2017 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

实验室于 2005 年在生态与农业研究室生物技术实验室和生理生化分子生物学实验室基础上创建。实验室所从事的寒区旱区生物适应极端环境的分子机理、生理响应和生态过程的研究，具有明显的区位优势，不仅对推动相关学科的发展、稳定和培养高水平人才队伍具有重要的意义，为抗逆育种、生物资源利用和退化生态系统的恢复提供理论依据和科技支撑。

2.1 实验室目标

- 阐明寒区旱区生物抗逆的机理、揭示其特有的逆境适应机制
- 为开展抗逆基因与生态学研究提供理论基础
- 为寒旱区恢复生态学研究、试验示范提供平台及技术支撑
- 为我省抗逆育种、生物资源利用提供理论和科技支撑
- 凝聚扎根于甘肃的一支创新团队

2.2 主要研究方向

针对我省极端环境特征，开展寒区旱区生物对环境胁迫的生理应答机理、极端环境生态格局与过程、生物多样性维持机理的研究，为寒区旱区生物资源利用、作物育种和生态恢复与重建提供理论支撑。 具体研究方向包括：

1）生物适应极端环境的分子基础

主要研究寒区旱区生物的逆境生理响应、信号调控、基因功能、个体发育及相互作用的分子机理；

2）寒区旱区生物多样性与遗传分化

主要研究寒区旱区不同生态种群的遗传多样性与群落的生物多样性，从分子遗传角度揭示物种与种群适应不同生态环境的过程与机理；

3）逆境农业生物技术与脆弱生态系统保护

开发利用寒区旱区抗逆基因资源，选育和创制具有高抗逆性的生物品种，研发其产业化关键技术，建立基于分子生态学机理的脆弱生态系统保护和退化生态系统持续恢复的技术模式，为逆境农业发展和生态环境保护提供理论依据和技术支撑。

2.3 主要研究内容

1）寒区旱区生物生态适应的分子机制

基于经典和现代遗传学理论，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，研究寒区旱区生物的抗逆生理和遗传变异，揭示生物适应极端环境的分子机制。

2）极端环境下生物相互作用的分子机理

针对寒区旱区长期演化形成的物种分布格局及特点，应用分子生物学手段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。

3）生态分化的生物学过程与遗传学基础

利用生物信息学、基因组学和进化生物学理论，开发多种分子标记，研究不同生境下生物的遗传分化和进化模式，阐明个体变异与种群演化的过程，解析极端环境下物种的适应性和遗传多样性的维持机制。

4）抗逆生物资源的保育、创制与分子育种

开展极端环境抗逆生物资源收集、筛选及评估，开发与有效利用寒区旱区抗逆基因资源，进行分子设计育种，提高目标生物的抗逆性，促进寒区旱区生物技术产业的发展。

5）寒区旱区生物多样性演变与退化生态系统恢复机制

开展寒区旱区生物多样性的形成、格局、过程及其机理的研究，探索脆弱生态系统保护与退化生态系统恢复的可持续性维持技术与模式，并且进行试验与示范。

三、实验室学术委员会组成

3.1 实验室主任

李新荣，1995 年在 Moscow State University 获博士学位。现为中科院寒旱所二级研究员，博士生导师，国家重点基础研究发展计划 973 项目首席科学家、国家杰出青年基金、重点基金获得者、人事部“新世纪百千万人才工程”国家级人才、国务院政府津贴获得者、甘肃省先进工作者、甘肃省领军人才、甘肃省欧美学会副会长、甘肃省优秀专家。先后在澳大利亚联邦科工组织水土所、美国宾夕法尼亚州立大学、德国柏林工业大学进修和高访。2009 年获德国 Stiftung Alfried Krupp Kolleg 高级研究员奖，并在格拉夫斯沃德大学进行为期一年的合作研究。 主要从事干旱区植被生态学和沙地生态水文学研究。发表论文 100 余篇，SCI 收录 70 余篇，出版专著 4 部。获国家科技进步二等奖 1 项，省部级自然科学一等奖 1 项和科技进步一等奖 1 项。

3.2 实验室学术委员会组成

2017 年实验室学术委员会委员、西北农林科技大学康振生教授当选中国工程院院士。

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 33 名，全部拥有博士学位，支撑系列工程师 7 名，总共 74 名固定人员。

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
1	李新荣	男	研究员	生态学	博士	恢复生态学
2	谢忠奎	男	研究员	生态学	博士	农业生态学
3	赵学勇	男	研究员	生态学	博士	恢复生态学
4	陈国雄	男	研究员	遗传学	博士	分子遗传学
5	马小飞	男	研究员	分子生态学	博士	分子生态学
6	王若愚	男	研究员	微生物学	博士	生物防治学
7	王新平	男	研究员	生态水文学	博士	生态水文学
8	周海燕	女	研究员	生理生态学	博士	生理生态学
9	张景光	男	研究员	生态学	博士	生态学
10	刘立超	男	研究员	生态学	博士	生态学
11	张铜会	男	研究员	生态学	博士	生态学
12	李玉霖	男	研究员	生态学	博士	生态学

13	张志山	男	研究员	生态学	博士	生态学
14	左小安	男	研究员	生态学	博士	生态学
15	何明珠	男	研究员	生态学	博士	生态学
16	刘玉冰	女	研究员	分子生物学	博士	分子生物学
17	李玉强	男	研究员	生态学	博士	生态学
18	李小军	男	研究员	生态学	博士	生态学
19	刘新平	男	副研究员	生态学	博士	生态学
20	杨 果	男	副研究员	畜牧	博士	畜牧
21	赵 昕	女	副研究员	生理生化学	博士	生理生化学
22	王亚军	女	副研究员	生态学	博士	农业生态学
23	谭会娟	女	副研究员	生理学	博士	植物生理学
24	潘颜霞	女	副研究员	生态学	博士	水文生态学
25	贾荣亮	男	副研究员	生态学	博士	生态学
26	王 进	男	副研究员	细胞生物学	博士	细胞生物学
27	赵鹏善	男	副研究员	分子生物学	博士	分子生物学
28	黄 磊	男	副研究员	生态学	博士	生态学
29	张玉宝	男	高级工程师	分子生物学	博士	分子生物学
30	赵 洋	男	副研究员	生态学	博士	生态学
31	黄文达	女	副研究员	生态学	博士	生态学
32	胡宜刚	男	副研究员	生态学	博士	生态学
33	王少昆	男	副研究员	生态学	博士	生态学
34	回 嵘	女	副研究员	生态学	博士	生态学

35	陈翠云	女	助理研究员	分子生物学	博士	分子生物学
36	石玉兰	女	助理研究员	分子生物学	博士	分子生物学
37	郭志鸿	男	助理研究员	分子生物学	博士	育种学
38	何玉惠	女	助理研究员	生态学	博士	生态学
39	冯 丽	女	助理研究员	生态学	博士	生态学
40	黄承红	女	助理研究员	分子生物学	博士	分子生物学
41	罗亚勇	男	助理研究员	生态学	博士	生态学
42	连 杰	男	助理研究员	生态学	博士	生态学
43	潘成臣	男	助理研究员	生态学	博士	生态学
44	王增如	男	助理研究员	生态学	博士	生态学
45	张 鹏	男	助理研究员	生态学	博士	生态学
46	高艳红	女	助理研究员	生态学	博士	生态学
47	毛 伟	男	助理研究员	生态学	博士	生态学
48	曲 浩	男	助理研究员	生态学	博士	生态学
49	虎 瑞	女	助理研究员	生态学	博士	生态学
50	苏洁琼	女	助理研究员	生态学	博士	生态学
51	杨昊天	男	助理研究员	生态学	博士	生态学
52	张亚峰	男	助理研究员	生态学	博士	生态学
53	冯 静	女	工程师	生态学	学士	检测
54	苏 娜	女	工程师	生态学	学士	检测
55	李启森	男	助理研究员	生态学	本科	科技推广
56	陈怀顺	男	助理研究员	生态学	本科	科技推广

57	樊恒文	男	高级工程师	科研管理	本科	科研管理
58	李爱霞	女	高级工程师	会计	本科	会计
59	高永平	男	工程师	气象监测	本科	气象监测
60	云建英	女	工程师	数据管理	本科	数据管理
61	赵金龙	男	工程师	农业管理	本科	农业管理
62	邱阳	男	助理研究员	生态学	博士	生态学
63	刘美玲	女	助理研究员	生态学	博士	生理生态学
64	罗永清	男	助理研究员	生态学	博士	生态学
65	陈敏	男	助理研究员	生态学	博士	生态学
66	赵霞	女	助理研究员	微生物学	博士	微生物分子生态学
67	钱朝菊	女	助理研究员	生态学	博士	分子生态学
68	赵杰才	男	助理研究员	生态学	博士	育种学
69	马旭君	男	助理研究员	生理生态学	博士	恢复生态学
70	刘良旭	男	助理研究员	生态学	博士	生态学
71	周建伟	男	助理研究员	草业科学	博士	畜牧
72	张成琦	男	助理研究员	地球系统科学	博士	环境变化与碳循环
73	周琴	女	助理研究员	生态学	博士	分子生物学
74	宋光	男	助理研究员	生态学	博士	生态学
75	王立龙	男	助理研究员	生态学	博士	分子生物学

五、实验室研究生培养

2017 年实验室继续重视人才培养、国际国内学术交流和科普宣传活动，2017 年新招 10 名硕士研究生、9 名博士研究生；毕业博士生 6 人，硕士生 6 人。目前在读研究生 59 人。

表三 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

2017 年毕业答辩博士、硕士研究生

1）解淀粉芽孢杆菌挥发性化合物介导的植物基因表达响应研究

答辩人：郝海婷　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

2) 全球气候变化背景下野生大麦早花的适应性进化机制

答辩人：钱朝菊　申请学位：理学博士

导师：马小飞　研究员

答辩委员会主席：李新荣　研究员

3) 中国主要沙区植被恢复对土壤碳的影响研究

答辩人：陈永乐　申请学位：理学博士

导师：李新荣　研究员

答辩委员会主席：杨 保 研究员

4) 固沙植被生态水文阈值研究

答辩人：张定海　申请学位：理学博士

导师：李新荣　研究员

答辩委员会主席：杨 保 研究员

5) 中国北方植被变化及其对干旱的响应

答辩人：徐浩杰 申请学位：理学博士

导 师：王新平　研究员

答辩委员会主席：李新荣　研究员

6) 干扰对生物结皮覆盖区土壤种子库的影响

答辩人：陈孟晨 申请学位：理学硕士

导 师：张景光 研究员

答辩委员会主席：李新荣　研究员

7) 沙埋对干旱沙区生物结皮层细菌群落结构和多样性的影响

答辩人：滕嘉玲 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

8) 低温及降雪对生物土壤结皮生理生化特性的影响

答辩人：谢 敏 申请学位：理学硕士

导 师：刘立超 研究员

答辩委员会主席：李新荣　研究员

9) 红砂响应干旱和 UV-B 辐射双重胁迫的基因转录表达分析

答辩人：刘 丹 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

10) 科尔沁沙地植物生长对风速和降水变化的响应

答辩人：魏水莲　申请学位：理学硕士

导师：刘新平　副研究员

答辩委员会主席：王涛 研究员

11) 科尔沁沙地农林复合系统碳截存潜力——以奈曼旗为例

答辩人：张建鹏　申请学位：工程硕士

导师：李玉强　研究员

答辩委员会主席：王涛 研究员

12）东方百合索邦中抗病关键基因的克隆和相互作用研究

答辩人：王乐　申请学位：理学博士

导师：谢忠魁 研究员

答辩委员会主席：李新荣 研究员

表四　2017年博士生开题、考核、中期报告题目

序号	**姓名**	**报告题目**	**指导老师**
1	张继伟	沙米表皮毛生物学功能研究	陈国雄
2	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
3	尹晓月	基于多组学探究沙米生态适应性分化机制	马小飞
4	李文美	干旱胁迫下兰州百合的适应机制。	谢忠奎
5	吕　朋	科尔沁沙地退化植被恢复及其管理对土壤氮矿化的影响	左小安
6	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
7	王艳莉	一年生植物砂蓝刺头对环境变化的生活史对策及响应机制	李新荣
8	王旭洋	中国北方农牧交错带土壤有机碳储量变化研究	李玉强
9	何钊全	半干旱沙地农田玉米农业生产潜力优化的节水途径对比研究	张铜会
10	陈娟丽	科尔沁沙地和乌拉特荒漠草原三种植物对水分胁迫的响应	赵学勇
11	张　蕊	荒漠草原生态系统碳通量对降水变化的响应	赵学勇
12	管　超	生物结皮覆盖土壤呼吸对增温及降水模式变化的响应	李新荣

13	周媛媛	植物固沙对沙漠生态系统碳通量的影响	李新荣
14	刘少芳	解淀粉芽孢杆菌诱导植物抗盐的分子机理研究	王若愚
15	卢 翔	胞外多糖在解淀粉芽孢杆菌促进植物抗逆作用中的研究	王若愚
16	韩亚楠	拉伸和填埋对地膜机械、降解特性、微生物多样性的影响及地膜的微生物降解	谢忠奎
17	岳喜元	典型草原与荒漠草原植物功能性状及其多样性对极端干旱事件的响应	左小安
18	周 琴	大麦角质层基因的遗传定位及生理功能研究	陈国雄
19	刘璐璐	退耕还林政策对农户脆弱性与可持续生计的影响—以甘肃会宁县为例	李锋瑞
20	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
21	宋 光	生物土壤结皮对相邻荒漠草原区植物定居过程的影响”	李新荣
22	金艳霞	荒漠灌木蒸散耗水特征的尺度转换研究	王新平
23	石 薇	腾格里沙漠东南缘人工固沙植被区土壤水分动态研究	王新平
24	岳 靓	解淀粉芽孢杆菌在植物系统诱导性抗旱机制中作用的研究	王若愚
25	马雄忠	阿拉善高原红砂与珍珠根系动态研究	王新平
26	焦 丹	冷应激对绵羊能量代谢通路的分子作用机制	谢忠奎
27	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加速草地退化的机制	谢忠奎
28	赵生龙	温带荒漠草原植被与土壤对不同放牧强度的响应	张铜会
29	于海伦	科尔沁沙地光梗蒺藜草和刺萼龙葵入侵途径及适应性对比研究	赵学勇
30	张润霞	干旱荒漠区城镇化建设对区域生态水文过程的影响——以兰州新区为例	赵学勇
31	程清平	基于未来“气候-水文-经济-生态环境”情景下黑河流域水资源可持续发展评估	左小安
32	孙靖尧	生物土壤结皮斑块镶嵌分布的小尺度空间格局研究	李新荣
33	赵丽娜	土壤结皮生物类群演变对沙地生态恢复的指示意义	李新荣

表五 2017 年终硕士生开题、考核、中期报告

序号	姓名	报告题目	指导老师
1	马晓俊	干旱沙区土壤微生物群落组成和氮转化功能基因对植被恢复的响应	李小军
2	周丽靖	生物炭对农田退化土壤的改良作用研究	王亚军
3	姬凯茜	冷应激下绵羊 PRDM16 和 ELOVL6 基因的表达特征与其基因启动子区序列特征的研究	杨 果
4	吕星宇	干旱沙区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	张志山

		计量研究	
5	孙沛沛	半干旱区蒿类植被建成的土壤微生物多样性规律	马小飞
6	杨红玲	添加混合凋落物对科尔沁沙地沙丘草地土壤碳矿化的影响	李玉霖
7	龚相文	科尔沁植被净初级生产力时空特征及其影响因子研究	李玉强
8	车力木格	半干旱沙质草地一年生植物生殖生长对降水变化的响应	刘新平
9	赵　芸	腾格里沙漠人工固沙植被区生物土壤结皮 NDVI 时空变化特征	贾荣亮
10	都　军	沙区不同类型生物土壤结皮对表层土壤理化性质及碳氮循环关键过程的影响	李小军
11	宁志英	科尔沁沙地沙质草地植被–土壤碳、氮、磷化学计量特征研究	李玉霖
12	牛亚毅	沙质草地生态系统碳通量特征及其影响因子	李玉强
13	魏文斐	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	刘立超
14	张雯莉	混合盐胁迫对两种枸杞叶片生理特性的影响	刘玉冰
15	华翠平	邻苯二甲酸介导的兰州百合“自毒”分子应答及他感协同作用研究	王亚军

六、2017 年实验室新增科研项目

2017 年在各项在研项目顺利进行的同时，新增 36 项，其中国家自然科学基金面上及青年基金 6 项，国家重点研发计划课题 2 项，中国科学院前沿科学重点研究计划 1 项，中科院百人计划 1 项，其他项目 26 项，经费合计 5446 万元。

表六　2017 年新争取课题/项目统计表

编号	课题名称	编号	负责人	起止时间	经费万元	类别
1	中国荒漠主要植物群落调查	2017FY100200	赵学勇	2017–2020	2177	科技基础资源调查
2	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	2016YFE0203400	王新平	2017–2020	1005	国家重点研发计划
3	西北内陆河流域评价		左小安	2017–2020	185	中科院战略性先导科技专项专题
4	内蒙古库伦旗光伏扶贫试验示范	Y729981001	张铜会	2017–2018	200	中国科学院科技扶贫项目

5	内蒙古库伦旗科技扶贫试验示范	Y729971001	张铜会	2017–2018	317	中国科学院科技扶贫项目
6	固沙先锋植物栽培选育	2016YFE0203400—06	陈国雄	2017–2020	52.50	国家重点研发计划课题
7	半干旱沙质草地土壤微生物功能群和氮转化对增减雨变化的协同响应	41771117	王少昆	2018–2021	71	国家自然科学基金
8	半干旱区沙地灌丛凋落物分解过程对季节性增温和极端干旱的响应及其生物机制研究	41773086	潘成臣	2018–2021	68	国家自然科学基金
9	温带荒漠建群灌木红砂的生态物种形成研究	31770416	马小飞	2018–2021	62	国家自然基金项目
10	干旱荒漠区灌木生物量与土壤水分动态耦合研究	41771101	王新平	2018–2021	71	国家自然科学基金
11	生物土壤结皮层丛枝菌根真菌(AMF)群落结构多样性及其驱动机制研究	41771105	刘立超	2018–2021	71	国家自然科学基金
12	UV–B 增强对荒漠地区隐花植物多样性及其结皮生态功能的影响	41701104	回嵘	2018–2020	23	国家自然科学基金青年科学基金
13	固沙微生物菌种分离、纯化、筛选和扩繁研究	QYZDJ–SSW–SMC011—01	王进	2016–2020	100	中科院前沿科学重点研究项目课题
14	内蒙古沙地治理技术及生态演变分析评估		刘新平	2017–2018	50	内蒙古自治区科技重大专项课题
15	西北荒漠–绿洲动态变化过程及其稳定性维持机制	2017YFC0504301	张志山	2017–2020	250	国家重点研发计划课题
16	西北荒漠–绿洲生态–水文过程耦合机制	2017YFC0504301–2	胡宜刚	2017–2020	60	国家重大研发计划项目
17	阿拉善高原–河西走廊荒漠主要植物群落调查	2017FY100203	李小军	2017–2020	370	国家重大基础资源调查专项课题
18	绿洲作物–土壤–水分耦合作用机制及水土高效利用研究	2017YFC0504302–01	王增如	2017–2020	60	国家重点研发计划专题
19	沙米自然群落高温耐受表型分化的分子遗传基础机制		赵鹏善	2017–2022	80	青促会项目
20	海源百合资源开发及脱毒种源		王亚军	2017	60.	宁夏农业发展

	繁殖示范					办公室
21	滩羊营养标准建立与不同生长阶段精准饲喂配方研发示范，		杨果	2017	55	宁夏农业发展办公室
22	基于有机混合物的沙丘快速治理技术原理及试验示范	2016YFE0203400	谢忠奎	2017	52.5	国家重点研发计划重点专项
23	水溶性微生物制剂对设施蔬菜病害的生物防治示范推广		王若愚	2017	35	宁夏农业发展办公室
24	盐碱地适生植物种质资源收集及栽培技术研究	2016YFC0501403-3	王若愚	2017	28	国家重点研发计划子项目
25	沙化草地综合治理	Y739AS1001	张铜会	2017-2019	50	奈曼旗科技局
26	沙地植物-土壤系统生态过程及对区域环境变化的响应	Y451H31003	左小安	2018-2021	60	中国科学院“百人计划”项目
27	沙地植物过程对生境变化的响应	1100000036	左小安	2018-2021	30	中国科学院青年创新促进会
28	科尔沁沙地植物群落调查	2017FY100205-6	黄文达	2017-2020	30	科技基础资源调查
29	西鄂尔多斯荒漠植被DNA条形码采集		赵昕	2017-2020	35	国家基础资源调查专项
30	基于有机混合物的沙丘快速治理技术原理及试验示范	2016YFE0203400-09	王少昆	2017-2020	52.5	国家重点研发计划
31	奈曼旗沙产业持续发展	Y739AR1001	赵学勇	2017-2019	20	奈曼旗科技局
32	不同演替阶段结皮对增强UV-B辐射的生理生态响应		回嵘	2017-2020	3	宁夏青年科技人才托举工程
33	芽孢杆菌提高植物抗旱性的分子作用机制和应用研究		赵霞	2017-2019	15	西部之光B类
34	乌拉特荒漠草原植物与土壤微生物响应降水变化的协同机制		马旭君	2018-2021	15	“西部青年学者”B类
35	沙蓬表皮毛缺失型突变体对干旱和高温的响应		赵杰才	2017-2020	15	“西部青年学者”B类

七、实验室获得主要科研成果

1、科研奖励成果

1）沙坡头站科研人员完成的“生物土壤结皮形成机理、生态作用及在防沙治沙中的应用”项目荣获 2017 年度宁夏回族自治区科技进步一等奖。

主要完成者：李新荣、刘立超、张志山、贾荣亮、谭会娟、潘颜霞、赵洋、王进、何明珠、回嵘、张鹏、胡宜刚、杨昊天、张亚峰、黄磊

2）沙坡头站科研人员参加的“基于水分平衡的低覆盖度治沙理论及其防风固沙技术模式研究与示范”项目获得 2017 年度甘肃省科技进步一等奖。

3）2017 年本实验室甘肃省重点实验室评估优秀奖，奖励 50 万元。

4）皋兰站王若愚研究员的中科院百人计划项目《植物病害生物防治的分子生物学研究》获得中国科学院 2017 年度“百人计划”终期评估优秀。

5）2017 年乌拉特荒漠草原站左小安研究员的中科院 “百人计划”项目《沙地植物-土壤系统生态过程及对区域环境变化的响应》终期评估获得优秀，并获得 60 万元科研经费奖励。

