素,光合器官的N含量对于植物适应干旱环境具有非常重要的作用^[12]。因此,研究植物功能性状变化有助于揭示不同功能群和群落对环境变化的响应和适应,对于退化植被恢复及管理 and 植物生物生理特征及其过程的影响具有重要的理论及实践意义。

科尔沁沙地位于内蒙古东部的西拉木伦河西岸和老哈河之间的三角地带,总面积约 5×10^4 km²。有关科尔沁沙地植物功能性状的研究已有大量报道,主要集中在不同生境或不同生活型之间植物功能性状的比较及其相关性分析^[9,13]、植物功能性状及多样性对氮素利用效率的影响^[14]、植物功能性状尺度变异与生境变化的关系^[15]等方面。然而,科尔沁沙地地处我国温带半干旱草原区,受人类活动和气候变化的影响,不仅存在各类型沙丘,也发育了以多年生禾本科植物为主的湿草甸、典型草原、疏林草地以及一年生植物为主的沙质草地^[16],但涉及典型草地中不同生活型、生态型来分析植物功能性状的研究报道较少。本文以科尔沁沙地不同草地生境19种植物为研究对象,测定植物高度、SLA、LDMC、LNC和LNN 5项植物功能性状,分析了科尔沁沙地

① 收稿日期:2017-03-16; 修订日期:2017-05-31

基金项目:国家自然科学基金项目(41571106,41622103);国家重点研发计划重点专项课题(2016YFC0500506)资助

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三江源区退化天然草地和人工草地生物量碳密度特征

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摘要: 生物量碳密度是生态系统表征碳截存能力的重要功能特征之一。为明晰三江源区高寒草地生物量碳密度特征, 选取源区内3个县(玛沁县、甘德县、达日县)的退化天然草地(黑土滩)、退化人工草地、未退化天然草地为研究对象, 通过野外调查取样和室内分析相结合的方法, 对样区地上生物量、根系生物量及其碳密度进行测定与分析。结果表明:“黑土滩”地上生物量高于退化人工草地和天然草地;“黑土滩”活根和死根生物量都低于天然草地和退化人工草地。退化人工草地、“黑土滩”和天然草地的总生物量碳密度分别为719.47、706.57和2 233.09 g/m²。草地退化不仅改变了生态系统的生物量分配, 而且改变了地上部分、活根和死根中的碳密度分配比例。退化人工草地和天然草地的活根和死根碳密度占总生物量碳密度的90%以上, “黑土滩”活根和死根碳密度占79.41%。活根碳密度与总生物量碳密度的比值在3种不同草地群落间的变化较地上植被和死根的大, 因此, 活根碳密度比例可以作为草地退化的敏感指标。

关键词: 三江源区; 退化人工草地; “黑土滩”; 天然草地; 生物量碳密度

中图分类号: S812

文献标志码: A

文章编号: 1000-3037(2018)02-0185-10

三江源区是长江、黄河和澜沧江的发源地, 被誉为“中华水塔”, 也是亚洲、北半球乃至全球气候变化的敏感区和重要启动区^[1]。三江源区内可利用天然草地的面积为2 637.48×10⁴hm², 但从20世纪90年代开始, 由于不合理的开发利用和气候变化, 草地呈大面积退化趋势。其中, 失去经济价值和生态服务功能的“黑土滩”草地约为490.87×10⁴hm²^[2-4]。“黑土滩”是极度退化高寒草地, 主要以毒杂草为植物群落, 草毡层消失, 黑土滩退化草地大面积发生加剧了青藏高原生物多样性的减少和水土流失^[5-6], 对青藏高原生态环境安全和草地畜牧业的持续发展构成了极大的威胁^[7-8]。

植被碳储量对生态系统碳平衡具有重要调节作用, 全球过去100 a的植被碳储量在整体上呈增加趋势^[9]。草地生物量碳储量包括地上部分和地下部分生物量碳储量^[10], 其中地下生物量是草地植被碳储存的重要组成部分^[11]。草地生态系统中植被所储存的碳量约为

收稿日期: 2016-12-19; 修订日期: 2017-03-11。

基金项目: 国家重点研发计划课题(2016YFC0501906); 国家自然科学基金项目(41671508, 41541003); 青海省重点研发与转化计划项目(2017-NK-149-2)。[Foundation items: National Key Research and Development Projects of China, No. 2016YFC0501906; National Natural Science Foundation of China, No. 41671508 and 41541003; Qinghai Key R & D and Transformation Program, No. 2017-NK-149-2.]