6）2017 年乌拉特荒漠草原站左小安研究员获得了“中科院青促会优秀会员”称号，获得了 30 万科研经费的后续支持。

2、专利

表七 实验室 2017 年申报、授权专利一览表

专利状态	专利名称	专利类型	授权号或申请号	申请日	授权公告日	技术联系人
授权	一种干旱沙区固沙植物栽植方法	发明专利	ZL201510280853.X		2017	李新荣
授权	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		2017	赵 洋
授权	一种百合复合病毒半定量检测金标卡的制备方法.	发明专利	ZL201510951214.1.		2017.11.14	张玉宝
授权	一种百合李属坏死环斑病毒 PNRSV 半定量检测金标卡的	发明专利	ZL201510951192.9.		2017.11.14	张玉宝

	制备方法.					
授权	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.		2017.11.10	张玉宝
授权	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.		2017.10.10	张玉宝
受理	一种羊消化代谢笼	实用新型	201721392832.8			杨　果
授权	一种简易降雨模拟试验装置	实用新型	201621202230.7	2016-11-08	2017-05-17	刘新平
授权	一种平衡式保水蓄水渗透装置	实用新型	201621183976.8	2016-11-04	2017-05-24	何钊全
授权	一种用于试验土样的筛选装置	实用新型	201621166651.9	2016-11-02	2017-06-06	何钊全
授权	一种用于退化草地快速恢复的凋落物网袋	实用新型	201620526639.8	2016-06-01	2016-10-26	曲　浩
受理	一种兰州百合与玉米/蚕豆套种的三年轮作方法	发明专利	201611089039.0	2016-12-01		王亚军
授权	一种用于 PVC 管刻度线的绘制装置	实用新型	201621323544.2	2016-12-05	2017-06-06	何钊全
受理	一种与土壤贯通的半封闭式多功能植树袋	发明专利	201710055975.8	2017-01-25		王增如
授权	一种与土壤贯通的半封闭式多功能植树袋	实用新型	201720096491.3	2017-01-25	2017-09-08	王增如
受理	一种野外模拟地下滴灌的便携式装置	发明专利	201710055970.5	2017-01-25		王增如
授权	一种野外模拟地下滴灌的便携式装置	实用新型	201720096492.8	2017-01-25	2017-09-12	王增如
受理	一种提高人工培育藓类结皮抗旱能力的方法	发明专利	201611191838.9	2016-12-21		贾荣亮
授权	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	201720236561.0	2017-03-13		王炳尧
授权	一种使用聚乳酸可降解纤维沙障构建的流动沙丘固定系统	实用新型	201621118520.3	2016-10-11	2017-04-19	曲　浩
受理	一种便于小面积农田覆膜的	实用	201720541359.9	2017-05-16		何钊全

	机具	新型				
受理	一种兰州百合专用的缓释微量元素颗粒肥料及其制备方法	发明专利	201710695456.8	2017–08–15		邱阳
受理	一种碱性土壤使用的颗粒型缓释铁肥及其制备方法	发明专利	201710695531.0	2017–08–15		邱阳
受理	一种悬挂直插式地下滴灌灌溉系统	发明专利	201710768248.6	2017–08–31		王炳尧
受理	一种悬挂直插式地下滴灌灌溉系统	实用新型	201721103518.3	2017–08–31		王炳尧
受理	沙米脱粒机构、脱粒机及脱粒方法	发明专利	201710406758.9	2017–06–02		赵昕
授权	沙米脱粒机构以及脱粒机	实用新型	201720637547.1	2017–06–02	2017–11–22	赵昕
受理	一种便携式可控瘤胃液采集装置	实用新型	201721392847.4	2017–02		周建伟

2017 年实验室科研人员所获得奖励

- 黄磊、李小军、王进、张玉宝副研究员分别在美国和澳大利亚进行访问学者。
- 李新荣同志被评为中科院兰州分院 2017 年度“优秀共产党员”。
- 张铜会获得 2017 年奈曼旗优秀科技工作者奖
- 赵洋副研究员被中卫市科技协会评为 2017 年优秀科技工作者。
- 赵鹏善副研究员入选中科院中科院青年创新促进会
- 赵昕获得兰州资源环境大型仪器区域中心和所级中心 2017 优秀工作者奖
- 博士生徐浩杰获得中国科学院大学“院长优秀奖”。
- 博士生王艳莉、硕士生都军获得中国科学院大学 2017 年“三好学生”奖。
- 博士生徐浩杰、宋光和硕士生赵芸、牛亚毅获得国家奖学金。

八、2017 年实验室发表学术论文

SCI 论文目录：

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核心期刊

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著作

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九、学术会议和学术交流活动

1、主办学术会议

5 月 27 日–5 月 28 日中国科学院重点科技设施建设项目“中国北方沙区水量平衡自动模拟监测系统—Lysimeter 群” 中期检查会在沙坡头站召开。

8 月 2–4 日甘肃省地理学会 “丝绸之路”生态环境与地理实践研讨会在沙坡头站召开, 50 多位专家学者参加了会议。

8 月 13–17 日冰冻圈科学系列丛书及冰冻圈科学发展战略讨论会议在在沙坡头站召开，来自全国各地的 24 位专家参会。

8 月 18 日，应沙坡头站李新荣研究员邀请，中科院院士秦大河为沙坡头站科研人员作了题为“冰冻圈科学与极地探险”的报告。

9 月 8–10 日，甘肃省生态学学会第五次会员代表大会暨第四届“甘肃生态论坛”在在沙坡头站召开。来自中科院、省内各高校、研究院所、林业管理局、自然保护区、草原工作站等相关单位的 120 余人参会，做了 16 场特邀报告、大会报告和学术报告，收到 60 余篇科研论文和会议摘要。

9 月 29–30 日，由沙坡头站李新荣研究员担任首席科学家的国家重点基础研究发展计划“植物固沙的生态–水文过程、机理及调控”在北京召开课题结题验收会议。

10 月 30 日，由沙坡头站王新平研究员担任首席科学家的国家重点研发计划项目“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”在甘肃兰州召开项目启动会议

2、学术交流活动记录

2 月 23–24 日，左小安、岳喜元在沈阳参加“极端干旱对草原生态系统影响”2016 年学术年会，作报告“草原优势植物羊草的功能性状对极端干旱的响应”。

3 月 1–3 日，贾荣亮副研究员参加了在银川举行的宁夏青联第十届委员会全体会议并当选为常务委员会委员。

4 月 10–12 日，王少昆在美国美布拉斯加州林肯市参加了“Water for Food Global Conference”，墙报展示了“Restoration of degraded semi–arid agro–pastoral ecosystems through microbial organic compound amendments in Inner Mongolia, China”的相关研究。

5 月 20 日，吕朋、张晶和岳喜元在奈曼旗奈曼站实验室进行的定氮仪实验方法和操作规程培训。

5 月 16–21 日贾荣亮副研究员参加北京植物所举行的 CERN 生物观测指标、规范与技术交流研讨会。

5 月 18 日和 23 日贾荣亮、王增如参加中科院青藏所第二次青藏高原科考，第一、二次

讨论会。

5 月 27 日至 6 月 11 日，在中国科学院西北生态环境资源研究院王涛院长的带领下，实验室赵学勇副主任、马小飞研究员（课题 3《沙化土地稳定恢复生态机理及关键生物技术》负责人）、李玉霖研究员（课题 7《种养一体化与沙化土地稳定恢复技术集成及产业示范》负责人）、左小安研究员、刘新平副研究员、黄文达副研究员以及博士生钱朝菊和尹晓月等人对我国北方典型沙化地区毛乌素沙地、库布齐沙漠东部、科尔沁沙地中西部和呼伦贝尔沙地等防沙治沙基地和野外实验站进行实地野外考察。

5 月 29 日–6 月 2 日应哈萨克斯坦植物生物学与生物技术研究所 Kabyl Zhambakin 博士和 Yerlan Turuspekov 博士的邀请，张继伟博士代表陈国雄研究员课题组赴哈萨克斯坦阿拉木图市参加了第四届植物基因国际会议 2017 (The 4th international conference “Plant genetics, genomics, bioinformatics and biotechnology” (PLANTGEN 2017))。会议期间，张继伟博士代表陈国雄研究员围绕沙蓬的驯化做了详细的大会报告，引起各国科学家的兴趣与关注。讨论中针对沙蓬适应沙漠环境的机制，包括根和叶的结构以及种子的落粒性展开。

6 月 9–11 日李新荣研究员应邀在天水师范学院做学术报告。

6 月 14 日左小安、陈敏、黄文达在北京参加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启动会。

6 月 23–25 日马小飞、钱朝菊在天水师范学院参加甘肃省植物学会 2017 年学术年会暨会员代表大会。

6 月 25–29 日潘颜霞副研究员参加在青岛大学举办的第三届水资源环境国际会议（The 3th International Conference on Water Resource and Environment (WRE 2017))。

6 月 28–30 日左小安参加国家生态系统研究网络（CNERN）平台 2016 年度野外站考核会议，参加了国家生态系统研究网络（CNERN）平台 2016 年度野外站考核会议，学习了其他国家站的先进管理经验和成果。

6 月 29–30 日王少昆在美国 Eastern Nebraska Research and Extension Center，参加 “Innovative Research and Extension Programs to Protect the Environment” 的学术论坛及现场示范参观。

7 月 1 日左小安研究员和张晶博士参加了中国科学院青年创新促进会西北研究院小组在乌拉特后旗一中开展的科普报告会。

7 月 1 日陈敏参加了中国科学院青年创新促进会西北研究院小组在乌拉特后旗一中开展的科普报告会就荒漠植物的繁殖对策进行科普报告。

7 月 2–3 日左小安在北京参加了中国科学院先导 A 类项目四：全景美丽中国下设课题五《大数据驱动的“美丽中国”全景评价与决策支持》可行性研论证会。

7 月 6–8 日左小安在张掖参加首届“中国科学院丝绸之路青年论坛”及学术交流。

7 月 8–14 日左小安参加了内蒙古呼伦贝尔草原生态系统国家野外科学观测研究站建站 20 周年的学术研究讨会，就与中国农科院区划所的庾强教授进一步开展北方草原生态系统对全球变化的响应的联网研究进行了深入的讨论，并确定了相应的实验方案。

7 月 16–22 日连杰、王旭洋、龚相文在北京师范大学参加第七届陆表卫星遥感数据反演理论与方法暑期学校。

7 月 23–29 日马小飞、黄文达、钱朝菊、赵芸在深圳参加第 19 届国际植物学大会。马小飞在遗传进化相关分会做主题报告。

7 月 26 日至 28 日李新荣研究员受中国科学院亚热带农业生态研究所王克林研究员的邀请，到环江喀斯特生态系统观测研究站访问并进行学术交流。

8 月 6–11 日王少昆参加美国生态学年会 Ecological Society of America (ESA) annual meeting 2017，在会上做了题为“Ecological restoration of degraded sandy land using microbial organic compound in Horqin Sandy Land, Northern China”的学术报告。

8 月 16–18 日高艳红在亚洲通量网（AsiaFlux）2017 年年会和中国通量观测研究联盟（ChinaFLUX）成立 15 周年联合会议中做了大会展板，同时论文“Evapotranspiration over artificially planted shrub communities in the shifting sand dune area of the Tengger Desert, north central China”获得 ChinaFLUX&CERN 优秀论文三等奖。

8 月 24 日左小安在“中科院寒旱区野外监测平台建设研讨会”上，围绕冰缘荒漠绿洲生态系统联合观测网络的建设部署进行了讨论，并就乌拉特站建设荒漠草原区水气碳通量观测进行了部署。

8 月 24 日–9 月 1 日李新荣、赵洋、谭会娟、回嵘、杨昊天前往巴西伊瓜苏参加国际恢复生态学会 2017 年会。

8 月 25–30 日左小安在云南大理参加了第九届西部地区植物科学与资源利用研讨会，并与西部知名学者就未来北方荒漠草原区的植物资源利用进行了广泛的交流。

9 月 7 日赵学勇、贾荣亮在鄂尔多斯参加《联合国防治荒漠化公约》第十三次缔约方大会《中国科技治沙边会》。贾荣亮做了题目为《Long–term ecological research guides ecological reconstruction and restoration in sandy areas of northern China》的报告，接受了中新社的采访，相关报道见《综述：中国治沙专家为世界输送“治沙经验”》。

9 月 25 –27 日在青海省海东市平安县召开的中国科学院西北研究院 2017 年度野外台站工作会议，沙坡头站获得优秀站。

10 月 10–12 日杨昊天博士参加在鹤山站开展土壤监测技术培训及土壤监测指标方法规范修订研讨会暨 STS 指标研讨会。

10 月 30 日–11 月 2 日马小飞、钱朝菊在中国科学院华南植物园参加第二届“全国自然杂交与生物多样性学术讨论会”。

11 月 10–12 日，主题为“面向全球变化的水系统创新研究”的第十五届水论坛在深圳召开，沙坡头站王新平研究员、潘颜霞副研究员参加了会议。

12 月 28 日宁夏回族自治区人民政府办公厅文件宁政办发【2017】218 号文件，批准以沙坡头站为载体，建立“宁夏沙坡头生态保护和建设院士工作站”。

九、国内外来访交流大事记

3 月 9–11 日南昌市科学技术局调研员胡向萍教授、亚热带风沙化土地综合开发南昌试验站站长朱国平等一行到沙坡头站访问考察。

3 月 24 日《人民日报》以《沙坡头沙漠研究试验站站长李新荣 沙漠里书写“草根”论文》报道沙坡头站李新荣研究员的先进事迹。

4 月 10 日奈曼旗畜牧工作站的黄保平等 2 人来奈曼站参观访问。

4 月 29 日湖南师范大学韩广等 2 人来奈曼站参观访问

4 月 9 日–5 月 10 日兰州交通大学，青春波和余沛东来奈曼站开展实验。

4 月 9 日–7 月 6 日西北师范大学赵欣鑫和杨欢来奈曼站开展实验。

5 月 2 日中国科学院地理科学与资源所国家重点研发计划项目组一行 7 人到沙坡头站。

5 月 3–6 日本鸟取大学干燥地研究中心钱塔拉和苟晓伟来奈曼站开展实验。

5 月 3 日–5 月 6 日鸟取大学干燥地研究中心 Tsunekawa Atsushi 来奈曼站参观访问

5 月 9 日奈曼旗畜牧工作站，黄保平来奈曼站参观访问

5 月 12–15 日北京大学张宏昇来奈曼站参观访问

5 月 12–15 日北京大学鞠婷婷来奈曼站开展实验。

5 月 16–30 日兰州交通大学余沛东来奈曼站开展实验。

5 月 14 日兰州大学草地农业科技学院副院长沈禹颖教授一行 6 人到沙坡头站考察；宁夏大学农学院刘成敏书记、曹兵院长等一行 15 人来站考察。

5 月 19 日兰州大学资源环境学院国家“千人计划”特聘教授贺缠生、美国西密西根大学（Western Michigen University）的 Amanda Sugan Barkman、Michael John Roberts 和 David Antoine Shelmon 等一行 6 人赴沙坡头站进行调研考察。

5 月 20 日内蒙古农牧业科学院，奈曼旗政府翟琇、路战远、白华一行 16 人来奈曼站参观访问

5 月 21 日武汉外国语学校师生 20 余人到站参观学习

5 月 24 日–8 月 12 日西北师范大学张立超来奈曼站开展实验。

5 月 28 日马来西亚博特拉大学（UPM）Liang Juan Boo 教授来皋兰站进行学术交流。报告题目：Use of naturally produced lovastatin for mitigation of enteric methane production。

6 月 2–4 日中国科学院西北生态环境资源研究院，王涛、马小飞、左小安等来奈曼站指导交流

6 月 4–8 日北京市第 101 中学师生 94 人到奈曼站参观学习，进行科普夏令营。

6 月 9 日央视一套中国影像，方志、鲁镐、周克讷、包呼生、霍艳东共 5 人及奈曼旗科技技术协会杨秀媛、陈学林 2 人来奈曼站参观采访

6 月 11–14 日日本鸟取大学彭飞来奈曼站布置样地。

6 月 12–19 日鲁东大学高军凯、侯孟孜、朱婧婧、白雪莲、王理想来奈曼站做实验。

6 月 17 日在防治沙漠化和干旱日央视记者直播沙坡头站科研进展和治沙成果。

6 月 14–19 日鲁东大学常学礼来奈曼站做实验。

6 月 26–27 日中科院大气物理研究所李宝江、李来港来奈曼站开展气象站维护。

7 月 3 日中科院西高所所长张怀刚研究员一行 6 人到沙坡头站考察

7 月 5 日光明日报社记者来奈曼站采访。

7 月 5 日中卫市宣传部袁海青副部长陪同央视记者到站。

7 月 7 日中山大学地理科学与规划学院 30 余名师生在董玉祥教授带领下到沙坡头站参观学习。

7 月 7 日–8 月 12 日西北师范大学刘洪庆、王培玉、赵贺、史佳、培婕、王雪萍、李逢帅来奈曼站开展实验。

7 月 13 日兰州大学新闻与传播学院暑期社会实践小分队一行 6 人到达沙坡头。

7 月 13 日–8 月 3 日内蒙古民族大学，闫雨东、汪冬至、曹万德，来奈曼站开展实验。

7 月 13–18 日银川唐徕回民中学高一师生 65 人到沙坡头站进行暑期社会实践。

7 月 16–18 日天水师范学院一行 5 人来沙坡头站合作交流。

7 月 16–24 日兰州交通大学闫志强、余沛东来奈曼站开展实验。

7 月 20 日陕西师范大学“风沙地貌研究团队 2017 年度野外科考”一行 20 余人到站

7 月 23 日山东卫视《调查》栏目组一行 4 人到站拍摄

7 月 24 日中卫市委宣传部和中央电视台“中国治沙五十年”摄制组一行到站拍摄。

7 月 24 日由中国科学院主办，西北生态环境资源研究院承办的 2017 年度“发展中国家沙漠化研究与治理国际培训班”的 20 余名学员和工作人员赴沙坡头站进行野外考察和参观学习。这些学员来自丝绸之路经济带沿线国家乌兹别克斯坦、哈萨克斯坦、巴基斯坦、伊朗、伊拉克、蒙古国、尼泊尔、卢旺达、苏丹等 9 个国家。

7 月 27 日北京市海淀区科协组织的 25 名小学生到沙坡头站进行暑期实践

7 月 30 日中国科学院地球环境研究所所长刘禹研究员一行 10 人到沙坡头站进行调研访问

7 月 26 日–8 月 3 日内蒙古民族大学张燕、张建辉、张伟阳、周建春来奈曼站开展实验。

8 月 9 日北京大学曹晓峰，柴立伟，黄木柯，张梦君来奈曼站开展实验。

8 月 11-12 日中国科学院微生物研究所，杨处长、钟研究员来奈曼站参观。

8 月 13 日中科院沈阳应用生态研究所所长朱教君一行 7 人来站考察；甘肃省武威市民勤县委书记、县长黄霓，纪委书记俞天平、宣传部部长刘瑞光、副部长张永文、林业局局长杨青文、连古城管理站副站长张世虎等一行 10 余人在宁夏回族自治区中卫市沙坡头区区委领导的陪同下到沙坡头站考察。

8 月 13-18 日中央电视台地理中国栏目组等 7 人拍摄专题片《百年地理大发现之风吟大漠》。

8 月 16-18 日北京市海淀区科普教育协会 20 余名师生到站进行野外科学实践

8 月 23-26 日中科院青藏所汪诗平研究员等 6 人到站进行学术交流。

8 月 27 日在宁夏农林科学院荒漠化治理研究所所长蒋齐研究员的带领下，参加“2017 年阿拉伯国家防沙治沙技术培训班”的国外学员及陪同人员一行共 30 人前来沙坡头站参观、学习。

8 月 29-30 日复旦大学历史地理研究中心副主任杨伟兵教授一行 7 人到沙坡头站调研。

9 月 1 日中科院成都山地所张信宝研究员与中科院普定喀斯特生态系统观测研究站站长彭韬及该站研究人员陈佳一行 3 人参观访问了沙坡头站。

9 月 9-10 日美国内布拉斯加大学，TaLa Awada, Rhae A Drijber（2 人）来奈曼站交流访问。

9 月 20 日中科院西安分院院士专家团“助推宁夏生态环境建设服务行” 一行 20 余考察沙坡头站， 专家组成员主要有安芷生院士、周卫健院士、山仑院士、中科院西安分院党组书记杨星科、中科院成都分院党组书记王学定、中科院水土保持研究所副所长冯浩等。

9 月 27-28 日国际知名生态学家骆亦其教授到沙坡头站进行学术交流。

十、实验室条件

主要实验仪器超过 500 多台/套，单价超过 2 万元的仪器近 140 台套，如野外大型观测设施 ENVIS 梯度气象站、涡度相关观测系统、碳通量观测系统、有机碳测定仪、激光雷达、元素分析仪等；室内红外热成像仪、低温冷室、莱卡激光共聚焦显微镜、智能人工气候室、

凝胶成像系统、酶标仪、Nanodrop 微量核酸定量仪、高效液相色谱仪、气相色谱、实时荧光定量 PCR 仪、紫外分光光度计、双向蛋白电泳仪、低温高速离心机等，总价值逾 2000 余万元。

此外，实验室还包括沙坡头沙漠试验研究站、奈曼沙漠化研究站、皋兰综合试验与农业研究站和一个植物标本室，野外台站为不同尺度上开展逆境生态研究提供基地，实验室为深入推进生理生态学向分子生物学水平拓展提供平台。

实验室仪器设备的管理是在实验室主任负责制下，下设专职管理员进行日常具体的管理。每件套大型仪器实行操作员岗位责任制，建立有仪器运行日志制度、维修与更新制度、运转事故与运行机时统计制度等。

表八　部分实验室仪器设备记录

序号	名称	型号	产地	原值(万元)	购置日期	运行状况
1	涡度相关观测系统	CST-3	美国	400	2006	良好
2	碳通量观测系统	LI-7500	美国	100	2005	良好
3	ENVIS 梯度气象站	ENVIS	德国	80	2004	良好
4	有机碳测定仪	--	美国	50	1998	良好
5	激光雷达系统	--	日本	50	1995	良好
6	激光粒度分析仪	S3500	美国	50	1995	良好
7	植物小气候生长室	TPG-500-TH	澳大利亚	45	2001	良好
8	光合呼吸测定仪	LI-6400	美国	42	2002	良好
9	高效气相色谱仪	Agilent	美国	40	2007	良好
10	人工降雨模拟系统	DIK-6000	日本	40	2008	良好
11	土壤碳通量测定系统	LI-8100	美国	40	2009	良好

12	半自动定氮仪	1026	德国	35	1998	良好
13	高效液相色谱仪	Waters600	美国	30	2006	良好
14	便携式叶绿素荧光仪	PAM–2000	德国	30	2002	良好
15	高速低温离心机	H–2050R	中国	4.5	2008	良好
16	凝胶成像系统	380C	中国	4.4	2008	良好
17	生物安全柜	SG403	德国	5.0	2008	良好
18	PCR 仪	Biometra	德国	5.6	2008	良好
19	冷冻高速离心机	Beckman J–25	德国	23	2008	良好
20	超低温冰箱	Haris ELT–13V	德国	5.6	2008	良好
21	超低温冰箱	Thermo	美国	5.0	2008	良好
22	超纯水机	Milli–Q	美国	5.0	2008	良好
23	超声波仪	Virsonic 100	德国	2.96	2008	良好
24	q–Real–Time PCR 仪	strategene MP3000	美国	27.0	2009	良好
25	梯度 PCR 仪	ABI 梯度	美国	10.0	2008	良好
26	普通 PCR 仪	ABI–2020	美国	3.0	2008	良好
27	Nanodrop	2000C	美国	7.0	2008	良好
28	纯水系统	UPR－I－20T	中国	2.0	2008	良好
29	智能人工气候植物箱	HP 1500GS－B	中国	3.0	2008	良好
30	红外热相仪	Vci－480	德国	23.4	2008	良好
31	高通量组织研磨器	MM400	德国	4.91	2008	良好

32	台式高速冷冻离心机	primo R	美国	9.0	2008	良好
33	超纯水系统	18.2MQCM	英国	3.42	2008	良好
34	全自动高压灭菌锅	MLS－3750	日本	3.45	2008	良好
35	PCR 核酸扩增仪	Icycler	美国	14.40	2008	良好
36	核酸扩增仪	C1000	美国	8.4	2008	良好
37	凝胶成像系统	Imagequant300	美国	6.65	2008	良好
38	分子杂交箱	WTB-BINDER	美国	3.35	2008	良好
39	离心浓缩系统	CENTRIVAP	美国	3.35	2008	良好
40	超低温冰箱	SANYO	日本	4.8	2008	良好
41	蛋白质电泳系统	BioRad Powerpac 3000	美国	5.0	2008	良好
42	高通量测序仪	Illumine Miseq	美国	111.6	2015	良好
43	元素分析仪	ECS4010	意大利	50	2014	良好
44	扫描电镜	FEI, MLA650	美国	291.4	2016	良好
45	激光共聚焦显微镜	莱卡 sp8	德国	147	2014	良好
46	光合呼吸测定仪	LI-6400	美国	96	2013	良好
47	水分碳氮分析仪	Vario Toc	德国	28	2013	良好
48	超低温冰箱	Thermofisher	美国	14	2012	良好
49	光照培养箱	Boxun	国产	4.0	2012	良好
50	高速离心机	Sigma	美国	5.2	2014	良好
51	小型发酵罐	INFOS	瑞士	23	2013	良好
52	流式细胞仪	BD 公司 C6	美国	34.72	2015	良好

2017 年实验室科研突破与创新进展

一、中国北方风沙危害区生态重建与恢复理论研究

中国北方风沙危害区主要包括四大沙地和相邻的农牧交错带，以及贺兰山以西的荒漠/沙漠与绿洲的过渡区，面积达 32 万平方公里，是沙漠化最为严重和发展最快的地区。植被建设是遏制沙化进一步发展和促进风沙区生态重建与恢复的有效途径和主要手段，人工植被的可持续性事关防沙治沙的成败。

中国科学院沙坡头沙漠研究试验站李新荣研究员主持的 973 计划项目“植物固沙的生态水文过程、机理和调控”于 2017 年 11 月 21 日顺利通过了科技部组织的验收。项目回答了不同沙区土壤水分的植被承载力、人工植被的生态和水文过程的相互作用机理，以及如何界定维持固沙植被稳定性的生态水文阈值等科学问题。首次探明了植物固沙的规模与土壤水植被承载力之间的关系，为识别人工植被退化与稳定提供了依据；从植物对风沙环境和水文过程的响应，水文过程对植被的影响以及植物种间关系等方面揭示了降水、土壤水、地下水和植物的水分利用对固沙植被演变的驱动机理，率先提出土壤生境恢复是判别沙区生态重建成功与否的新观点；在国际上首次提出了人工植被稳定性维持的“生态水文阈值”的概念，明确了不同气候带适宜固沙植被的生态水文阈值，提出了不同沙区的植物固沙范式。项目共发表 SCI 论文 160 篇，出版专著 3 部，发明专利 7 项，项目主要负责人和骨干获基金委创新研究群体资助，1 人获“杰青”，1 人获“优青”资助。获省部级一等奖 2 项目，修订了《国家造林技术规程》(GB/T 15776–2016)，为国家防沙治沙做出了贡献。

二、基于长期观测资料，探明了荒漠灌木树干茎流的动态变化特征

土壤水分在调控植被时空分布格局并影响气候–土壤–植被系统的复杂动态过程中起关键作用。准确认识生物量与土壤水分的动态耦合特征，是揭示荒漠生态系统稳定性及可持续性的基础。因此，在未来气候（降水格局）变化情景下，生物量与土壤水分动态的随机耦合关系，是干旱区生态水文学领域的前沿科学问题。基于长期观测资料，刻画了沙坡头地区随机降水的泊松分布特征，并在综合考虑植物冠层对降水截留、植物根区土壤导水率及持水性能的基础上，确定了耦合土壤水分调节作用的单位生物量增长和损失因子、单位生物量蒸

腾耗水等关键参数，界定了生物量、土壤水分的稳态及瞬态变化范围，揭示了生物量–土壤水分动态非线性变化的概率分布规律，构建了耦合土壤水分的生物量动态随机微分方程，预测了降水格局变化情景下生物量和土壤水分的变化趋势。(Wang et al., PNAS, 2017, 114(25): E4944–E4950)。

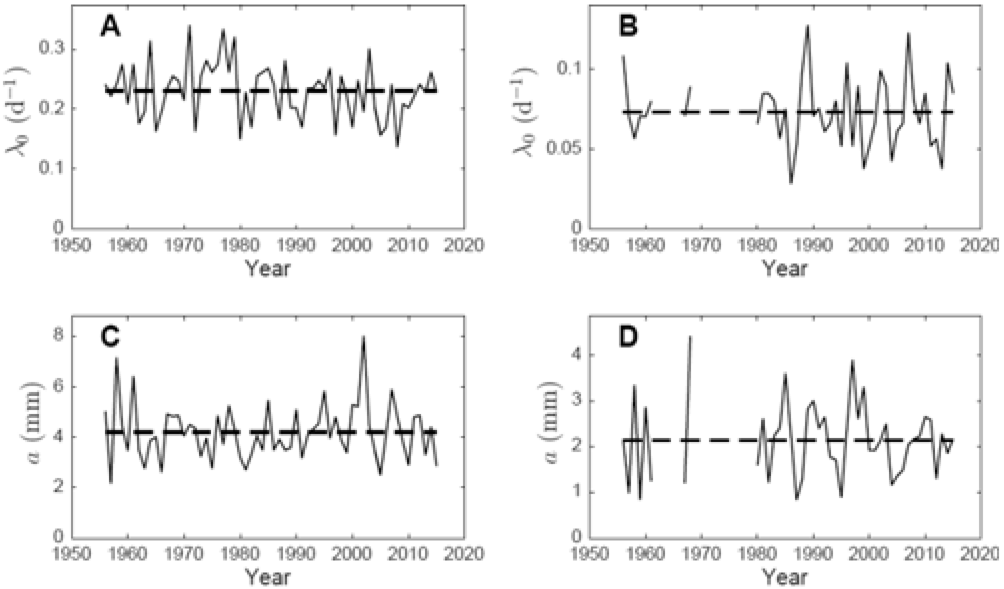


图 1 研究区多年平均降水日数(A，湿润季；B，干旱季)及降水日的日平均降水量(C，湿润季；D，干旱季)动态

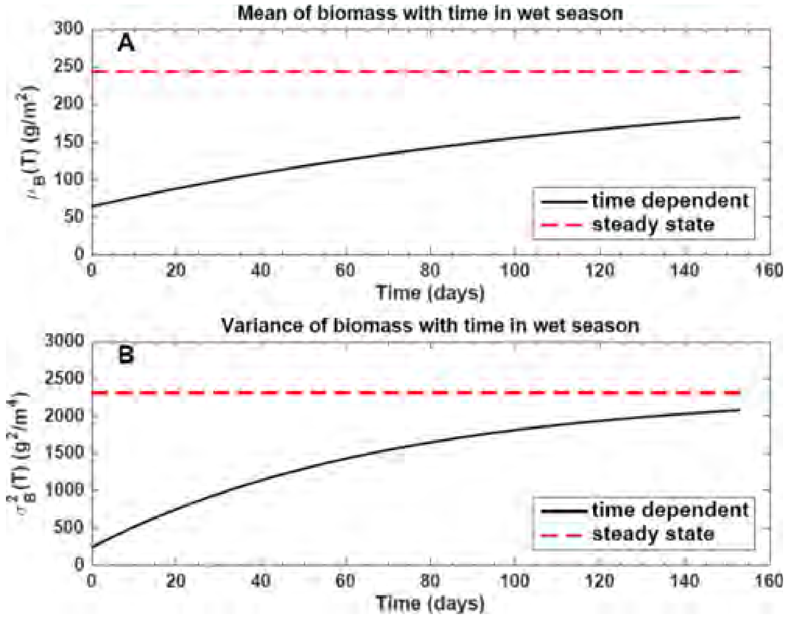


图 2 随时间变化的生物量均值(A)及方差(B)与稳态值比较

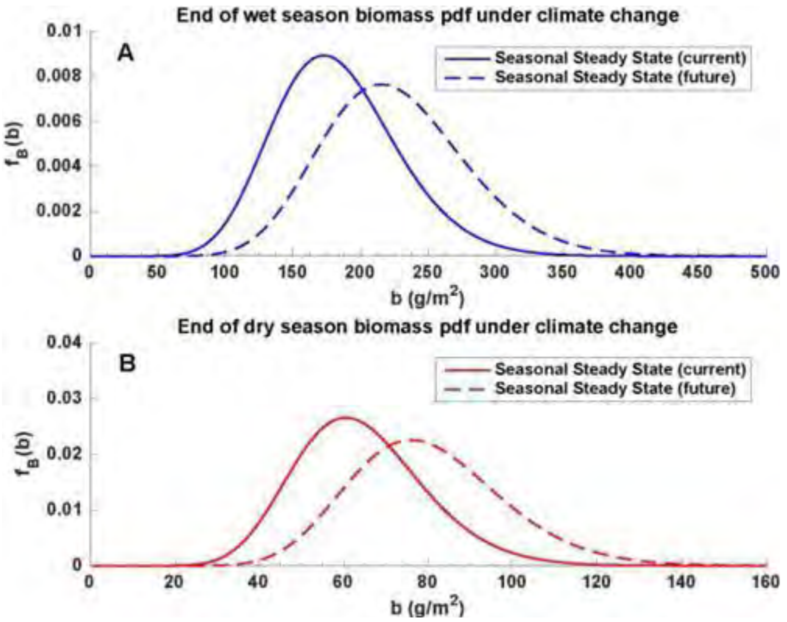
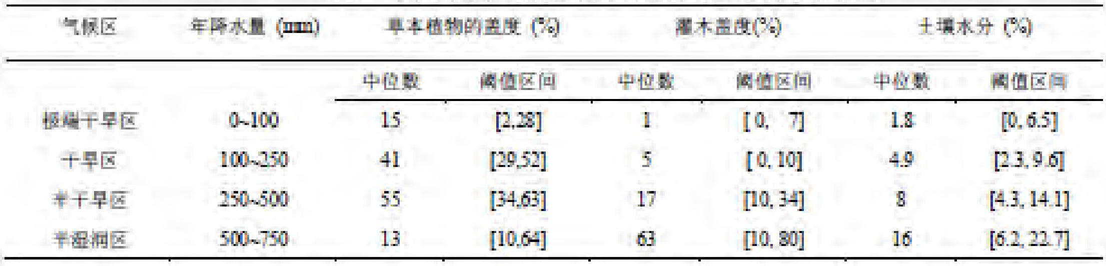


图 3 降水变化情景下湿润季末(A)和干旱季末(B)生物量分布

三、通过对已建立的生态水文模型的模拟，确定了我国不同气候区典型固沙植被的生态水文阈值，评估了不同气候区固沙植被的稳定性

通过建立耦合固沙植被盖度和土壤水分的生态水文模型探讨了以天为尺度的随机降水格局对人工固沙植被建立后的植被盖度和土壤水分动态的影响。模型模拟结果表明，草本植被的盖度、固沙灌木的盖度和土壤水分均随年降雨量的增加呈现非线性的增长趋势。其中，草本植被的盖度随年降雨量的增加呈现先增加后减少的趋势，固沙灌木的盖度随年降雨量的增加呈现幂律增长的趋势，土壤水分随年降雨量的增加呈现指数增长的趋势。同时，通过对已建立的生态水文模型的模拟，确定了我国不同气候区典型固沙植被的生态水文阈值。生态水文阈值的确立不仅可以促进目前我国干旱生态系统的管理和防风固沙效益的可持续发展，而且可以为未来我国风沙危害区植被恢复和建设提供可量化的依据（Li et al., Ecological Indicators, 2017, 83: 404–415）。

表 1 中国不同气候区固沙植被的生态水文阈值



气候区	年降水量 (mm)	草本植物的盖度 (%)		灌木盖度(%)		土壤水分 (%)	
		中位数	阈值区间	中位数	阈值区间	中位数	阈值区间
极端干旱区	0~100	15	[2,28]	1	[0, 7]	1.8	[0, 6.5]
干旱区	100~250	41	[29,52]	5	[0, 10]	4.9	[2.3, 9.6]
半干旱区	250~500	55	[34,63]	17	[10, 34]	8	[4.3, 14.1]
半湿润区	500~750	13	[10,64]	63	[10, 80]	16	[6.2, 22.7]

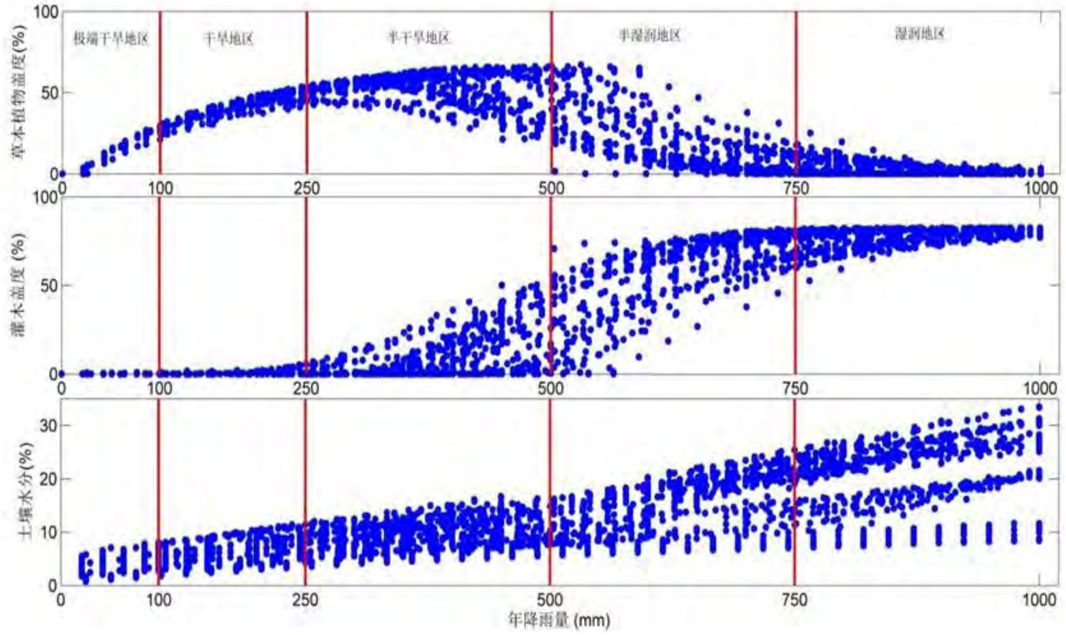


图 4 草本植物的盖度（A）、灌木盖度（B）和土壤水分（C）随年降水量的变化规律

表 2　6 个典型的野外研究区固沙植被的生态水文阈值

指标	荒漠绿洲边缘 (临泽)	古尔班通古特 (阜康)	腾格里沙漠 (沙坡头)	毛乌素沙地 (盐池)	科尔沁沙地 (奈曼旗)	科尔沁沙地 (章古台)
年均降水量（mm）	117	160	186.6	295	366.4	469
降水区间（mm）	[80,150]	[100,200]	[140.220]	[180,330]	[250,450]	[350,550]
实际草本盖度（%）	28	33	35	40	43	35
草本的阈值区间（%）	[24,39]	[28,45]	[33,48]	[43,58]	[38，63]	[23，64]
实际灌木盖度（%）	12	18	9	30	33	35
灌木的阈值区间（%）	[0,13]	[0,15]	[7,18]	[14,32]	[10,38]	[15,50]
实际土壤水分（%）	2.24	3.65	2.3	4.3	3.4	5.2
土壤水分的阈值区间（%）	[2.07,8.44]	[2.16,8.84]	[2.23,9.6]	[3.48,11.4]	[3.24,13.67]	[5.05,15.23]
土壤水分的阈值区间（%）	[2.07,8.44]	[2.16,8.84]	[2.23,9.6]	[3.48,11.4]	[3.24,13.67]	[5.05,15.23]

四、植物角质层系统研究

干旱区植物在长期进化过程中形成了独特的水分胁迫适应机制，是认识干旱区生态水文过程的基础，而角质层作为植物水分关系的生态界面却被长期忽视。2017 年在植物角质层方面的系统研究成果如下：

1) 揭示了植物叶片角质层的保水功能

在生理生态水平上，展示了角质层结构对角质层保水功能的重要贡献，拓展了荒漠植物水分关系研究的内涵；在遗传水平上，确定了相关基因在染色体上的位置，突破了着丝粒附

近克隆基因难关，创造性地利用遗传分析与转录组分析相结合的方法，克隆了 GDSL 酯酶基因；在分子水平上，发现了该基因在表皮细胞表达，确认了其编码蛋白位于角质层，证明了该酯酶在角质网结构建成中的重要作用，阐明了叶片表皮细胞细胞壁外角质网构建的分子机制，论证了角质网对角质层结构形成的重要性；在进化水平上，分析了该基因在陆生植物中的保守性，论证了该基因在植物对干旱环境适应过程中的意义（Li et al., 2017. Plant Direct, https://doi.org/10.1002/pld3.25）。

2) 揭示了植物叶片角质层蜡质晶体形成的分子基础

阐明了叶片表面蜡质晶体形态对叶片疏水性及叶片持水能力的决定性作用，证明了叶片表面蜡质晶体形成及其形态与蜡质组成有关，明确了 β 双酮是细棒状蜡质晶体的主要成分；精细定位了相关基因在染色体上的区间，提出了候选基因，为深入研究 β 双酮的生物合成基因及其合成通路奠定了雄厚的基础（Zhou et al.,2017.Theoretical and Applied Genetics,130: 1169–1178）。

3) 揭示了植物叶片角质转运相关基因与系统获得性抗性有关

展示了角质单体全分子转运蛋白基因 ABCG31 突变促进系统获得性抗性相关基因的表达，论证了它们之间的相关性，提出了 ABCG31 介导的获得性抗性模式；用比较转录组方法验证了 ABCG31 基因克隆的准确性，提出了克隆自然突变基因的新方法（Zhou et al., 2017. Genetics and Molecular Biology, 40: 834–843）。

五、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（Qian CJ et al, Journal of Systematics and Evolution，2018）。

六、通过植物的种内变异将群落尺度的功能多样性和生产力变化建立了相关性

全球环境变化对植物种内性状引起的功能多样性变化和群落内共存物种生态位幅度的影响最终将改变群落尺度的功能多样性和生产力。基于此，我们计算了氮素添加和冬季降雪增加后沙质草地优势物种和亚优势物种的功能多样性、共存物种的生态位重叠、和生产力的变化。结果表明，氮添加增加了一年生植物的生产力从而使得整体群落生产力增加，也增加了一年生植物和多年生植物种内性状变化的功能多样性（FDITV）和生态位重叠（图 5，图 6）。这一结果指示氮添加后，更多喜氮植物可以存活，正由于喜氮植物比例增加且均依赖于对氮的获取，因此群落内的物种之间的竞争强度增加，表现为生态位重叠增加（图 7）。然而降雪增加没有显著改变多年生植物的生产力和种内功能多样性变化，反而增加了一年生植物的种内功能多样性和性状重叠（图 6，图 7）。冬季增雪并没有明显增加土壤氮含量，因此对群落的影响较弱，只是通过影响一年生植物而改变群落生产力。本研究证实了在沙质草地一年生植物功能性状的迅速改变是其获取高生产力的重要途径。优势的一年生植物对环境条件的改变更加敏感，将在很大程度上决定群落的功能多样性、生态位重叠和群落生产力。此外，我们的研究也再次验证了优势植物对环境的响应决定了群落功能多样性的变化方向。（Mao W et al, Frontiers in Plant Science, 2017, 8(28821).）