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沙坡头生态水文学研究进展及水量平衡 自动模拟监测系统

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摘要: 在中国科学院野外站网络重点科技基础设施建设项目的支持下, 沙坡头沙漠研究试验站建成了以 36 台大型称重式蒸渗仪为主体的中国北方不同气候带沙区水量平衡自动模拟监测系统——Lysimeter 群。概述了沙坡头生态水文学研究进展。介绍了 Lysimeter 群建设的科学目标、构建思路、建设内容和预期研究方向。Lysimeter 群由大型称重式蒸渗仪、各类探头、移动大棚和降水模拟器等组成, 具有集成性和唯一性。该平台可全自动模拟控制降水和地下水位, 量化植物水分来源; 自动监测蒸散发、植物蒸腾、土壤水渗漏、土壤水分、温度和电导率等。该平台的建成将提升在不同尺度上认知中国沙区生态和水文过程、植被重建的生态水文学和环境胁迫生理生态学机理等相关领域的研究能力, 回答不同沙区土壤水分植被承载力和人工植被稳定性维持的生态水文阈值等国家在防沙治沙实践中所面临的核心科学问题。

关键词: 沙区; lysimeter 群; 模拟实验; 生态水文学; 生理生态学

文章编号: 1000-694X(2018)06-1119-17

DOI: 10.7522/j.issn.1000-694X.2018.00065

中图分类号: P414.8

文献标志码: A

0 引言

蒸渗仪(lysimeter), 全称蒸发渗漏仪, 是一种设在田间自然环境或人工模拟环境(如温室)下装满土壤的大型仪器。仪器中的土壤表面或裸露或种植植物, 用来测量裸土蒸发量或植被的蒸散量、潜在蒸散量及深层渗漏量, 被认为是研究水量平衡最为重要的工具。蒸渗仪分为称重式和非称重式两种。非称重式蒸渗仪又称排水型蒸渗仪, 缺乏称重设备, 通过控制地下水位来测定补偿的水量, 测量结果只能由排水的深度随时间的变化来反映, 精度较低; 称重式蒸渗仪由土柱系统、称重系统、观测系统、供排水系统和数据采集及传输系统组成, 采用高精度传感器和专用的测量设备来称量土柱的质量变化, 得到土柱中土壤水分存储的变化量, 并采集渗漏量, 从而得到计算蒸散量所需的水分平衡因子, 具有较高的准确性和时间分辨率^[1-2]。较之其他方法如微气象法和湿度相关法, 土壤蒸渗仪是陆地生态系统中测定蒸散发的最为可靠的方法^[3]。

在中国科学院野外站网络重点科技基础设施建设项目“中国北方沙区水量平衡自动模拟监测系

统——Lysimeter 群建设(KFJ-SW-YW005, 2016-2018年)”支持下, 中国科学院西北生态环境资源研究院沙坡头沙漠研究试验站(以下简称沙坡头站)已建成以 36 台大型称重式蒸渗仪为主体的中国北方不同气候带沙区水量平衡自动模拟监测系统。它的建成将搭建我国联网监测研究和数据共享平台, 提升生态水文学、逆境生理生态学、恢复生态学、生物地球化学循环等相关学科研究能力, 解决国家在防沙治沙和生态环境建设中的重大科技需求。

1 建设蒸渗仪群的重要性

1.1 北方沙区防沙治沙实践和生态环境建设的重大科技需求

中国北方风沙区面积约 170 万 km², 包括八大沙漠和四大沙地; 横跨极端干旱、干旱、半干旱和半湿润气候带, 年降水量 50~500 mm, 区域差异明显^[4]。由于自然环境严酷, 且易受气候变化和不合理的人类活动影响, 北方风沙区是中国生态环境最为脆弱的区域。自 20 世纪 50 年代开始, 国家实施了“三北”防护林工程、“退耕还林(草)”工程、“京

收稿日期: 2018-03-20; 改回日期: 2018-05-30

资助项目: 中国科学院野外站网络重点科技基础设施建设项目(KFJ-SW-YW005); 国家自然科学基金项目(41621001)

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科尔沁沙地几种常见植物茎叶吸水特征

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摘要: 植物通过茎叶吸水能够极大地改善自身水分条件。为研究科尔沁沙地植被茎叶吸收水分变化特征, 于2017年7—8月选取科尔沁沙地常见植物差不嘎蒿(*Artemisia halodendron*)、小叶锦鸡儿(*Caragana microphylla*)、猪毛菜(*Salsola collina*)通过自然降雨、茎叶隔雨、根部隔雨的控制试验, 运用压力室法测定了降雨前后的植物水势(Ψ)变化。结果表明:(1)根部隔雨试验中, 差不嘎蒿、小叶锦鸡儿和猪毛菜降雨后的水势值与降雨前相比分别升高了约66.7%、59.5%和87.9%。在降雨后第2天的水势值与降雨前相比分别升高了约73.2%、86.7%和90.6%。(2)差不嘎蒿和猪毛菜在不同部位隔雨试验中的茎叶水势值差异不明显($P>0.05$), 小叶锦鸡儿茎叶水势值存在显著差异($P<0.05$)。(3)差不嘎蒿、小叶锦鸡儿和猪毛菜都存在茎叶吸水现象。小叶锦鸡儿比差不嘎蒿和猪毛菜更能够适应科尔沁沙地的生存环境。