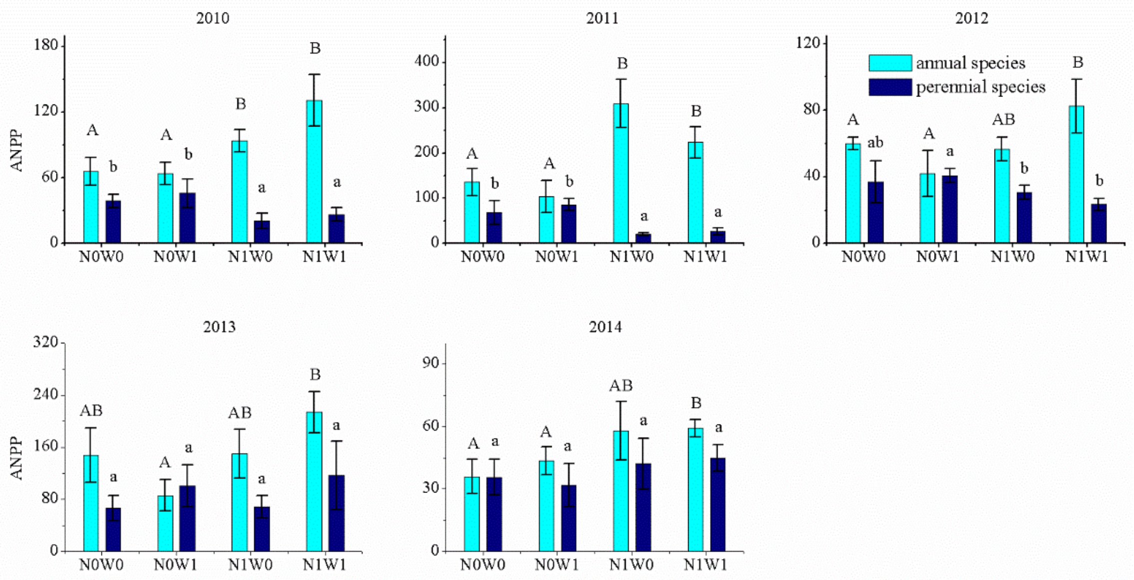


图 5 沙质草地生态系统一年生植物和多年生植物的生产力

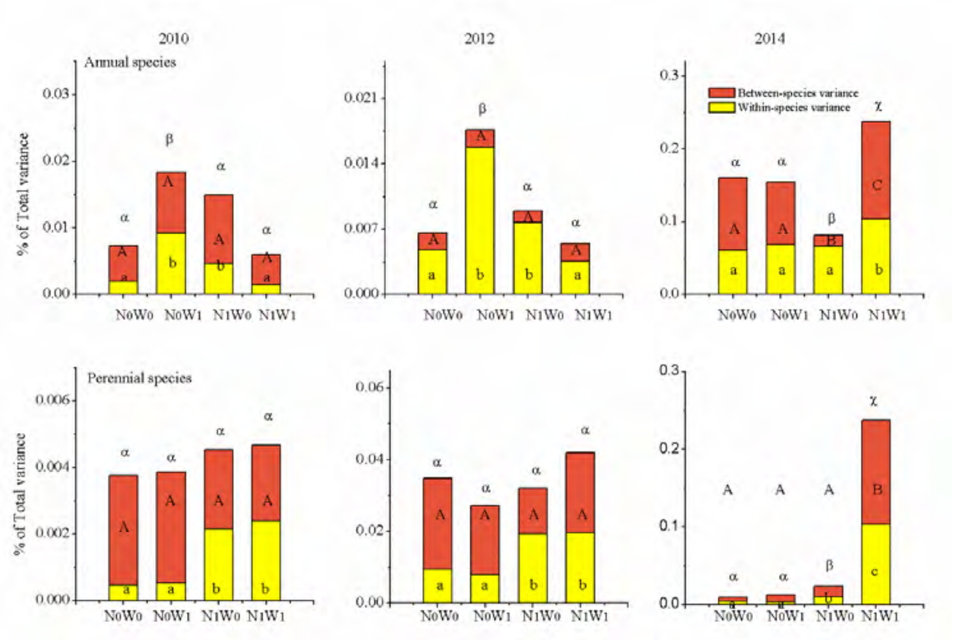


图 6 氮素增加和冬季增雪后沙质草地一年生植物和多年生植物的种内功能多样性和种间功能多样性

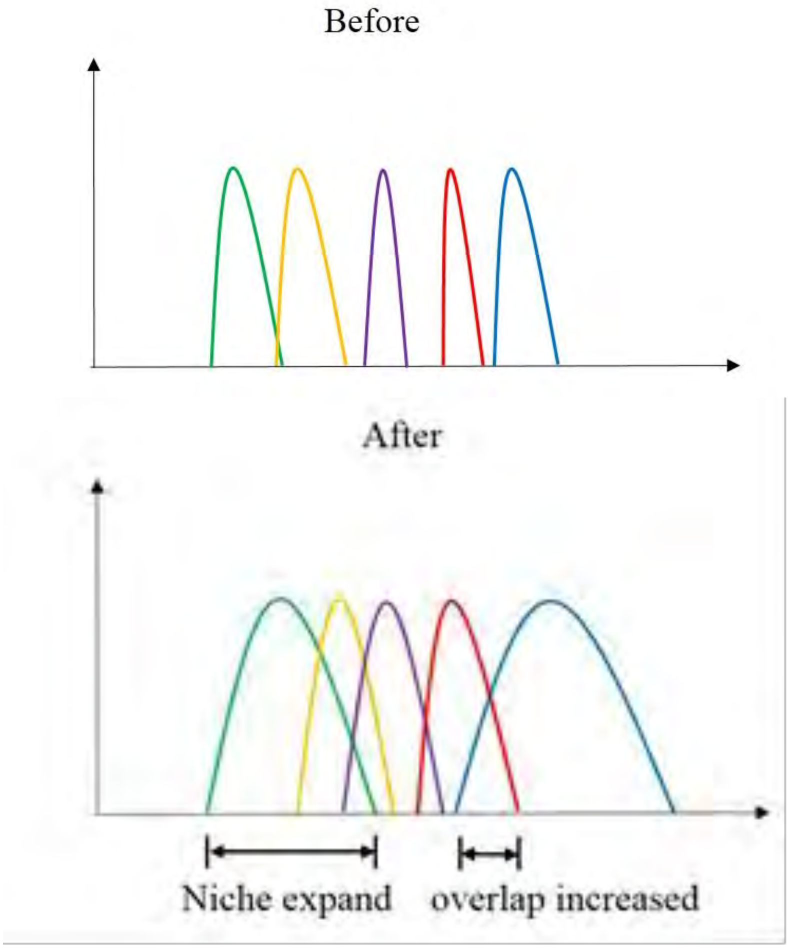


图 7 氮素增加和冬季增雪后沙质草地群落共存物种生态位重叠的变化

七、揭示了沙地不同生境类型植被对降水和温度增加的响应特征

为深入了解半干旱退化沙质草地植物对温度和水分增加的响应，我们研究了在流动沙丘、固定沙丘和草地 3 种生境维管植物对气候变暖、降水增加的响应。植物生物量，特别是地上生物量，在沙丘种类中差异显著($P < 0.05$)。固定沙丘和草地的总植物密度为流动沙丘的 1.9 和 1.7 倍（图 8）。物种丰富度变化较小但差异性显著($P < 0.05$)。增加 30%对任何植物变量没有显著影响。相比之下，温度增加显著降低了地下生物量、总生物量、物种丰富性和植物总密度（图 9）。在半干旱沙质草地，降水量增加对植物生长的影响较小，而温度升高显著抑制了植物的生长。土壤质地可能是降水异常低时决定这些反应的关键因素。（Luo YQ et al，Ecological Research, 2017, 32(6), 887–898）

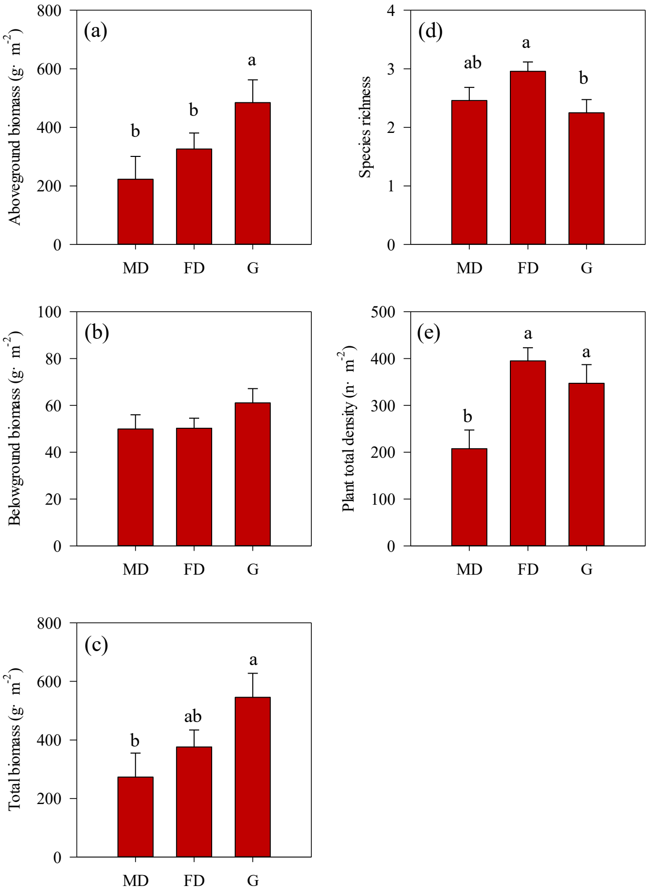


图 8 不同生境植物地上生物量(a)、地下生物量(b)、总生物量(c)、丰富度(d)和密度(e)特征

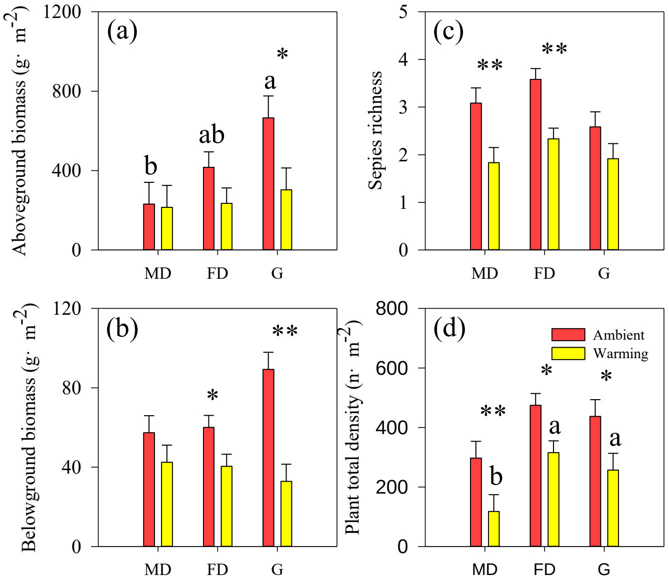


图 9 温度增加对不同生境植物地上生物量(a)、地下生物量(b)、丰富度(c)和密度(d)的影响

八、明确了沙化草地恢复和增温对小叶锦鸡儿生殖成功率的影响

随着科尔沁沙化草地的恢复，生态环境得到明显改善，植被盖度、物种丰富度显著增加，但小叶锦鸡儿传粉蜜蜂的物种丰富度和访花频率的变化趋势与植被结构的变化不一致。半固定沙丘与流动沙丘传粉蜜蜂的物种丰富度和访花频率没有显著差异，到固定沙丘阶段小叶锦鸡儿传粉蜜蜂的物种丰富度和访花频率显著增加（图 10），从而导致小叶锦鸡儿生殖成功率在固定沙丘阶段明显提高，而半固定沙丘与流动沙丘小叶锦鸡儿生殖成功率没有显著差异（图 11）。研究结果表明，增温使小叶锦鸡儿花朵密度显著降低，而对其座果率没有显著影响，导致小叶锦鸡儿种子产量显著降低（图 12）。传粉昆虫的变化与季节性花卉资源的变化密切相关，以上结果说明，在退化土地恢复过程中增加花卉资源和传粉昆虫的多样性和数量对植物的生存和繁殖具有重要意义，有利于退化土地指标的恢复。（Scientific Reports, 2017, 7: 2795）

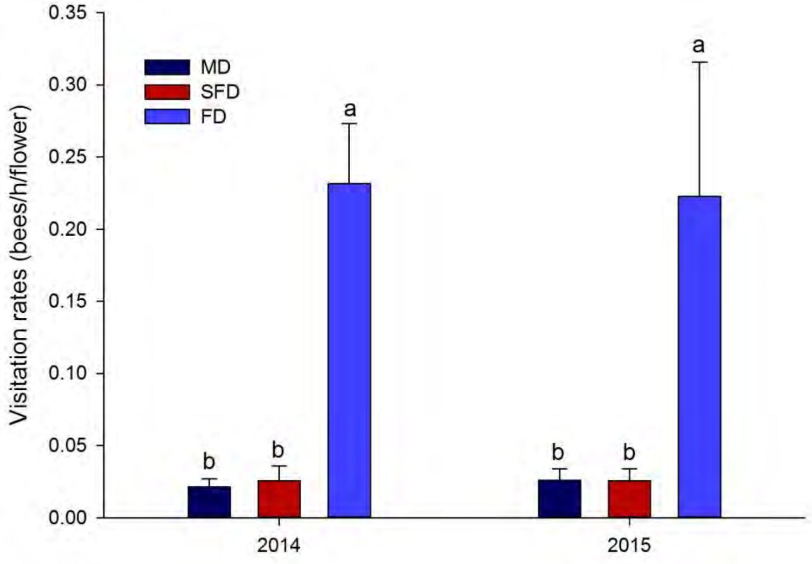


图 10 沙化草地恢复过程中小叶锦鸡儿传粉蜜蜂访花频率的变化

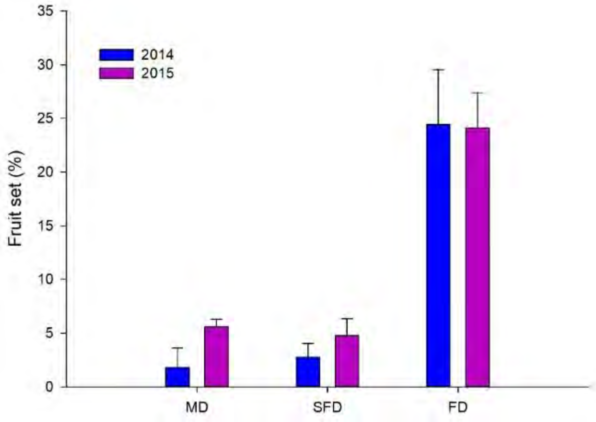


图 11 沙化草地恢复过程中小叶锦鸡儿座果率的变化

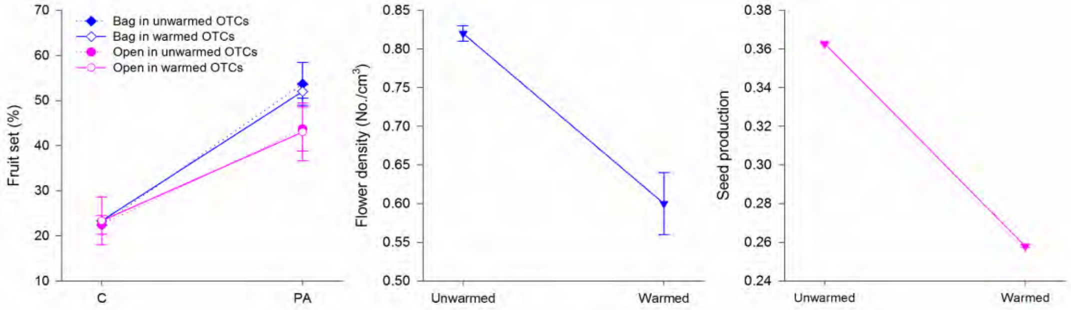


图 12 增温对小叶锦鸡儿生殖成功率、花朵密度和产量的影响

九、解淀粉芽孢杆菌诱导植物抗盐的分子机理

通过对 FZB42 处理的受盐胁迫植物中的耐盐相关生理指标和转绿组变化研究，以及分析 FZB42 对拟南芥突变体耐盐性的诱导，确定了植物响应 FZB42 诱导而提高自身盐耐受性时的信号通路。并通过研究 FZB42 生物被膜和乙偶姻突变体对植物耐盐性的影响，发现生物被膜是 FZB42 根际接菌诱导植物耐盐的重要物质，而乙偶姻可能不是 FZB42 挥发物发挥促生及增强植物耐盐的关键物质。主要研究内容如下：

在水培条件下，FZB42 可以增强拟南芥耐盐能力。在 100 mM NaCl 下，FZB42 处理的拟南芥生物量显著高于对照组，鲜重和干重分别增加了 24.7%和 27.2%。基于 Illumina 的 RNA-seq 方法对非盐和盐胁迫下拟南芥响应 FZB42 的差异表达基因进行分析，分别得到 1461 和 1288 个 DEGs。在 100 mM NaCl 下，FZB42 调控拟南芥中与光合作用、生长素、抗氧化酶、Na+隔离和渗透保护物质相关基因的表达，降低了植物对盐的敏感性，增强植物对盐环境的

适应性。同时，FZB42 使拟南芥中的 Na+浓度显著降低，并且促使 Na+/K+比率升高。此外，我们发现FZB42调控拟南芥中JA合成、响应JA的防御基因和ET合成及ET信号转导的DEGs全部表达上调，而 ABA 通路相关基因全部表达下调。转录组结果初步发现 JA/ET 在 FZB42 诱导植物耐盐过程中的重要作用。FZB42 诱导拟南芥突变体（etr1-3、eto1、 jar1-1 和 abi4-102）的耐盐结果进一步证实 FZB42 通过调控植物中 JA/ET 信号通路诱导植物耐盐性，并且该过程与 ABA 途径无关。

生物被膜在 PGPR 促进植物生长及诱导植物抗性的过程中发挥了重要作用。通过启动子融合和转座子等分子手段，研究获得与生物被膜相关的胶原样蛋白基因的调控基因 spoⅡGA、kinA 和 spo0A。这三个基因都影响 FZB42 中生物被膜的形成，△spoⅡGA、△kinA 的生物被膜比 WT 褶皱少，但△spo0A 完全不能产生生物被膜。在非盐和盐胁迫条件下，发现生物被膜的产生受到一定影响的△spoⅡGA 和△kinA 仍能促进植物生长，而完全不能产生生物被膜的△spo0A 丧失促进植物生长和诱导植物耐盐性的功能。说明生物被膜在 FZB42 发挥促生及诱导植物耐盐过程中的重要作用。

研究 FZB42 挥发物对植物耐盐性影响时，发现 VOCs 能显著增加受盐胁迫的拟南芥的生物量，说明 VOCs 能诱导植物的耐盐能力。VOCs 在提高植物耐盐性时，诱导植物中生长和耐盐相关的生理指标发生变化，包括叶绿素（Ca、Cb 和 Ca+b）含量升高、抗氧化酶活性（POD、CAT 和 SOD）增加和可溶性糖含量增加。同时，VOCs 通过调控植物中的 Na+/H+逆向转运蛋白基因（NHX1 和 HKT1）表达，降低拟南芥中 Na+浓度，增加 Na+/K+比率，进而缓解 Na+毒害。在 100 mM NaCl 下，VOCs 对拟南芥激素相关突变体（etr1-3、eto1、abi4-102、cre1-2、ga1、aux1-7、jar1-1、nahG 和 npr1-1/jar1-1）促生结果显示，挥发物不能促进茉莉酸相关突变体 jar1-1 和 npr1-1/jar1-1 的生物量的增加，初步证明 FZB42 挥发物可能是通过调控植物中 JA 通路来诱导植物耐盐性。此外，VOCs 调控受盐胁迫植物中的 JA 合成（LOX4）和响应 JA 的防御基因（JMT、PDF1.3、PDF1.2c 和 PDF1.2）表达，并且组织中 JA 含量升高，进一步证明 JA 信号通路在 FZB42 挥发物诱导植物耐盐过程中的作用。

乙偶姻是 FZB42 挥发物中第二大成分，为了验证乙偶姻是否是 FZB42 中促进植物生长和诱导植物抗性的信号物质，我们对 FZB42 中参与乙偶姻合成基因 alsD 和 alsS 进行敲除。

△alsD 产生乙偶姻能力下降，但仍能产生少量的乙偶姻，而△alsS 几乎不能产生乙偶姻。通过分析比较△alsD、△alsS 与 WT 挥发物对拟南芥促生和诱导耐盐胁迫的影响，发现与 WT 一样，△alsD 和△alsS 显著促进非盐和盐胁迫中植物生长，△alsD 和△alsS 挥发物处理的拟南芥生物量显著高于对照组。说明乙偶姻可能不是 FZB42 挥发物中发挥促生和诱导植物耐盐性的关键物质。

综上所述通过对转录组、生理代谢及拟南芥突变体数据分析，首次发现植物主要通过 JA 信号通路响应 FZB42 的诱导来增强自身耐盐性。该研究首次从植物如何响应 PGPR 诱导和 PGPR 自身如何诱导植物耐盐两方面揭示了 PGPR 诱导植物耐盐的分子机理，为 PGPR 在盐碱地的推广应用奠定理论基础(Liu SF et al, Scientific Reports. 2017, 13, 7(1):10795）。

十、寒区旱区农牧耦合与高效循环利用研究与示范

1）皋兰站开展冷应激下阿勒泰羊与湖羊能量与蛋白代谢机制研究

在我国北方寒区旱区，绵羊是最重要的草食家畜之一。由于受特殊的生态、气候与环境的限制，该地区绵羊饲养管理方式较为粗放，主要是在草地上终年放牧，很少补饲。经过成百上千年的自然和人工选择，北方土种绵羊已经形成了耐粗饲、抗严寒、生长快的特点。相关研究表明绵羊能量和蛋白代谢受环境温度的影响非常之大，在实际生产中，我们也发现阿勒泰羊对冷应激的耐受能力较湖羊强。基于此，本课题主要对比研究阿勒泰羊与湖羊对冷应激的响应机制，并探讨满足绵羊维持能量–越冬产热的能量需求与尿素代谢特征，为开发绵羊冬季补饲科学配方与饲料添加剂提供基础数据。

A. 消化代谢实验

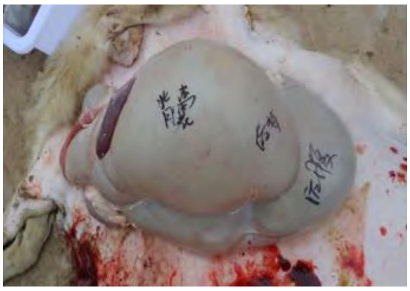

粪尿收集


尿液处理


粪便取样

B. 屠宰实验

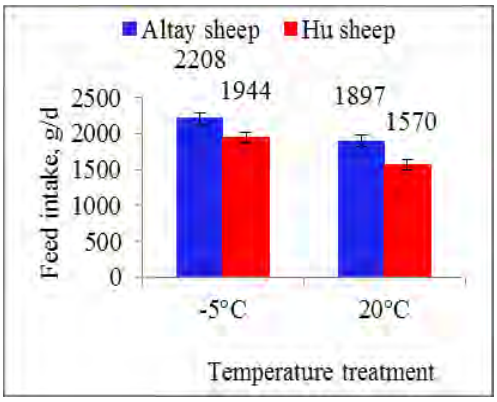
脂肪组织取样



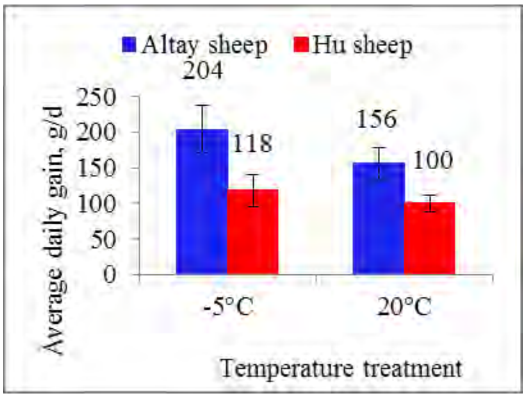
绵羊复胃

肠道分离

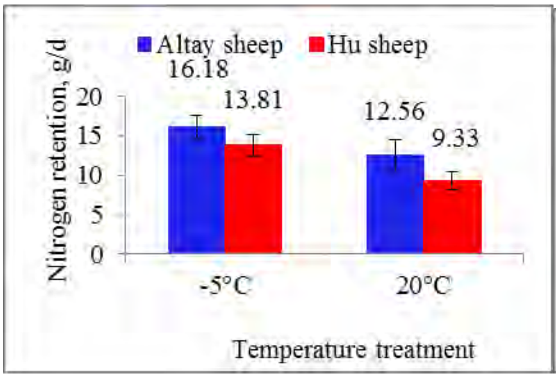
C. 研究结果



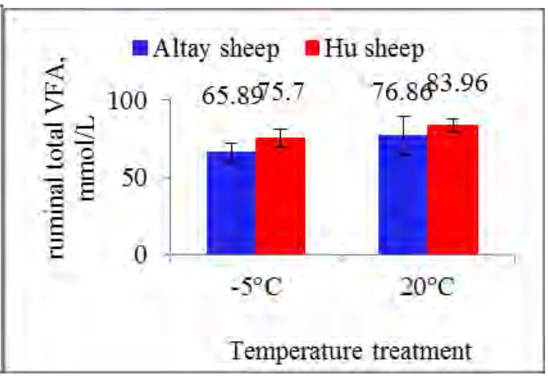
a.饲料采食量



b.生长性能



c.瘤胃液 VFA 浓度



d.氮沉积

a) 冷应激下，绵羊饲料采食量都显著增加，且阿勒泰羊采食量高于湖羊；与常温组相比，湖羊饲料采食量增加速率（20.83%）高于阿勒泰羊（13.58%），这表明阿勒泰羊和湖羊在寒冷胁迫下的能量维持需要、能量利用效率及其调控机制可能存在不同。

b) 自由采食条件下，阿勒泰羊生长性能优于湖羊；当环境温度为-5℃时，阿勒泰羊的生长速度最快，这说明阿勒泰羊对寒冷胁迫具有极强的适应性，其在低温下可能具有更加高

效的能量代谢及其调控机制。

c) 自由采食条件下，湖羊瘤胃液 VFA 浓度高于阿勒泰羊；寒冷胁迫下，绵羊 VFA 浓度显著降低，这是因为低温下需要更多的 VFA 用于氧化供能，进而促进了绵羊瘤胃中 VFA 吸收。

d) 自由采食条件下，阿勒泰羊氮沉积量显著高于湖羊，因而表现出更佳的生产性能；当环境温度为–5℃时，阿勒泰羊的氮沉积量最大。

2）中科院“第二粮仓农牧耦合改土技术”

农牧耦合改土技术主要通过牧草种植、牲畜饲养、粪肥还田等手段来改善土壤理化性质，从而提高砂姜黑土有机质含量，更新腐殖质，优化菌群结构，抑制土壤胀缩性。目前，在安徽省蚌埠市农亢农场种植苜蓿、白三叶、羊草、高丹草等牧草 100 亩，可移动式羊舍 2 栋（每栋面积 150 平米），养殖绵羊 100 多头，通过该研究，以期提高土壤肥力指标 5%以上、提高饲草转化效率 10%以上、提升经济效益 10%以上

3）中科院“呼伦贝尔生态草牧业示范工程”

自动称重系统

呼伦贝尔羊人工授精

呼伦贝尔羊
饲料配方手册

主编：杨果，刘虎，周建伟，赵凯，段子渊

中国科学院西北生态环境资源研究院
中国科学院西北高原生物研究所
中国科学院遗传与发育生物学研究所

呼伦贝尔羊饲料配方手册

澳巴羊
饲料配方手册

主编：周建伟，刘虎，杨果，赵凯，段子渊

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澳巴羊饲料配方

Probabilistic model predicts dynamics of vegetation biomass in a desert ecosystem in NW China

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The temporal dynamics of vegetation biomass are of key importance for evaluating the sustainability of arid and semiarid ecosystems. In these ecosystems, biomass and soil moisture are coupled stochastic variables externally driven, mainly, by the rainfall dynamics. Based on long-term field observations in northwestern (NW) China, we test a recently developed analytical scheme for the description of the leaf biomass dynamics undergoing seasonal cycles with different rainfall characteristics. The probabilistic characterization of such dynamics agrees remarkably well with the field measurements, providing a tool to forecast the changes to be expected in biomass for arid and semiarid ecosystems under climate change conditions. These changes will depend—for each season—on the forecasted rate of rainy days, mean depth of rain in a rainy day, and duration of the season. For the site in NW China, the current scenario of an increase of 10% in rate of rainy days, 10% in mean rain depth in a rainy day, and no change in the season duration leads to forecasted increases in mean leaf biomass near 25% in both seasons.

ecohydrology | stochastic dynamics | vegetation modeling | climate change impacts | soil moisture

In arid and semiarid ecosystems, successful use of limited water resources is of central importance in determining the evolutionary trends of vegetation. Soil moisture there is the principal limiting factor for vegetation restoration and plays a key role in controlling the spatiotemporal patterns of vegetation regulating the complex dynamics of the climate–soil–vegetation system (1, 2).

Characterizing the vegetation in water-limited ecosystems, with regard to quantity, species composition, and stability, is a long-standing problem in restoration ecology (3). Field surveys and different types of measurements have been taken for decades (4), but they have mostly yielded only descriptive results [e.g., links between soil moisture and accompanying biomass (5)].

Schaffer et al. (3) recently developed an analytical description of the transient joint behavior of plant biomass and soil moisture induced by stochastic rainfall dynamics. These analytical results allow for predictions of ecosystem behavior under changing climate conditions and also illuminate the sensitivities of the dynamics to plant physiology, as well as to climate and soil characteristics that govern the system. The objective of this study is first to test the accuracy of the analytical model under current conditions by comparing its predicted distribution for the biomass density in both the wet and dry seasons with the statistics observed in a long-term field experiment in northwestern (NW) China. Subsequently, using the climate change forecast of the field site, predictions will be made for the seasonal mean biomass and its variability in the future.

Ecosystem Characteristics: Climate, Soil, and Vegetation

Long-term detailed measurements of vegetation dynamics were carried out at the plant level in four plots located at the Shapotou Desert Research and Experiment Station in NW China. Meteorological 60-y records at the station provide an adequate characterization of the rainfall dynamics at the site. The mean annual rainfall is 182.6 mm, of which 82% falls in the rainy season (May 1–September 30) with an observed range between 60 mm and 270 mm and a SD of 57.1 mm. The mean rainfall during the wet season is 149.1 mm and during the dry season is 33.5 mm, with SDs of 51.5 mm and 16.9 mm, respectively.

The arrival of rainfall events is modeled as a Poisson process in which the rate λ_0 (d^{-1}) is constant over the course of a season, but varies between seasons. After accounting for interception (which acts as a censoring process), the rainfall arrival rate is transformed into the infiltration arrival rate λ (2); λ inherits the seasonal characteristics of λ_0, namely constant intraseason and variable interseason values.

The temporal structure within each rainfall event is ignored, with all water modeled as arriving in an instantaneous pulse with random depth. For values of the arrival rate typical of water-limited systems (such as those here), it will be rare for such a process to produce multiple arrivals in a given day, and so the continuous-in-time Poisson process can be correctly understood at the discrete daily scale. In this case, λ_0 (d^{-1}) represents the probability of having rain on a given day, and the distribution of rain depth during a pulse arrival is equivalent to the distribution of rain depth on any rainy day (6); in particular, this distribution is taken to be exponential with mean a (2). The fluctuations of λ_0 and a for both seasons at the site for the period 1956–2015 are shown in Fig. S1.

A detailed description of the field site, its climate, soil, and vegetation is given in *Field Site and Vegetation*. Based on the analysis

Significance

The temporal dynamics of vegetation biomass are of vital importance for evaluating the sustainability of arid and semiarid ecosystems. Field observations indicate that soil moisture and plant biomass fluctuate stochastically with the occurrence of rainfall events. Based on long-term field observations, we find that the dynamics of the vegetation biomass can be quantified by their analytically derived time-dependent probability distribution. This allows for the study of the impact of climate change scenarios on vegetation cover and plant water resource competition. It is found that in a restored desert ecosystem in northwest (NW) China, the growing season leaf biomass is expected to increase by nearly 25% compared to the present.

Author contributions: I.R.-I. designed research; X.-p.W. performed research; X.-p.W., B.E.S., Z.Y., and I.R.-I. analyzed data; X.-p.W., B.E.S., and I.R.-I. wrote the paper; and B.E.S. developed theoretical results.

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Research paper

The eco-hydrological threshold for evaluating the stability of sand-binding vegetation in different climatic zones

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ABSTRACT

Soil moisture dynamics are a determinant of the sustainable development of artificial sand-binding vegetation, which directly prevents and controls desertification and sand hazards, such as the sand burial of farmlands and pastures. How to maintain the stability of sand-binding vegetation is a challenge for ecologists and land managers. An eco-hydrological model coupling the dynamics of sand-binding vegetation cover and soil moisture was used to explore the effect of a stochastic daily precipitation regime on soil moisture and vegetation cover after the establishment of sand-binding vegetation. The simulation results indicate that herbaceous vegetation cover, woody vegetation cover and soil moisture increase nonlinearly with increasing annual rainfall. Specifically, herbaceous vegetation cover first increased and then decreased with increasing annual rainfall. Woody vegetation cover increased by a power-law function within the total community cover, and soil moisture increased exponentially. The eco-hydrological thresholds in different climatic zones and in typical revegetated sandy desert regions of China were determined using an eco-hydrological model. These indexes will not only help to promote dryland ecosystem management and maintain the sustainability of wind-breaks and sand-binding benefits but will also provide a quantifiable reference standard for vegetation recovery and reconstruction in sandy areas in the future.

1. Introduction

The main district requiring wind-sand hazard protection in northern China is approximately 320,000 km^2 in size. It includes sandy land or an agro-pasture ecotone east of Helan Mountain and transitional regions with sandy deserts or desert-steppe west of Helan Mountain (Li et al., 2014). The annual rainfall is more than 250 mm east of Helan Mountain and less than 250 mm west of Helan Mountain (Li et al., 2014). Introducing and establishing sand-binding vegetation is an effective method for preventing the hazard of wind-sand, controlling desertification and promoting regional ecological restoration and rehabilitation in sandy desert regions. Over the past 60 years, we have established artificial sand-binding vegetation on 6000,000 ha of wind-blown sand hazard areas of northern China, which serve as an important ecological barrier (Wang et al., 2008a; Cao et al., 2011). This barrier effectively controls wind-sand damage, promotes sandy land recovery and has achieved remarkable success (Cao, 2008; Wang et al., 2008a; Wang et al., 2008b; Cao et al., 2010; Wang et al., 2010; Cao et al., 2011; Assouline, 2013). However, many problems have arisen in practice, such as large areas of artificial sand-binding vegetation degrading over the decades (Cao et al., 2011; Li et al., 2014; Ding et al., 2015), groundwater levels beginning to decline (Li et al., 2014; Ding et al., 2015) and new desertification appearing in previously revegetated desert regions (Wang et al., 2008a; Li et al., 2014; Ding et al., 2015). Consequently, maintaining artificial sand-binding vegetation stability and the benefits of windbreaks and sand-binding sustainability has become a large challenge in ecological restoration and reconstruction in sandy areas (Cao, 2008; Wang et al., 2010; Tan and Li, 2015).

Artificial sand-binding vegetation is different from natural sand-binding vegetation (Hayse and Wissing, 1996; Li et al., 2000; Zeng et al., 2007; Dou, 2008; Li et al., 2010). Natural sand-binding vegetation is the result of adaption to long-term regional or local climatic conditions and the soil environment (Hayse and Wissing, 1996; Li et al., 2014). Natural sand-binding vegetation can maintain high stability in the context of small disturbances (Jonathan, 2003; Li et al., 2014).

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REGULAR ARTICLE

Precipitation and topsoil attributes determine the species diversity and distribution patterns of crustal communities in desert ecosystems

X. R. Li · G. Song · R. Hui · Z. R. Wang

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Abstract
Background and aims Despite the important role of biological soil crusts in desert ecosystems, the responses of the crustal composition and distribution to changes in both climatic and edaphic factors at different spatial scales are not well understood. The goal of our research was to study the drivers of crustal community diversity at different scales, determine how crustal diversity and distribution patterns are related to abiotic and biotic factors, and identify the characteristics of crustal communities along a precipitation gradient.
Methods We investigated the distribution and characteristics of crustal communities based on 457 soil samples that were randomly collected from six desert regions of northern China. These regions represent a precipitation gradient from 450 mm in the east to 80–100 mm in the west. The measured environmental variables included soil moisture, pH, clay and silt content, soil organic carbon (SOC), total N, total P, total K, $CaCO_3$ content, annual and perennial plant cover and crustal variables, including species richness, crustal cover and biomass. An ANOVA analysis, a stepwise regression and a redundancy analysis were used to analyse and interpret the response of biological soil crusts to environmental factors at two spatial scales.
Results Our results showed that the moss distribution and biomass were strongly related to the topsoil moisture content. The highest diversity of cyanobacteria and algae was observed at sites with relatively dry topsoil, and lichen diversity was promoted at sites with fine-textured soils. In addition, the cover and biomass of moss were positively correlated with perennial plant cover and higher topsoil moisture, which was expected because plant cover provides shade for the moss. The cover and biomass of lichens, cyanobacteria and algae were positively correlated with that of annual plants because these plants may create an ideal habitat and provide nutrients. The physiochemical properties of the topsoil greatly influenced the distribution pattern of the crustal communities at the regional scale. The species richness and biomass of the crustal mosses were positively correlated with precipitation, whereas the species richness and biomass of cyanobacteria and algae were negatively correlated with precipitation at the landscape scale.
Conclusions Rainfall largely determined the species richness and cover of the crustal cyanobacteria and mosses, whereas soil properties had a greater impact on the crustal lichens. Future changes to rainfall regimes could result in the conversion of biological soil crusts

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Biogeosciences

Development of bacterial communities in biological soil crusts along a revegetation chronosequence in the Tengger Desert, northwest China

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Abstract. Knowledge of structure and function of microbial communities in different successional stages of biological soil crusts (BSCs) is still scarce for desert areas. In this study, Illumina MiSeq sequencing was used to assess the compositional changes of bacterial communities in different ages of BSCs in the revegetation of Shapotou in the Tengger Desert. The most dominant phyla of bacterial communities shifted with the changed types of BSCs in the successional stages, from Firmicutes in mobile sand and physical crusts to Actinobacteria and Proteobacteria in BSCs, and the most dominant genera shifted from *Bacillus*, *Enterococcus* and *Lactococcus* to RB41_norank and JG34-KF-361_norank. Alpha diversity and quantitative real-time polymerase chain reaction (PCR) analysis indicated that bacterial richness and abundance reached their highest levels after 15 years of BSC development. Redundancy analysis showed that silt + clay content and total K were the prime determinants of the bacterial communities of BSCs. The results suggested that bacterial communities of BSCs recovered quickly with the improved soil physicochemical properties in the early stages of BSC succession. Changes in the bacterial community structure may be an important indicator in the biogeochemical cycling and nutrient storage in early successional stages of BSCs in desert ecosystems.

1 Introduction

Biological soil crusts (BSCs) are assemblages of cryptogamic species and microorganisms, such as cyanobacteria, green algae, diatoms, lichens, mosses, soil microbes and other related microorganisms that cement the surface soil particles through their hyphae, rhizines/rhizoids and secretions (Eldridge and Greene, 1994; Li, 2012; Pointing and Belnap, 2012; Weber et al., 2016). Due to their specialized structures and complicated assemblages of their members, BSCs constitute one of the most important landscapes and make up 40 % of the living cover of desert ecosystems, even exceeding 75 % in some special habitats (Belnap and Eldridge, 2003).

It is well known that BSCs play critical roles in the structure and function of semiarid and arid ecosystems (Eldridge and Greene, 1994; Li, 2012). They provide ecological services such as soil stabilization, reduction of wind and water erosion, and facilitation of higher plant colonization (Belnap, 2003; Belnap and Lange, 2001; Maier et al., 2014; Pointing and Belnap, 2012). BSCs are functionally important and variable, and may be a useful model system for diversity-function research. Their functional attributes are relatively well known, and estimation and manipulation of biodiversity in experiments are feasible, at least within some groups of BSC biota (Bowker et al., 2010). This relationship is more easily interpreted in artificially constructed BSCs. There are primary successional stages for BSCs in desert ecosystems: mobile sand, algal crust, lichen crust and moss crust (Lan

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Recovery of microbial community structure of biological soil crusts in successional stages of Shapotou desert revevegetation, northwest China

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ABSTRACT

Microbial community structure of biological soil crusts (BSCs) in successional stages of Shapotou desert revegetation, northwest China, was assessed using Illumina MiSeq sequencing. Bacterial diversity and richness were highest after 15 years, while those of fungi increased along a chronosequence of stabilized dunes. Hierarchical clustering and principal coordinate analysis showed significant differences in bacterial communities between biocrusts and physical crusts, whereas fungal communities clustered into four groups. Each age of BSCs exhibited the same dominant phyla at different proportions. The recovery time for bacteria was more than 15 years, whereas that for fungi ranged from decades to centuries, indicating that fungal richness might be a potential indicator for predicting the degree of BSC recovery.

Biological soil crusts (BSCs) constitute one of the most important landscapes (Belnap and Eldridge, 2003), having critical roles in semi-arid and arid ecosystems (Eldridge and Greene, 1994; Li, 2012; Weber et al., 2016). In general, BSCs encounter the main successional stages in desert ecosystem: mobile sand, physical crust, algal, lichen, and moss crust (Lan et al., 2012; Liu et al., 2006). Recent estimates suggest that the recovery time of cyanobacterial soil crusts is 15–50 years, whereas that of soil lichens range from decades to centuries (Pointing and Belnap, 2012). However, there is no information about when the microbial community structure can reach a stable state in the recovery process of BSCs in desert ecosystems. Bacteria and fungi are the major microorganisms in BSCs (Bates et al., 2010; Gundlapally and Garcia-Pichel, 2006). During the BSC successional process, microbial species composition and community structure significantly change (Gundlapally and Garcia-Pichel, 2006; Moquin et al., 2012; Zhang et al., 2016). Most of the research on prokaryotic diversity of BSCs has mainly focused on cyanobacteria-dominated biocrusts in arid and semi-arid regions (Abed et al., 2010; Garcia-Pichel et al., 2001; Nagy et al., 2005; Steven et al., 2013; Yeager et al., 2004). Recent studies on the bacterial community structure of bryophyte or lichen-dominated crusts have indicated that lichen-associated communities encompass wide taxonomically diverse bacteria (Bates et al., 2011; Cardinale et al., 2008; Maier et al., 2014). However, studies on fungal diversity during BSC development in desert zones are relatively few (Abed et al., 2013; Grishkan et al., 2015). Thus, what are the changes in microbial community composition and function in different successional stages of BSCs? In addition, what is the effect of these changes on the recovery process of BSCs in desert revegetation in temperate zones?

To answer these questions, we selected BSCs in Shapotou restored vegetation, located on the southeast fringe of Tengger Desert, northwest China. The unirrigated vegetation system was established in 1956 and extended in 1964, 1973, 1981, and later on by planting shrubs (Li et al., 2007b; Liu et al., 2006). In the revegetation area, BSCs varied with the ages of restored vegetation enclosures, and bacteria and fungi were selected to study the BSC microbial community. We hypothesized that the BSC microbial community structure reaches a steady state after a certain developmental period, and is of particular importance to vegetation stability and soil properties during the successional stages of revegetation in desert ecosystems. We sampled BSCs at the revegetation established in 1964, 1981, 1987, 2000, and 2010 in November 2015, and named them according to fixed-sand time as 51 YR (51-year-old revegetation), 34 YR, 28 YR, 15 YR, and 5 YR, respectively. Mobile sand (MS) was employed as a control (Fig. S1).