关键词: 叶片吸水; 茎叶水势; 科尔沁沙地

文章编号: 1000-694X(2018)05-1017-07

DOI: 10.7522/j.issn.1000-694X.2018.00069

中图分类号: Q945.79

文献标志码: A

0 引言

茎叶吸水是植物获取水分的重要策略^[1], 对植物生长发育过程具有重要的作用^[2-3]。茎叶吸水能使植物获益于小降雨事件, 从而极大地改善植物水分条件, 提高光和作用效率, 降低气孔导度, 更好地应对自然环境胁迫^[4-6]。关于茎叶吸水的研究, 1676年首次明确提出, 之后的多数研究主要集中于茎叶从湿润空气中获取的水分特征分析^[5, 7-9]。Luo等^[9]测量苘麻(*Abutilon theophrasti* Medik)水势值, 发现潮湿空气中的水势值比干燥空气中的大0.2 MPa; 郑玉龙等^[7]发现, 西双版纳地区附生植物在喷雾5 h后水势值升高接近0.1 MPa, 并且随喷雾时间的延长水势值会持续提高。Breshears等^[2]发现, 美国西海岸的乔木刺柏(*Juniperus*)吸收降雨后的水势值有超过1 MPa的提高, 并首次指出植物能够跳过根系通过叶片吸水直接获取降水。此外, 随着对植被茎叶吸水研究的增加, 发现越来越多的不同种类植物叶片可以直接吸收水分^[1, 10-12], 尤其是处于干旱缺水环境中的植物^[2]。在中国北方干旱和半

干旱沙漠(沙地)地区, 自然条件相对严酷, 生态环境脆弱, 降水少且蒸发量大, 植被对降雨的依赖性更强。但目前关于这些地区植物茎叶吸水现象及特征方面的研究还相对匮乏。

IPCC第五次研究报告指出, 未来50年全球气温变化引起的大气环流格局和水文过程的改变将会导致降水格局发生变化, 表现在降水变率和极端降水事件增加, 降水频率降低、间期增长^[13], 而这种降水格局的改变必然会影响到植物的生长发育过程。科尔沁沙地作为中国北方重要的天然生态屏障, 地处生态脆弱区和自然过渡带^[14], 当地植被对气候变化的响应更加敏感^[15]。科尔沁沙地近50年来降水量数据分析结果显示, 该区域年际降水波动较大, 其中小降水事件(<10 mm)占全年降水的64.41%, 即降水能通过入渗到达沙地植物根部的有效降水占全年降水的比例很少^[16-17]。那么, 沙地植物如何适应这种小降水居多的生存环境? 是否存在直接通过茎叶吸水来维持自身生长和发育的现象? 有多少种植物具有茎叶吸水功能? 基于以上科学问题, 本文以科尔沁沙地为研究区, 通过控制试验开展了沙地植

收稿日期: 2018-04-03; 改回日期: 2018-06-04

资助项目: 内蒙古自治区科技重大专项课题(Y749BJ1001); 内蒙古草原生态大数据平台构建与应用开发研究和内蒙古植物种质资源保护、开发利用及产业化示范; 国家重点研发计划课题(2016YFC0500907); 国家自然科学基金项目(41371053)

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内蒙古库伦旗科技扶贫活动的 实践与思考

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摘要 库伦旗是中国科学院在内蒙古自治区定点帮扶的旗县。文章回顾和总结了2013—2018年中国科学院在库伦旗开展科技扶贫工作的主要内容及成效,分析了在精准扶贫、精准脱贫方略引领下科技扶贫面临的挑战,认为解决贫困农牧民的发展观念,发挥产业配套经营、分工合作、互利共赢的优势以及将科技扶贫与人才扶贫相结合,才能促进库伦旗长久、根本脱贫和社会经济持续发展。

关键词 科技扶贫, 脱贫攻坚, 荞麦产业, 草牧业, 农牧交错带

DOI 10.16418/j.issn.1000-3045.2018.10.012

库伦旗位于内蒙古自治区通辽市南部,地处科尔沁沙地与辽西浅山黄土丘陵区的过渡区,是我国北方农牧交错带的典型区^[1]。1994年起库伦旗被国家确认为592个国家级贫困旗县之一^[1,2]。根据《关于做好新一轮中央、国家机关和有关单位定点扶贫工作的通知》(国开办发〔2012〕78号)文件安排,自2013年起中国科学院在内蒙古自治区的定点与对口帮扶旗县确立为库伦旗。

从2013年起,中国科学院(简称“中科院”)结合当地科技需求及产业发展方向,以科技扶贫为引领,确立发挥地方特色资源优势、改进与完善传统产业效能、引进

与展示先进技术等脱贫理念。重点通过推进科技成果转移转化,科学合理布设引领项目,以发展壮大合作社及乡村集体经济,实现现有贫困农牧民精准脱贫^[1,3]。经过几年多方面的共同不懈努力,库伦旗的建档立卡贫困人口由2015年底的5633户14021人,减少到2018年9月的2618户6848人。

本文就近年来中科院在库伦旗所开展的科技扶贫工作与实践活动进行回顾与总结,并对目前库伦旗科技扶贫面临问题及其解决途径进行分析,以期将现有成功的技术模式、产业发展构型及不断改进与完善的新技术,

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资助项目:中国科学院科技扶贫项目

修改稿收到日期:2018年10月6日