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Co-variation of fine-root distribution with vegetation and soil properties along a revegetation chronosequence in a desert area in northwestern China

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ABSTRACT

This study investigated the changes in the distributions of fine roots and explored their responses to changes in vegetation and soil properties along a 46-year revegetation chronosequence in a desert area in northwestern China. Fine roots and soil samples at depths of 0–3.0 m soil profile were obtained from revegetated sand-binding areas and compared with those from moving sand dunes, natural undisturbed vegetated dunes, and a desert steppe. The soil physicochemical properties in the top 0.8 m layer were analyzed, and the soil water contents at depths of 0–3.0 m soil profile were measured. Redundancy and regression analyses were conducted to explore the relationships between fine roots, vegetation and soil properties. Both the cumulative fine-root length and mass in the 0–0.4 m layer and throughout the 0–3.0 m profile increased along the revegetation chronosequence, and those of the 1.0–3.0 m layer increased up to 29 years and then decreased. Additionally, the proportion of fine roots in the 0–0.4 m layer increased and the proportion of fine roots from 1.0–3.0 m decreased along the revegetation chronosequence. The fine-root length in 0–0.4 m layer was mainly influenced by herbaceous cover, while the fine-root mass at depth of 0–3.0 m was affected by shrub cover and biomass. The amounts of fine soil particles, soil organic carbon, and total nitrogen were the main edaphic factors that influenced the distribution of fine roots. The fine-root length and mass in the 0–0.4 m layer were weakly and positively correlated with soil water contents, while those in the 1.0–3.0 m layer had strong negative relations with the soil water contents in corresponding layers. Our results demonstrated that the fine-root distribution in revegetated sand dunes was regulated by the succession of the vegetation-soil system after revegetation.

1. Introduction

Fine roots play a crucial role in the exchange of materials and energy flow between plants and soil (Casper and Jackson, 1997; Waisel et al., 2002), and the distribution of fine roots with depth is among the most relevant aspects that influence water, carbon, and nutrient fluxes (Jackson et al., 1997; Norby and Jackson, 2000; Schenk and Jackson, 2002). Generally, the distribution of fine roots in a certain area results from the combined influences of climate, vegetation and soil (Schenk and Jackson, 2005). For instance, plants in water-limited ecosystems often present deep rooting and have relatively large root systems (Canadell et al., 1996; Chapin et al., 1993; Schenk and Jackson, 2002), particularly in coarse-textured soils in which soil water and nutrients are regularly scarce (Collins and Bras, 2007; Wilcox et al., 2004). Currently, changes in vegetation are mainly characterized by shifts between woody and herbaceous species, and associated soil changes are ongoing in water-limited ecosystems (Sala and Maestre, 2014). Studies of the potential consequences of such changes under certain climate conditions on root distributions are urgently needed.

Changes in plant life forms typically alter the rooting depth and biomass of fine roots (Canadell et al., 1996; Jackson et al., 1996,

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Abbreviations: BSCs, Biological soil crusts; MSD, Moving sand dunes; R20, Sand-binding dunes revegetated in 1990 (20 years old); R29, Sand-binding dunes revegetated in 1981 (29 years old); R46, Sand-binding dunes revegetated in 1964 (46 years old); Ref, Undisturbed naturally vegetated sand dunes; Ste, Desert steppe; SWC, Soil water content; FRLD, Fine-root length density per cubic meter ($m\ m^{-3}$); FRMD, Fine-root mass density per cubic meter ($kg\ m^{-3}$); FRL, Fine-root length per square meter ($m\ m^{-2}$); FRM, Fine-root mass per square meter ($m\ m^{-2}$).

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Variations of N_2O fluxes in response to warming and cooling in an alpine meadow on the Tibetan Plateau

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Abstract Little is known about the impacts of climate change especially for cooling on N_2O emissions from alpine meadows on the Tibetan Plateau. Along a slope of Qilian mountains, China, we transferred intact soil cores covering different vegetation types (graminoid, shrub, forb, and sparse vegetation) downhill (warming) and uphill (cooling) across a 600-m elevation gradient to examine the responses of soil-atmosphere N_2O exchange rates to climate warming and cooling. N_2O fluxes were measured during two growing seasons from May to October in 2008 and 2009. The Tibetan alpine meadow acted as a net N_2O source at an average rate of

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Stemflow volume per unit rainfall as a good variable to determine the relationship between stemflow amount and morphological metrics of shrubs

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A B S T R A C T

In this study, we determined the relationship between stemflow amount and morphological metrics of plants. Previous studies on this issue generally neglected the influence of differential rainfall amounts on stemflow, which somehow bias the relationship between stemflow amount and morphological metrics. Here, field observation of stemflow in two xerophytic shrubs (*Caragana korshinskii* and *Artemisia ordosica*) of varying sizes were conducted during three growing seasons in 2011–2013 to evaluate this relationship by using a simple variable, i.e., stemflow volume per unit rainfall (SfVPR, mL mm^{-1}). This stemflow index directly defines the influence of rainfall depth on the morphological metrics of plants, and it has the following advantages over the conventional stemflow coefficient that has been used to determine the influence of tree/shrub morphological metrics on the stemflow amount: (1) it avoids the bias caused by the influences of differential rainfall amount on stemflow yield and (2) it is suitable for use in hydrological models. Our results showed that SfVPR can well be used to determine the relationship between stemflow amount and shrub morphological metrics. Moreover, by using multiple regression model, we found that projected canopy area (or canopy volume, or basal area), plant area index, and stem diameter are the most influential factors for the stemflow amount of *C. korshinskii*, whereas no significant explanatory variables were found for that of *A. ordosica*.

1. Introduction

Stemflow refers to a part of rainfall that is intercepted by leaves, twigs, and branches and eventually channeled into soil through trunk or stem, which further could be transported and redistributed into deeper soil layers through preferential pathways such as roots. Although volumetrically minor, stemflow is an important source of soil moisture and nutrients for plant growth, this being particular important in arid and semiarid ecosystems (Aboal et al., 1999; Navar and Bryan, 1990; Navar et al., 2009; Navar, 2011; Whitford et al., 1997; Zhang et al., 2016). The hydrological and biogeochemical importance of stemflow was systematically reviewed by Levia and Frost (2003).

Stemflow amount is a function of canopy structure, rainfall characteristics, and meteorological variables (Crockford and Richardson, 1990; Navar, 1993; Levia and Frost, 2003). The influence of individual canopy structure metrics on stemflow amount is difficult to determine (Germer et al., 2010; Levia et al., 2013). Simple regressions were first performed between a conventionally used stemflow coefficient (the total volume of stemflow during the observation periods) and the morphological metrics of plants, and then a multiple linear regression model was developed after eliminating colinearity between these metrics (e.g., Aboal et al., 1999; Martinez-Meza and Whitford, 1996; Wang et al., 2013; Yang et al., 2008). However, by using the accumulated stemflow volumes during the observational periods, the previous authors neglected the influence of differential rainfall amount on the stemflow amount that obscures the morphology effects because it is well known that stemflow significantly increases with the rainfall amount after a threshold value for stemflow generation (e.g., Li et al., 2008; Manfroi et al., 2004; Navar, 2011; Zhang et al., 2013, 2015). As such, the contribution of rainfalls with high depths was probably overestimated, whereas that of rainfall with low depths was underestimated or under-represented. In terms of accurate

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Spatial distribution of *Agriophyllum squarrosum* Moq. (Chenopodiaceae) in the straw checkerboards at a revegetated land of the Tengger Desert, northern China

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Abstract: The present study focuses on straw checkerboards established in the Shapotou Desert Research and Experimental Station at the southeastern edge of the Tengger Desert and their effects on the species richness and the abundance of *Agriophyllum squarrosu* Moq. Specifically, detailed analyses on the spatial distribution of *A. squarrosum* and the related soil properties were carried out at a small scale in the straw checkerboards. *A. squarrosum* is an excellent pioneer plant for revegetation in desert areas. However, the distribution pattern of *A. squarrosum* and the influencing factors have not been sufficiently delineated. The results showed that the species richness and the abundance of *A. squarrosum* were decreased exponentially from the border to the center of the straw checkerboards. At the micro-geomorphological scale, the soil texture, soil organic matter (SOM), soil nutrients (nitrogen, phosphorus and potassium), and soil infiltration rate in the topsoil tended to increase from the center to the border within a straw checkerboard, while soil moisture presented an opposite tendency. The soil seed bank of *A. squarrosum*, soil bulk density, electrical conductivity, sand content, $CaCO_3$ accumulation, and pH showed no significant difference ($P>0.05$) between the border and the center of the straw checkerboards. Multiple linear regression analysis indicated that the abundance of *A. squarrosum* was mainly determined by the concentrations of SOM, nitrogen, and the infiltration rate, implying that nutrient acclimation was the optimal competitive strategy of *A. squarrosum* for surviving in a barren natural environment of an arid desert region.

Keywords: *Agriophyllum squarrosum*; seed banks; soil moisture; soil infiltration rate; nutrient acclimation

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1 Introduction

Vegetation spatial patterns are considered as common and well-defined characteristics of many landscapes (Foti and Ramírez, 2013). The spatial patterns of vegetation are the results of the interaction between biotic factors and abiotic factors and also the results of long-term vegetation successions (Li et al., 2007, 2013). Vegetation spatial patterns in arid desert regions can be either periodic or random (Borgogno et al., 2009). For example, in the Chihuahuan Desert, covering parts of Mexico and the United States, in the Negev Desert in southern Israel, and in other water-limited areas, vegetation distributions generally exhibit multitude patterns, such as banded,

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Differential intra-specific stemflow funnelling efficiencies of *Caragana korshinskii* within arid desert ecosystems

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ABSTRACT

Stemflow is known as a highly localized point input of rainwater and solutes around tree/shrub bases where roots are concentrated, thus having considerable effects on hydrology and biogeochemistry of vegetated ecosystems. Stemflow shows a pronounced inter-specific variation due to morphological differences among species, while the intra-specific variation of stemflow has been poorly explored. We systematically examined the effects of shrub morphological metrics on intra-specific funnelling efficiencies by quantifying the stemflow of nine shrubs of *Caragana korshinskii* within a water-limited arid desert ecosystem of northern China. Stemflow volume was used to compare the absolute amount of stemflow generated by shrubs of varying size, and funnelling ratio was used to assess their funnelling efficiencies. Both rainfall depth and shrub morphological metrics significantly affected stemflow volume, while funnelling ratio was more associated with shrub morphology. Under the same rainfall condition, smaller shrubs produced lower volumes of stemflow, while gaining access to rainfall via higher funnelling ratio than larger shrubs. Our findings highlight a large variation in funnelling efficiency among individual shrubs within the same species, and in particular, smaller shrubs might profit more from sporadic small rainfall events than larger shrubs.

Key words | *Caragana korshinskii*, desert ecosystem, funnelling ratio, morphological metrics, stemflow

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INTRODUCTION

Drylands cover about 41% of Earth's terrestrial surface (Reynolds *et al.* 2007; Huang *et al.* 2015), characterized by a two-phase mosaic composed of vegetated patches interspersed with bare patches (Aguiar & Sala 1999; Tongway *et al.* 2001; Rietkerk & Van de Koppel 2008), where precipitation is scarce and typically unpredictable and hence a key limiting factor of ecosystem functioning (e.g., Noy-Meir 1973). Shrubs are the dominant vegetation over the vast drylands, and play a crucial role in the hydrological and biogeochemical cycles in terms of redistributing incident precipitation (Schlesinger & Pilmanis 1998; Llorens & Domingo 2007; Zhang *et al.* 2016a). Precipitation falling on the shrub canopy either is intercepted and subsequently evaporated (interception loss) or reaches the ground diffusely by throughfall or concentrated by funnelling down the stems in the form of stemflow.

Stemflow is volumetrically small (normally 5–10% of incident precipitation) in comparison to the other components of the canopy water balance; it is, however, of high eco-hydrological and chemical importance due to its very local input to nature (Johnson & Lehmann 2006; Levia & Germer 2015). Nutrient-enriched stemflow funnels down the shrub stems and infiltrates into deep soil layers through preferential pathways such as roots, creating islands of soil moisture and nutrients (e.g., Mauchamp & Janeau 1993; Navar 2011; Schwärzel *et al.* 2012; Zhang *et al.* 2013, 2016b). Stemflow is thus considered to be an important biological transfer mechanism in contributing to the

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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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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 CO_2 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 CO_2 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 CO_2 emission in the water-limited desert ecosystem.

Key Words: biological soil crusts, C cycling, CO_2 emission, desert ecosystem, precipitation amount, soil water content

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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 CO_2 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 CO_2 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 CO_2 emission may contribute a significant portion of the total annual CO_2 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 eve-

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Allometric models for estimating shrub biomass in desert grassland in northern China

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ABSTRACT

The development of shrub allometric models is crucial for accurate biomass assessment, as well as for scientific studies of carbon storage and carbon cycling of desert ecosystems. The aim of the present study was to construct allometric models to predict biomass using easily measured variables for xerophytic shrubs. The 12 most widespread shrub species of northern China were selected and a total of 385 individuals were harvested to obtain the weight of its components (leaves, twigs, branches, and roots), the crown area (CA) and plant height (H). Based on a high coefficient of determination (R2), a low standard error of estimate (SEE), and low Akaike information criterion (AIC) values, 72 species-specific and 24 multispecies models with CA and H as independent variables were developed. The function lnW (biomass of different components) = a + b × lnX (predictor variable) was selected as optimal model. CA was revealed as the best independent variable for the biomass of leaves and twigs, and V (CA × H) was the best predictor variable for branches, aboveground, belowground, and total biomass. In conclusion, for the first time species-specific and multispecies models were constructed with a high goodness of fit of leaves, twigs, branches, aboveground, belowground, and total biomass for 12 shrub species in northern China. Compared to multispecies models, species-specific models had improved accuracy. Since biomass quantification is the basis of carbon stocks estimation, the models presented here can be considered as alternative tool for assessing carbon storage and carbon cycling of desert ecosystems.

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KEYWORDS
Biomass estimation; desert ecosystems; multispecies; species-specific; xerophytic shrub

Introduction

In China, shrub land covers an area of $2 \times 10^6\,\text{km}^2$, which is twice that covered by forests, and the majority of it is located within arid areas (Hou 1982). Shrubs naturally are the dominant species and should be considered ecological key species within desert ecosystems. They can provide several important ecosystem and social service functions such as: (1) the reduction of wind erosion and promotion of sand-fixation as well as effective conservation of soil and water (Whitford 2002); (2) the influence of micro-climate through temperature amplitude changes and redistribution of rainfall (Canadell and Raupach 2008); (3) the generation of good habitats for co-occurring plant, animal, and microorganism

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Combined application of cyanobacteria with soil fixing chemicals for rapid induction of biological soil crust formation

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ABSTRACT

Combined applications of cyanobacteria with soil fixing chemicals were investigated to generate artificially induced biological soil crust (BSC). Polyvinyl alcohol (PVA) and Tacki-Spray (TKS7) chemicals composed of bio-polysaccharides and tackifiers were examined under laboratory conditions. Following singular applications of chemicals, the mean weight diameter values of soil treated with TKS7 were 1.4–2.5 times higher than those of soil treated with PVA and thus TKS7 was selected for further tests for application with cyanobacteria (*Nostoc* Vaucher ex Bornet & Flahault, *Phormidium* Kützing ex Gomont, and *Scytonema arcangeli* Bornet ex Flahault). Combined application of cyanobacteria and different concentrations of TKS7 enhanced soil aggregate stability, resulting in mean weight diameter values of 0.58–0.69 mm and was comparable to TKS7 singular application (0.18–0.40 mm). Surface hardness values were also highly improved by the combined application of cyanobacteria with TKS7 (4.5 MPa) compared to singular treatment of cyanobacteria (2.3 MPa). In addition, superabsorbent polymer (SAP) was applied as a water-holding material and nutrient supplement in soil. The SAP promoted cyanobacterial cell growth under dry conditions. Chlorophyll *a* content of soil was improved by the addition of SAP (CST1: 2.93 μg g^{-1}) compared to singular treatment of cyanobacteria (C: 2.25 μg g^{-1}). These results suggest that combined application of cyanobacteria with TKS7 and SAP can induce BSC formation faster than singular application of cyanobacteria. The novel method presented herein can be applied to restoration of degraded soils in arid and semiarid areas.

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KEYWORDS
Artificial biological soil crust; cyanobacteria; land degradation; soil fixing chemicals; soil stabilization

Introduction

Artificial induction of biological soil crusts (BSCs) has been suggested as a solution for rehabilitation of damaged soil in arid and semiarid regions. For this reason, rapid induction of artificial BSCs using moss and cyanobacteria has been attempted by many researchers. Chen et al. (2006) generated cyanobacterial crusts within 20 days in Inner Mongolia, China by inoculating *Microcoleus vaginatus* Gomont ex Gomont onto unstable sand dunes. Wang et al. (2009) also conducted a feasibility study by inoculating cyanobacteria with straw checkerboards in desert areas. Xiao et al. (2011) examined artificial induction of BSCs in the Loess Plateau of China by inoculating moss-dominant BSCs.

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Color versions of one or more of the figures in the article can be found online at www.tandfonline.com/uasr.

RESEARCH ARTICLE

Rapid development of cyanobacterial crust in the field for combating desertification

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Abstract

Desertification is currently a major concern, and vast regions have already been devastated in the arid zones of many countries. Combined application of cyanobacteria with soil fixing chemicals is a novel method of restoring desertified areas. Three cyanobacteria, *Nostoc* sp. Vaucher ex Bornet & Flahault, *Phormidium* sp. Kützing ex Gomont and *Scytonema arcangeli* Bornet ex Flahault were isolated and tested in this study. Tacki-Spray^{TM} (TKS7), which consists of bio-polysaccharides and tackifiers, was used as a soil fixing agent. In addition, superabsorbent polymer (SAP) was applied to the soil as a water-holding material and nutrient supplement. Application of cyanobacteria with superabsorbent polymer and TKS7 (CST) remarkably improved macro-aggregate stability against water and erodibility against wind after 12 months of inoculation when compared to the control soil. The mean weight diameter and threshold friction velocity of the CST treated soil were found to be 75% and 88% of those of the approximately 20-year-old natural cyanobacterial crust (N-BSC), respectively, while these values were 68% and 73% of those of the N-BSC soil after a single treatment of cyanobacteria alone (CY). Interestingly, biological activities of CST were similar to those of CY. Total carbohydrate contents, cyanobacterial biomass, microbial biomass, soil respiration, carbon fixation and effective quantum yield of CST treated soil were enhanced by 50–100% of the N-BSC, while those of control soil were negligible. Our results suggest that combined application of cyanobacteria with soil fixing chemicals can rapidly develop cyanobacterial crust formation in the field within 12 months. The physical properties and biological activities of the inoculated cyanobacterial crust were stable during the study period. The novel method presented herein serves as another approach for combating desertification in arid regions.

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Introduction

Desertification is a global environmental issue in which land in arid, semiarid and dry subhumid areas is degraded by factors such as climatic variations and anthropogenic activities [1]. Problems associated with desertification include loss of biodiversity, low soil productivity, dust storms and economic losses. Drylands cover 41.3% of all land and are home to more than 2.5

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ORIGINAL ARTICLE

The abundance of certain metabolites responds to drought stress in the highly drought tolerant plant *Caragana korshinskii*

Jiwei Zhang[1,2] · **Guoxiong Chen**[1] · **Pengshan Zhao**[1] · **Qin Zhou**[1] · **Xin Zhao**[1,3]

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Abstract Metabolomics offers opportunities for studying the systematic response of an organism to a genetic and/or an environmental change. Here, the metabolic consequences of drought stress were characterized in the highly drought tolerant plant *Caragana korshinskii.* The time-of-flight mass spectrometry platform employed identified several hundred metabolites in extracts of the leaf, stem, root collar, and root of plants which had been either subjected to drought stress or were well-watered. Each of the four organs harbored a number of potential metabolite markers for the drought response. An increased abundance of various small carbohydrates and soluble amino acids in each of the four organs was induced by the stress; these compounds may act as compatible solutes or antioxidants. Across the whole plant, there was a fall in the content of several Krebs cycle and glycolysis intermediates, as well as in that of the amino acids glutamic acid and aspartic acid. Pathway analysis suggested that most of the potential metabolite markers were involved in energy metabolism and amino-acid metabolism. The implication was that energy metabolism and photosynthesis are compromised during the adaptation of *C. korshinskii* to drought stress. Given the different spectrum of metabolites associated with the drought response in the four organs, it was concluded that each organ employs a distinct strategy to cope with drought stress.

Keywords Metabolomics · *Caragana korshinskii* · Drought stress · Metabolite markers · Organs · Energy metabolism

Introduction

The perennial xerophytic shrub *Caragana korshinskii* is widely distributed across the arid and semi-arid zones of north-western China and Mongolia (Wang et al. 2007; Zhang et al. 2009), where it is frequently used as a soil stabilizer (Li et al. 2003; Wang et al. 2004). Its tolerance to various abiotic stresses, and especially drought, makes it attractive as a model for the study of the plant response to stress (Li et al. 2004). Seedlings are able to maintain a level of photosynthetic activity even when exposed to fairly severe moisture stress (Fang et al. 2011). Mature plants

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SOILS, SEC 1 • SOIL ORGANIC MATTER DYNAMICS AND NUTRIENT CYCLING • RESEARCH ARTICLE

Climate change affects soil labile organic carbon fractions in a Tibetan alpine meadow

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Abstract

Purpose Changes in bioactive soil C pools and their temperature sensitivities will dominate the fate of soil organic C in a warmer future, which is not well understood in highland ecosystems. This study was conducted in order to evaluate climate change, especially cooling effects, on soil labile organic C (LOC) pools in a Tibetan alpine meadow.

Materials and methods A short-term reciprocal translocation experiment was implemented to stimulate climate warming (downward translocation) and cooling (upward translocation) using an elevation gradient on the Tibetan Plateau. Variations in soil microbial biomass C (MBC), dissolved organic C (DOC) and LOC were analyzed.

Results and discussion Over the range of soil temperature from 0.02 to 5.5 °C, warming averagely increased soil MBC, DOC and LOC by 15.3, 17.0 and 3.7 % while cooling decreased them by 11.0, 11.9 and 3.2 %, respectively. Moreover, warming generally increased the proportion of DOC in LOC but cooling had an opposite effect, while the response of the MBC proportion to DOC and LOC varied depending on vegetation type. Soil MBC, DOC and LOC pools were positively related to soil temperature and showed a hump-shaped relationship with soil moisture with a threshold of about 30–35 %. Although soil DOC was more sensitive to warming (5.1 % $°C^{-1}$) than to cooling (3.0 % $°C^{-1}$), soil LOC showed a symmetrical response due to regulation by soil moisture.

Conclusions Our results indicated that climate change would not only change the size of soil LOC pools but also their quality. Therefore, cooling effects and regulation of soil moisture should be considered to evaluate the fate of soil organic C in Tibetan alpine meadows in a warmer future.

Keywords Alpine meadow · Climate change · Reciprocal translocation · Soil labile organic C

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ORIGINAL RESEARCH

Biological soil crusts determine the germination and growth of two exotic plants

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Abstract

In arid and semiarid ecosystems, the potential threats of exotic invasive species are enhanced due to increasing human activities. Biological soil crusts (BSCs), acting as arid ecosystem engineers, may play an important role in preventing the establishment of exotic invasive plants. Our goal was to examine whether BSCs could inhibit the establishment of probable exotic plant species originating from adjacent grasslands located along the southeast edge of the Tengger Desert. In our study, we investigated the effects of three BSC types (cyanobacteria, lichen, and moss crusts) under two disturbance conditions (intact and disturbed) on the establishment of two exotic plant species (*Ceratoides latens* and *Setaria viridis*) using indoor experiments. We found both negative and positive effects of BSCs on the establishment of the two exotic plant species. Compared with the disturbed BSCs, the germination percentages of *C. latens* and *S. viridis* were reduced by 54% to 87% and 89% to 93%, respectively, in intact BSCs. In contrast, BSCs significantly promoted the height growth and aboveground biomass of the two exotic plant species ($p < .05$) by enhancing the soil water and nutrient availability for the exotic plants. Our results confirm that BSCs strongly suppress the rapid expansion of exotic plant populations by inhibiting germination of seed with big size or appendages and have a weak inhibitory effect on exotic plant with small and smooth seeds. This may decrease the threat of propagation of exotic species. In the meantime, BSCs promote the growth of a few successful engraftment seedlings, which increased the beta diversity. Our work suggests that better understanding the two opposing effects of BSCs on the establishment of exotic plant species in different growth stages (germination and growth) is important for maintaining the health and stability of revegetated regions.

KEYWORDS
biological invasion, biological soil crust, biotic resistance, disturbance, exotic plant, germination percent

1 | INTRODUCTION

Biological soil crusts (BSCs) are photosynthetic and diazotrophic organisms that include cyanobacteria, green algae, lichens, and mosses and that have adapted to the environmental stresses of high light, temperature, and desiccation (Belnap & Lange, 2003; Belnap, Phillips, & Troxler, 2006; Li, Jia, Long, & Zerbe, 2005). In arid and semiarid ecosystems, cryptogamic species of BSCs are considered ecosystem pioneers

PLOS ONE

RESEARCH ARTICLE

Effect of biological soil crusts on seed germination and growth of an exotic and two native plant species in an arid ecosystem

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Abstract

Biological soil crusts (BSCs) can improve the stability and health of native plant communities in arid ecosystems. However, it is unknown whether BSCs can also inhibit invasions of exotic vascular plants on stabilized reclaimed sand dunes. To answer this question, we conducted a greenhouse experiment to test the effects of cyanobacteria-dominated BSCs on 1) seed germination and biomass of an exotic grass (*Stipa glareosa* P. Smirn.), and 2) individual biomass of the exotic *S. glareosa* growing with two native plants, *Eragrostis poaeoides* Beauv. and *Artemisia capillaris* Thunb. Our experiment included three BSC treatments (intact crust, disturbed crust, and bare soil) and five species trials (native *E. poaeoides* alone, *E. poaeoides* mixed with exotic *S. glareosa*, native *A. capillaris* alone, *A. capillaris* mixed with exotic *S. glareosa*, and *S. glareosa* alone). The results showed that cyanobacteria-dominated crusts can significantly reduce the cumulative percent germination of the exotic grass ($P<0.001$) and native plants ($P<0.001$). Maximum cumulative percent germinations of the exotic grass and two native plants were found in bare soil, and minimum in intact crusts. The interaction of crust treatment × species trials on shoot biomass of the two native plants was significant ($P<0.05$). These results indicate that the presence of BSCs on stabilized sand dunes may reduce the germination of the exotic and two native plants. The effect of reducing exotic and native plant seeds germination would maintain more diverse plant communities and contribute to the formation of clumped vegetation patterns. We conclude that BSCs act as a natural regulator for vegetation patterns and thus promote ecosystem stability and sustainability.

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Introduction

Drylands, areas with a severe and fragile ecological environment, cover more than one third of the terrestrial land surface [1,2]. Drylands are characterized by a sparse presence of vascular plants due to low water availability, and low rates of nutrient turnover or a limited ability to acquire resources due to extreme temperatures [3,4]. The soil surface in drylands is often

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Research Article

Comparative transcriptome profile of the leaf elongation zone of wild barley (*Hordeum spontaneum*) *eibi1* mutant and its isogenic wild type

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Abstract

The naturally occurring wild barley mutant *eibi1/hvabcg31* suffers from severe water loss due to the permeable leaf cuticle. *Eibi1/HvABCG31* encodes a full ATP-binding cassette (ABC) transporter, HvABCG31, playing a role in cutin deposition in the elongation zone of growing barley leaves. The *eibi1* allele has pleiotropic effects on the appearance of leaves, plant stature, fertility, spike and grain size, and rate of germination. Comparative transcriptome profile of the leaf elongation zone of the *eibi1* mutant as well as its isogenic wild type showed that various pathogenesis-related genes were up-regulated in the *eibi1* mutant. The known cuticle-related genes that we analyzed did not show significant expression difference between the mutant and wild type. These results suggest that the pleiotropic effects may be a compensatory consequence of the activation of defense genes in the *eibi1* mutation. Furthermore, we were able to find the mutation of the *eibi1/hvabcg31* allele by comparing transcript sequences, which indicated that the RNA-Seq is useful not only for researches on general molecular mechanism but also for the identification of possible mutant genes.

Keywords: ABC transporter, defense genes, desiccation tolerance, plant cuticle, RNA-Seq.

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Introduction

The cuticle covers aerial plant organs and acts as an effective barrier against pests and pathogens (Reina-Pinto and Yephremov, 2009; Metraux *et al.*, 2014). The cuticle mainly consists of wax and cutin. Cutin is made up of polyesters whose monomer composition is mainly C16 and C18 ω-hydroxylated fatty acid, and is typically modified by hydroxy- or epoxy groups in mid-chain positions (Yeats and Rose, 2013). Moreover, cutin contains glycerol and a small amount of phenolic compounds (Nawrath, 2006; Yeats and Rose, 2013).

A spontaneous cuticle mutant (*eibi1*) from wild barley (*Hordeum spontaneum*) genotype 23-19 has been cloned via a map-based approach (Chen *et al.*, 2009, 2011b,). The *eibi1* mutant suffers from severe water loss related to a reduced cuticle thickness and a decreased amount of cutin monomers, and shows twisted leaves, dwarf plant, low fertility, reduced spike and grain size, and germination delay. The gene, named as *Eibi1/HvABCG31* is mapped to a pericentromeric region on chromosome 3H, where a mutation in an ABCG31 transporter gene is associated with the *eibi1* mutant phenotype. This PDR (pleiotropic drug resistance) transporter family, as well as its homologs in Arabidopsis and rice, AtABCG32 and OsABCG31, plays an important role in cutin deposition during the development of a functional cuticle (Bessire *et al.*, 2011; Chen *et al.*, 2011a; Garroum *et al.*, 2016). Analysis of *Eibi1* gene expression shows abundant transcripts in the elongation zone (EZ) but only traces in non-elongation zones (NEZ) and emerged blade (EmBL) of a growing leaf, and none in the mature root (Chen *et al.*, 2011b). Cutin but not wax deposition occurs mostly in the EZ (Richardson *et al.*, 2007). Cutin deposition is already established by the time the EZ is formed, and the defect of the *eibi1* mutant cuticle is apparent in the EZ (Chen *et al.*, 2011b). However, gene transcription in *eibi1* EZ is poorly understood.

A comparative transcriptomic analysis of the second leaves of near-isogenic *eibi1* and the wild type lines has been conducted using the 22-k Barley1 Affymetrix

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ORIGINAL ARTICLE

Characterization and genetic mapping of the β-diketone deficient *eceriferum-b barley* mutant

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Abstract

Key message **The barley** ***eceriferum-b.2*** **(*****cer-b.2*****) mutant produces glossy leaf sheaths and is deficient in the cuticular wax component 14,16-hentriacontanedione. The mutated gene maps to a 1.3-cM interval on chromosome 3HL flanked by the genes MLOC_10972 and MLOC_69561.**

Abstract The cuticular wax coating of leaves and stems in many grass species is responsible for the plants' glaucous appearance. A major component of the wax is a group of β-diketone compounds. The barley *eceriferum-b.2* (*cer-b.2*) mutant produces glossy leaf sheaths and is deficient for the compound 14,16-hentriacontanedione. A linkage analysis based on 708 gametes allowed the gene responsible for the mutant phenotype to be mapped to a 1.3-cM interval on chromosome 3HL flanked by the two genes MLOC_10972 and _69561. The product of the wild type allele may represent a step in the β-diketone synthesis pathway.

Introduction

All aerial organs of plants are covered by the cuticle: leaf and stem of plants are covered by the waxy cuticle, which restricts water loss and forms a physical barrier against pathogens (Bernard and Joubès 2013; Kunst and Samuels 2009; Riederer and Schreiber 2001; Xu et al. 1997). Some of the wax is deposited outside the cuticle (epicuticular wax) and some within it (intracuticular wax) (Bernard and Joubès 2013; Broun et al. 2004; Jenks et al. 2002; Jetter and Schäffer 2001). The epi- and intracuticular waxes are responsible for the glaucous appearance of the surface by refracting the incident light (Bianchi and Figini 1986; Jenks et al. 2002; Jetter and Schäffer 2001). The chemical constitution of cuticular wax comprises very long chain (C_{20}–C_{34}) fatty acids, primary and secondary alcohols, aldehydes, alkanes, ketones and alkyl esters (Kunst and Samuels 2003; Li-Beisson et al. 2010; Yeats and Rose 2013). The precursor fatty acids of chain length C_{16}–C_{18} are synthesized by fatty acid synthase in the plastids, from where they are exported to the cytoplasm and elongated in the endoplasmic reticulum (Bernard and Joubès 2013; Kunst and Samuels 2003, 2009). The barley C_{29}–C_{33} β-diketones are synthesized by an enzyme complex which features of both fatty acid elongase and polyketide synthase (PKS) (Mikkelsen 1979; Schneider et al. 2016; von

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The differential effects of sand burial on CO_2, CH_4, and N_2O fluxes from desert biocrust-covered soils in the Tengger Desert, China

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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 CO_2, CH_4, and N_2O from the desert biocrust-covered soils. Based on measurements of the fluxes of three greenhouses 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 CO_2 and a negative effect on uptake of CH_4 by soils covered with the two types of biocrusts ($P < 0.05$), but had a differential effect on N_2O fluxes depending on burial depth. Shallow burial dramatically increased N_2O emissions from the biocrust-covered soils ($P < 0.05$), but the opposite was observed under deep burial. As burial time increased, the increase of CO_2 emissions decreased, but changes in fluxes of CH_4 and N_2O varied with biocrust types and burial depths, respectively. In addition, results showed that CO_2 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, CH_4 and N_2O 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 N_2O and CH_4 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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ORIGINAL RESEARCH
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SNP Discovery and Genetic Variation of Candidate Genes Relevant to Heat Tolerance and Agronomic Traits in Natural Populations of Sand Rice (*Agriophyllum squarrosum*)

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The extreme stress tolerance and high nutritional value of sand rice (*Agriophyllum squarrosum*) make it attractive for use as an alternative crop in response to concerns about ongoing climate change and future food security. However, a lack of genetic information hinders understanding of the mechanisms underpinning the morphological and physiological adaptations of sand rice. In the present study, we sequenced and analyzed the transcriptomes of two individuals representing semi-arid [Naiman (NM)] and arid [Shapotou (SPT)] sand rice genotypes. A total of 105,868 pairwise single nucleotide polymorphisms (SNPs) distributed in 24,712 Unigenes were identified among SPT and NM samples; the average SNP frequency was 0.3% (one SNP per 333 base pair). Characterization of gene annotation demonstrated that variations in genes involved in DNA recombination were associated with the survival of the NM population in the semi-arid environment. A set of genes predicted to be relevant to heat stress response and agronomic traits was functionally annotated using the accumulated knowledge from *Arabidopsis* and several crop plants, including rice, barley, maize, and sorghum. Four candidate genes related to heat tolerance (heat-shock transcription factor, *HsfA1d*), seed size (DA1-Related, *DAR1*), and flowering (early flowering 3, *ELF3* and *late elongated hypocotyl, LHY*) were subjected to analysis of the genetic diversity in 10 natural populations, representing the core germplasm resource across the area of sand rice distribution in China. Only one SNP was detected in each of *HsfA1d* and *DAR1*, among 60 genotypes, with two in *ELF3* and four in *LHY*. Nucleotide diversity ranged from 0.00032 to 0.00118. Haplotype analysis indicated that the NM population carried a specific allele for all four genes, suggesting that divergence has occurred between NM and other populations. These four genes could be further analyzed to determine whether they are associated with phenotype variation and identify alleles favorable for sand rice breeding.

Keywords: sand rice, physiological adaptation, climate change, single nucleotide polymorphism, allele diversity, natural variation, candidate genes

RESEARCH ARTICLE

A comparative transcriptomic analysis reveals the core genetic components of salt and osmotic stress responses in *Braya humilis*

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Abstract

Braya humilis is a member of the Euclidieae tribe within the family Brassicaceae. This species exhibits a broad range of adaptations to different climatic zones and latitudes as it has a distribution that ranges from northern Asia to the arctic-alpine regions of northern North America. In China, *B. humilis* is mainly found on the Qinghai—Tibetan Plateau (QTP) and in adjacent arid regions. In this study, we sequenced a sample from an arid region adjacent to the QTP using the Illumina platform generating a total of 46,485 highly accurate unigenes, of which 78.41% were annotated by BLASTing versus public protein databases. The *B. humilis* transcriptome is characterized by a high level of sequence conservation compared with its close relative, *Arabidopsis thaliana*. We also used reciprocal blast to identify shared orthologous genes between *B. humilis* and four other sequenced Brassicaceae species (i.e. *A. thaliana*, *A. lyrata*, *Capsella rubella*, and *Thellungiella parvula*). To enable precise characterization of orthologous genes, the early-diverging basal angiosperm *Amborella trichopoda* was also included. A total of 6,689 orthologous genes were identified before stricter criteria for the determination of e-values, amino acid hit lengths, and identity values was applied to further reduce this list. This led to a final list of 381 core orthologous genes for *B. humilis*; 39 out of these genes are involved in salt and osmotic stress responses and estimations of non-synonymous/synonymous substitution ratios for this species and *A. thaliana* orthologs show that these genes are under purifying selection in *B. humilis*. Expression of six genes was detected in *B. humilis* seedlings under salt and osmotic stress treatments. Comparable expression patterns to their counterparts in *Arabidopsis* suggest that these orthologous genes are both sequence and functional conservation. The results of this study demonstrate that the environmental adaptations of *B. humilis* are mainly the results of preexisting genetic components. Future work will be required to characterize the expression patterns of these orthologous genes in natural populations and will provide further insights into the adaptive mechanisms underlying the wide range of *B. humilis* adaptations.

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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.

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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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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 × 10^8 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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ORIGINAL PAPER

Effects of gravel-sand mulching on soil bacterial community and metabolic capability in the semi-arid Loess Plateau, China

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Abstract Gravel and sand mulching is an indigenous technology used for the crop yield for at least 300 years in the loess area of northwest China; however, little is known about the changes of soil bacterial community and metabolic capability under the mulching. In this study, we investigated the soil microbial community structure and metabolic functional diversity during mulching using Illumina MiSeq sequencing and Biolog ECO method. Totally, 9417 OTUs were classified at 97% similarity level for soil samples after 0 (control), 4, 7, and 10 years of mulching. Dendrogram result indicated that mulching affected the soil bacterial community; and the higher richness and diversity of bacterial community were detected in mulching samples. The average abundance of soil bacteria (such as *Proteobacteria, Actinobacteria, Firmicutes* and *Nitrospirae*) in mulching samples was higher than samples without mulching. Besides, some microbial communities (such as *Rhodobacteraceae, Phenylobacterium, Pseudonocardia, Nonomuraea* and *Aeromicrobium*) were only present in the mulched soil samples. However, the lower metabolic capability was observed in mulching samples based on Biolog method, which the main reason for the opposite result might be that the soil objects detected by the two methods are different. In conclusion, these results demonstrated that gravel and sand mulching affected the structure and metabolic capability of bacterial community and was one reason for crop yield.

Keywords Gravel and sand mulching · Cultivated soil · Bacterial community structure · Metabolic diversity · High-throughput sequencing

Introduction

Mulching fields with different materials (crop residues, chemicals, and different sizes of gravel) are employed widely to increase crop yields in many parts of the world (Ghosh et al. 2006; Sinkevičienė et al. 2009; Tu et al. 2006). Increased crop yields due to mulching have been reported in groundnut (Ramakrishna et al. 2006a), wheat (Chakraborty et al. 2008; Huang et al. 2005) and maize (Li et al. 2000; Wang et al. 2009). In a previous study it was reported that mulching was able to increase crop yields, because mulching can effectively reduce soil evaporation, increase soil temperature and improve water use efficiency(Li 2003). In addition, mulching play a role in suppressing weed infestations and reducing the incidence of viruses and aphid infestations in some ways (Ramakrishna et al. 2006b; Saucke and Döring 2004).

In China, especially in the northwest region, gravel and sand mulching is a traditional farming practice employed for crop production due to the similar function mentioned above, which has been practiced for at least 300 years (Kemper et al. 1994; Li et al. 2001; Xie et al. 2010). Moreover, the

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SCIENTIFIC REPORTS

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Transcriptome profiling of genes involved in induced systemic salt tolerance conferred by *Bacillus amyloliquefaciens* FZB42 in *Arabidopsis thaliana*

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Plant growth-promoting *Bacillus amyloliquefaciens* FZB42 induces systemic salt tolerance in *Arabidopsis* and enhances the fresh and dry weight. However, the underlying molecular mechanism that allows plants to respond to FZB42 and exhibit salt tolerance is largely unknown. Therefore, we performed large-scale transcriptome sequencing of *Arabidopsis* shoot tissues grown under salt stress with or without FZB42 inoculation by using Illumina sequencing to identify the key genes and pathways with important roles during this interaction. In total, 1461 genes were differentially expressed (FZB42-inoculated versus non-inoculated samples) at 0 mM NaCl, of which 953 were upregulated and 508 downregulated, while 1288 genes were differentially expressed at 100 mM NaCl, of which 1024 were upregulated and 264 were downregulated. Transcripts associated with photosynthesis, auxin-related, SOS scavenging, Na^+ translocation, and osmoprotectant synthesis, such as trehalose and proline, were differentially expressed by FZB42 inoculation, which reduced the susceptibility to salt and facilitated salt adaptation. Meanwhile, *etr1-3*, *eto1*, *jar1-1*, and *abi4-102* hormone-related mutants demonstrated that FZB42 might induce plant salt tolerance via activating plants ET/JA signaling but not ABA-dependent pathway. The results here characterize the plant transcriptome under salt stress with plant growth-promoting bacteria inoculation, thereby providing insights into the molecular mechanisms responsible for induced salt tolerance.

Soil salinity is a major issue that affects agriculture and approximately 20% of agricultural land is salt-stressed at present[1, 2]. Indeed, salt has become one of the main abiotic stress factors that limit agricultural productivity. Mechanistically, apart from causing plant ion imbalance and osmotic stress, excess salinity inhibits metabolism, including photosynthesis, protein and lipid synthesis, thereby limiting the crop growth and yield, and it may even lead to plant death[3, 4].

In order to reduce the severe effects of salt stress on plants, many approaches have been developed. Many studies have addressed this issue by focusing on genetic engineering, but this approach is time-consuming and may cause possible environmental risks, so genetically engineered plants are rarely used in the field[5, 6]. Recently, the use of microbes has become a new alternative for improving stress tolerance in plants[7, 8]. Plant-growth-promoting rhizobacteria (PGPR) comprise a diverse group of rhizosphere-colonizing bacteria that promote plant growth via direct or indirect mechanisms[9, 10], which may be correlated with the ability to resist various pathogens, the production of phytohormones, the release of volatiles, and the production of phytase and siderophores to enhance the availability of minerals in the soil[11–14]. In addition to their growth-promoting activity, some PGPR are also

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Simultaneous detection of three lily viruses using Triplex IC-RT-PCR

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ABSTRACT

Viruses commonly infecting lily (*Lilium* spp.) include: Lily symptomless virus (LSV), Cucumber mosaic virus (CMV) and Lily mottle virus (LMoV). These viruses usually co-infect lilies causing severe economic losses in terms of quantity and quality of flower and bulb production around the world. Reliable and precise detection systems need to be developed for virus identification. We describe the development of a triplex immunocapture (IC) reverse transcription (RT) polymerase chain reaction (PCR) assay for the simultaneous detection of LSV, CMV and LMoV. The triplex IC-RT-PCR was compared with a quadruplex RT-PCR assay. Relative to the quadruplex RT-PCR, the specificity of the triplex IC-RT-PCR system for LSV, CMV and LMoV was 100% for field samples. The sensitivity of the triplex IC-RT-PCR system was 99.4%, 81.4% and 98.7% for LSV, CMV and LMoV, respectively. Agreement (κ) between the results obtained from the two tests was 0.968, 0.844 and 0.984 for LSV, CMV and LMoV, respectively. This is the first report of the simultaneous detection of LSV, CMV and LMoV in a triplex IC-RT-PCR assay. In particular we believe this convenient and reliable triplex IC-RT-PCR method could be used routinely for large-scale field surveys or crop health monitoring of lily.

1. Introduction

Lily (*Lilium* spp.) is an important ornamental flower crop throughout the world. In China, Lanzhou lily (*Lilium davidill* var. *unicolor*) is also an important edible bulb crop and a traditional medicinal plant with a 150-year cultivation history. The bulb crop is mainly grown in central Gansu province in Northern China (Wang et al., 2010a; Zhang et al., 2015a). Unfortunately lilies are often infected with viral diseases causing degeneration in the quality of many elite varieties. These infections can cause severe economic losses in terms of quantity and quality of flower and bulb production (Sharma et al., 2005; Wang et al., 2010a). More than ten different viruses have been reported to infect lilies worldwide(Ryu et al., 2002). Among the lily-infecting viruses, *Lily symptomless virus* (LSV), *Cucumber mosaic virus* (CMV) and *Lily mottle virus* (LMoV) are considered challenging viral pathogens for many cultivars of lily (Asjes, 2000; Kwon et al., 2013; Lim et al., 2016).

LSV (Genus *Carlavirus*, family *Flexiviridae*) is a filamentous particle, 640 nm in length and 17–18 nm in diameter. Leaves infected by the virus show vein-clearing characterized by light green inter-veinal striping (Fig. 1A). Many cultivars remain symptomless when infected with only LSV. Infected plants often have diminished growth, smaller flowers, pronounced lower bulb yield, and shorter vase life as cut flowers than uninfected plants (Ryu et al., 2002).

CMV (Genus *Cucumovirus*, family *Bromoviridae*) has the widest host range among plant viruses; it can infect more than 1000 plant species (Lin et al., 2003; Nouri et al., 2014; Kim et al., 2016). Leaves of infected CMV lily show chlorotic or yellow spotting, inter-veinal striping or vein-clearing and sometimes malformations. Later, in the plant's lifecycle, grey or brown necrotic spotting may develop (Fig. 1B). A coarse flower-breaking pattern may develop in some cultivars along with petal malformation (Ryu et al., 2002).

LMoV (Genus *Potyvirus*, family *Potyviridae*) is flexuous, non-enveloped, and rod-shaped; it is 11–15 nm wide and 680–900 nm long. LMoV infected lilies exhibit symptoms of leaf mottle, leaf mosaic, reddish-brown necrotic spots, vein clearing, chlorosis and yellow streaking, leaf curling and narrowing (Fig. 1C). Symptoms may be very mild, or plants may be symptomless during early growth stages (Zhang et al., 2016).

In the field, LSV, CMV or LMoV can occur singly or as mixed infections within lily plants. In fact, mixed infections with two or three of these viruses are present in over 60% of plants in some of the main planting areas of Lanzhou lily (Zhang, Y. B. unpublished data), and consequently cause more severe damage when they occur together (Zhang et al., 2014; Lim et al., 2016).

The management of a viral disease depends on a detection protocol that is rapid, reproducible and scalable to large number of samples (Viswanathan et al., 2013). Several techniques (ELISA, RT-PCR, and multiplex RT-PCR) have been developed to detect LSV, CMV or LMoV in

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Botanical Studies

ORIGINAL ARTICLE

Open Access

Characterization of *LhSorP5CS*, a gene catalyzing proline synthesis in Oriental hybrid lily Sorbonne: molecular modelling and expression analysis

Le Wang[1,2], Zhihong Guo[1], Yubao Zhang[1], Yajun Wang[1], Guo Yang[1], Liu Yang[1,2], Ruoyu Wang[1] and Zhongkui Xie[1*]

Abstract

Background: Abiotic stresses negatively affect plant growth and flower production. In plants, P5CS proteins are key enzymes that catalyzed the rate-limiting steps of proline synthesis, and proline is a well-known osmoprotectant that is closely related to abiotic stress tolerance. However, information about the P5CS genes, their effects on proline accumulation, and their role in abiotic stress tolerance in *Lilium* is still lacking.

Results: We isolated and characterized a novel gene (*LhSorP5CS*) from Oriental hybrid lily cultivar Sorbonne. Phylogenetic analysis indicated that *LhSorP5CS* is a member of the *P5CS* family. The three-dimensional structure of LhSorP5CS predicted by homology modeling showed high similarity to its correspondant human P5CS template. Further gene expression analysis revealed that *LhSorP5CS* expression was up-regulated by NaCl, mannitol, and ABA, and that stress-exposed plants accumulated proline at a significantly higher level than in the control.

Conclusions: *LhSorP5CS* characterized in this study is involved in proline synthesis in lily, and that it might play an important role in abiotic stress tolerance. However, there should be other *P5CS* homologues in the lily genome, and some of them could be highly stress-induced and more important for proline accumulation. Future studies on *P5CS* family genes would be of great importance to proline-related stress tolerance in lily.

Keywords: *LhSorP5CS* gene, Homology modeling, Proline, Abiotic stress, *Lilium* spp.

Background

Abiotic stresses such as salinity, drought, heat, and water-logging negatively affect plant growth. These environmental constraints further restrict the range of sites that are suitable for cultivation, and cause decreased agricultural productivity around the world (Zhu 2001). To protect themselves against adverse conditions, plants have evolved many physiological, cellular, and molecular mechanisms (Tan et al. 2013). One of the most well-studied protective mechanisms relates to proline metabolism. Stress responses in plants are often accompanied by the accumulation of proline in different tissues (Verbruggen and Hermans 2008). The accumulated proline can function as an intracellular osmolyte (Chinnusamy et al. 2005), a scavenger for reactive oxygen species (ROS) (Matysik et al. 2002), a maintainer of cell structure (Verslues et al. 2006), and a signaling molecule that primes multiple stress response pathways (Maggio et al. 2002). More recent findings have connected proline to redox status (Sharma et al. 2011; Shinde et al. 2016), and proline was considered as a storage of both energy and reducing potential (Szabados and Savoure 2010). Besides, proline metabolism was also involved in programmed cell death and plant-pathogen interaction. Accumulation of proline

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RESEARCH PAPERS

Isolation and Characterization of Two Distinct Class II *PR4* Genes from the Oriental Lily Hybrid Sorbonne[1]

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Abstract—Pathogenesis-related (PR) proteins are generally involved in the defense of plants and are important contributors in the disease resistance of plants. Among the 17 PRs that are currently recognized, the PR4 family of proteins is divided into two classes and features a conserved barwin domain. In this study, we isolated two Class II *PR4s* from the oriental hybrid lily cultivar Sorbonne using the rapid amplification of the cDNA ends (RACE) method, and designated these two PR4s *LhSorPR4a* and *LhSorPR4b*. *LhSorPR4a* and *LhSorPR4b* were 627 and 617 bp in length, respectively, and encoded two corresponding PR4s of 141 and 143 amino acids. These deciphered LhSorPR4a and LhSorPR4b protein sequences shared a sequence similarity of 90.7%, but their theoretical isoelectric points were distinctively different (7.74 and 4.08, respectively). The three-dimensional structures of LhSorPR4a and LhSorPR4b predicted by homology modeling showed high similarity to their corresponding papaya barwin-like protein template. Analysis of expression by qPCR revealed that both *LhSorPR4a* and *LhSorPR4b* were responsive to methyl jasmonate and ethephon treatments. The *LhSorPR4b* expression was also significantly induced by sodium salicylate (SS); however, *LhSorPR4a* was unresponsive to the SS treatment. Both LhSorPR4a and LhSorPR4b were expressed in *Escherichia coli* (*E. coli*) and successfully purified. The *PR4s* characterized in this study (*LhSorPR4a* and *LhSorPR4b*) are the first two *PR4* family genes isolated from the *Lilium* genus, and they could therefore play an important role in lily disease resistance.

Keywords: Lilium spp., PR4, disease resistance, homology modeling, gene expression analysis, prokaryotic expression

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INTRODUCTION

The sessility of plants make them vulnerable targets of biotic and abiotic stress. To adapt to changing environments, plants must build up robust defense systems to combat adverse conditions. Invasive pathogens and insects, which are major threats to agricultural and crop production, are responsible for 25% of crop loss globally [1]. Hence, a comprehensive understanding of molecular mechanisms that govern plant immune systems will facilitate plant research in diverse areas and underpin the improvement of agricultural productivity and crop production. Plants mainly use two central immune systems to scrutinize surrounding microorganisms and detect potential pathogens: the pathogen-associated molecular patterns (PAMP) triggered immunity (PTI) system and the effector-triggered immunity (ETI) system [2]. PTI and ETI activated in locally infected tissues often emanate signals systematically to uninfected areas to "warn" them of imminent danger. This disease resistance mechanism, which is conferred through signals that emanate from distally infected areas, is referred to as systematic acquired resistance (SAR) [3]. Generally, SAR is associated with the accumulation of pathogenesis-related (PR) proteins, which are important contributors to plant disease resistance. PR proteins are currently classified into 17 family groups that are based on their similarities in protein sequences, serological relationships, and their enzymatic activity and antimicrobial mechanisms [4]. Among these PR proteins, some are reported to directly interact with pathogens [5] and exhibit antimicrobial properties. PR4 family proteins combat pathogens by direct interaction. Proteins in

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[1] The article is published in the original.

[2] These authors contributed equally to this work.

Abbreviations: CBP—chitin-binding protein; ET—ethylene; ETH—ethephon; ETI—effector-triggered immunity; HEL—hevein-like protein; IMAC—immobilized metal (Ni^{2+}) affinity chromatography; JA—jasmonic acid; MeJA—methyl jasmonate; PAMP—pathogen-associated molecular patterns; PR—pathogenesisrelated; PTI—PAMP-triggered immunity; RMSD—root mean square deviation; SA—salicylic acid; SAR—systematic acquired resistance; SS—sodium salicylate.

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Botanical Studies

ORIGINAL ARTICLE

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Characterization of LhSorTGA2, a novel TGA2-like protein that interacts with LhSorNPR1 in oriental hybrid lily Sorbonne

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Abstract

Background: Non-expressor of pathogenesis-related genes 1 (NPR1) regulates expression of *pathogenesis-related (PR)* genes by interacting with TGA family proteins during systemic acquired resistance (SAR). However, no TGA-like proteins or their interacting partners have been characterized in lily.

Results: In the present study, LhSorTGA2, a novel TGA-like protein, was identified as an interacting partner of LhSorNPR1 (an NPR-like protein) by bimolecular fluorescence complementation (BIFC) and yeast two-hybrid assay (Y2H). Subcellular localization of GFP-tagged proteins targeted LhSorTGA2 to the nucleus, whereas GFP-labeled LhSorNPR1 was observed both in the nucleus and at the cytomembrane. Sequence alignment revealed that LhSorTGA2 was featured with a basic leucine zipper (bZIP) domain and two glutamine rich acid domains (QI and QII). Further phylogenetic analysis showed that TGA family proteins can be grouped into three subclades, within which LhSorTGA2 was clustered into subclade I, together with AtTGA2/5/6. Expression of *LhSorTGA2* was investigated in different tissues by qPCR, and the highest expression level was observed in stem. Besides, when treated with phytohormones (SA, MeJA, ETH and ABA) or fungal pathogen *Botrytis elliptica*, *LhSorTGA2* expression was also induced at different time points post treatments.

Conclusions: Collectively, these results suggested that LhSorTGA2 was an interacting partner of LhSorNPR1, which might function in regulating expression of *PR* genes in lily during SAR.

Keywords: Non-expressor of pathogenesis-related genes 1, TGA-like proteins, Protein interaction, Gene expression, Subcellular localization, *Lilium* spp.

Background

Infections at local sites often induce resistance against further invasions of pathogenic organisms in the distal uninfected parts of plants. This primed resistance, which protects plants from further invasion of a broad spectrum of pathogens at the whole-plant level, is referred to as systemic acquired resistance (SAR) (Fu and Dong 2013). The establishment of SAR is accompanied by accumulation of salicylic acid (SA) (Gao et al. 2015), and induction of *pathogenesis-related (PR)* genes. *PRs* encode for small proteins, of which some are endowed with direct antimicrobial activities. Since SA level, PR accumulation, and SAR are tightly linked, SAR-conferred resistance could be severely compromised either by interfering the level of SA synthesis or by disrupting signaling pathways control *PR* gene expression (Gaffney et al. 1993). Mutation of the *non-expressor of PR genes 1 (NPR1)* gene, a central node in SA-mediated defense signaling, blocks the priming of SAR (Cao et al. 1997). NPR1 lacks a DNA binding domain itself, but features with an ankyrin repeat domain and a BTB/POZ domain, both of which mediate protein–protein interaction (Pieterse and Van Loon 2004). The ankyrin repeat at C-terminus interacts with TGA2

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RESEARCH ARTICLE

Overexpression of *LhSorNPR1*, a *NPR1*-like gene from the oriental hybrid lily 'Sorbonne', conferred enhanced resistance to *Pseudomonas syringae* pv. tomato DC3000 in *Arabidopsis*

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Abstract The *non-expressor of the pathogenesis-related genes 1* (*NPR1*) is a master regulator in defense signaling of plants and plays a key role in basal and systemic acquired resistance. In this study, we isolated a *NPR1*-like gene from the oriental hybrid lily 'Sorbonne' (designated as *LhSorNPR1*) using rapid amplification of cDNA ends (RACE). The open reading frame of *LhSorNPR1* consisted of 1854 bp, encoding a protein of 617 amino acids. Multiple sequence alignment revealed that LhSorNPR1 shares high similarity to NPR1-like proteins and characteristics of the BTB/POZ domain and ankyrin repeats. A comparison between the intron/exon organization of *LhSorNPR1* and orthologs from other plant species demonstrated that *NPR1* genomic fragments (including *LhSorNPR1*) are all composed of 4 exons and 3 introns. We also identified sequence motifs involved in hormone response and binding sites for RAV1 proteins and WRKY transcription factors through the prediction of *cis*-regulatory elements in the *LhSorNPR1* promoter. Our gene expression analysis showed that *LhSorNPR1* transcript levels significantly differed in various tissues, and that *LhSorNPR1* expressions were induced by sodium salicylate, ethephon, and methyl jasmonate. Furthermore, we transformed *LhSorNPR1* into Col-0 wild-type *Arabidopsis* to conduct function analysis, and we observed enhanced resistance to the bacterial pathogen *Pseudomonas syringae* pv. *tomato* DC3000 in the *Arabidopsis* expressing *LhSorNPR1* gene. The enhanced disease resistance of *LhSorNPR1* expressing plants could correlate to elevated expression levels in *pathogenesis-related* genes (*PR1*, *PR2*, and *PR5*) in vivo.

Keywords *LhSorNPR1* · Lily · Systemic acquired resistance · Gene expression analysis · Transgenic *Arabidopsis*

Introduction

Signals from pathogen attacks at local infection sites are often transmitted to uninfected distal sites to protect plants from further invasion. This long-lasting, broad-spectrum defense response is referred to as systemic acquired resistance (SAR) (Fu and Dong 2013). The onset of SAR is accompanied by elevated levels of in vivo salicylic acid (SA) and induced expressions of *pathogenesis-related* (*PR*) genes (Gaffney et al. 1993; Rochon et al. 2006). Moreover, SA accumulation, at both infected and uninfected sites, has led to speculation that SA is the SAR signal molecule (Metraux et al. 1990; Rasmussen et al. 1991). Although much effort has been made in understanding the relationship between SA and SAR, there is to date no direct evidence of this. However, reducing SA levels by disrupting SA synthesis genes (Wildermuth et al. 2001) or by expressing bacterial salicylate hydroxylase genes (Vernooij et al. 1994) has compromised SAR phenotypes.

The *non-expressor of PR genes 1* (*NPR1*) was first identified in *Arabidopsis* by screening mutants that were not sensitive to SA or its analogues (Cao et al. 1994, 1997).

Le Wang and Zhihong Guo have contributed equally to this work.

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sustainability

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Article

Improvements in Soil Carbon and Nitrogen Capacities after Shrub Planting to Stabilize Sand Dunes in China's Horqin Sandy Land

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Abstract: *Caragana microphylla*, a native perennial leguminous shrub, is widely used for desertification control in China's Horqin Sandy Land. We investigated the effects of afforestation using *C. microphylla* in areas with fixed and active dunes on soil carbon (C) and nitrogen (N) storage in the soil total and light-fraction (LF) organic matter. Compared to the values in the control areas, soil organic carbon (SOC) storage to a depth of 100 cm increased by 88%, 74%, and 145% at 9, 15, and 31 years after shrub planting, respectively; the corresponding values were 68%, 61%, and 195% for total nitrogen (TN) storage, 109%, 199%, and 202% for LF organic carbon storage, and 203%, 337%, and 342% for LF nitrogen storage. The soil light-fraction (LF) organic matter contributed significantly to total SOC and TN storage, despite the low proportion of total soil mass accounted for by the LF dry matter. Thus, afforestation using *C. microphylla* was an effective way to sequester C and to restore degraded soils, but the process was slow; it would take more than 100 years to fully restore SOC storage in active dunes through afforestation with *C. microphylla* in the Horqin Sandy Land.

Keywords: desertification control; carbon sequestration; shrub plantation; semiarid ecosystem

1. Introduction

The increase in atmospheric carbon dioxide (CO_2) concentrations from 280 ppm in pre-industrial times to 391 ppm in 2011 has been attributed to numerous anthropogenic activities, including unsustainable land use, that have resulted in an increased severity and extent of soil degradation and desertification, and this increase has contributed greatly to global warming [1,2]. Arid and semiarid regions comprise 47.2% of the world's land and more than two-thirds of these fragile ecosystems have undergone degradation and desertification, primarily due to overgrazing, other unsustainable human activities, and climate change [3]. Lal [4] estimated that global desertification led to a total loss of 19 to 29 Pg·C from the plant-soil continuum. However, it is increasingly accepted that restoration of vegetation cover in the world's arid and semiarid regions could create a high potential C sink because of the vast area of this land combined with widespread degradation and desertification in these areas [5,6].

Many agroforestry management practices can be employed to sequester C and counteract land degradation. Afforestation (artificial planting of trees or shrubs) is one of the most effective ways because of the durability and large mass of the woody stems, combined with the ongoing contribution of organic matter to the soil. Afforestation is usually successful above the isohyet of 200 mm mean

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Earlier flowering did not alter pollen limitation in an early flowering shrub under short-term experimental warming

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In animal pollinated plants, phenological shifts caused by climate change may have important ecological consequences. However, no empirical evidence exists at present on the consequences that flowering phenology shifts have on the strength of pollen limitation under experimental warming. Here, we investigated the effects of experimental warming on flowering phenology, flower density, reproductive success, and pollen limitation intensity in *Caragana microphylla* and evaluated whether earlier flowering phenology affected plant reproduction and the level of pollen limitation using warmed and unwarmed open top chambers in the Horqin Sandy Land of Inner Mongolia, northern China. The results of this study indicated that artificial warming markedly advanced flower phenology rather than extending the duration of the flowering. Additionally, warming was found to significantly reduce flower density which led to seed production reduction, since there were insignificant effects observed on fruit set and seed number per fruit. Experimental floral manipulations showed that warming did not affect pollen limitation. These results revealed the negative effects of advanced phenology induced by warming on flower density and reproductive output, as well as the neutral effects on reproductive success and pollen limitation intensity of long surviving plants.

Global mean temperature has risen by 0.85 °C since the 1880s, and is predicted to increase an additional 1.8–4 °C by the end of this century[1]. The effects of global warming on ecosystem structure and function have received increasing attention world-wide. Global warming has resulted in a change in flowering phenology and/or a decline in flower production[2], leading to a change in reproductive output of plants. It has been frequently reported that the time of flowering could be either advanced or delayed by artificial warming[2–6]. These phenological shifts could potentially increase pollen limitation[7,8], which results in reduced fruit and seed sets caused by a scarcity of pollen receipt[9]. Many previous studies have recorded a shift in the reproductive output in response to warming[2,10,11]. However, the effect of the shift in flowering phenology induced by experimental warming on pollen limitation intensity has not been empirically examined. Shifts in flowering time may expose species to novel abiotic and biotic environments, and these components may interact to determine plant reproduction and pollen limitation[10]. It has been previously documented that plant populations suffering from pollen limitation experience disruptions in seed production[12]. Pollen limitation induced reproductive failure may lead to a reduction in population growth rates and their long-term viability[13,14]. Severe and consistent pollen limitation may even cause local extinctions[15]. It has been predicted that climate warming may drive thousands of plant species to the brink of extinction over the next century, due to changes in the timing of their life cycles, such as flowering phenology[16,17]. Therefore, research concerning the reproductive success and pollen limitation of endemic plants living in a warmer world is essential to the understanding and prediction of the consequences of the climate warming-mediated timing of plant life cycles, as well as the changes in the conservation of plant populations.

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ORIGINAL ARTICLE

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Plant responses to warming and increased precipitation in three categories of dune stabilization in northeastern China

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Abstract Rising temperatures and precipitation are important climate change processes around the world. The responses of plants to these trends are still unclear in semi-arid regions, especially in areas with degraded sandy grassland. To provide insights into the response in these regions, we investigated responses of vascular plants to warming and increased precipitation in mobile dunes, fixed dunes and grassland, which represent the series of sand dune stabilization by plants in semi-arid northeastern China. Plant biomass, especially the aboveground biomass, varied significantly ($P < 0.05$) among dune categories. Total plant density in the fixed dunes and grassland was 1.9 and 1.7 times that in the mobile dunes. Species richness differed slightly but significantly ($P < 0.05$) among the habitats. Increasing precipitation in a drought year (65.5% of the long-term average annual precipitation) by 30% did not significantly affect any plant variable. By contrast, warming significantly decreased the belowground biomass, total biomass, species richness and plant total density. In summary, in semi-arid region with sandy soil, additional precipitation slightly improved plant performance, but increased temperature decreased plant performance. Soil texture, which determines the balance between moisture retention and evaporation, may be a key factor in determining these responses when precipitation is unusually low.

Keywords Plant growth response · Precipitation · Sandy grassland · Restoration · Warming

Introduction

Sandy ecosystems are dominant landscape units in many parts of the world, and because of their large extent in China, which was estimated to be 36.9×10^4 km^2 in 2000 (Wang et al. 2004), they play a significant role in carbon sequestration (Zuo et al. 2015). However, vegetation performance, the primary component of carbon balance, is influenced by many variables, like soil texture, soil nutrients, temperature, precipitation regime, etc. in these ecosystems. The sandy ecosystem area is vulnerable to climate change, leading to uncertainty in their contributions to regional and global carbon budgets and their responses to climate change (Li et al. 2012a, b).

Sandy land can function as a large carbon (C) sink under beneficial conditions (Miao et al. 2015), but may also turn into a large C source under harmful conditions due to over-grazing (Li et al. 2012b; Zhao et al. 2011). For example, free-grazed sandy grasslands in the Horqin region of northeastern China have sustained heavy damage from overgrazing, resulting in serious degradation of the vegetation and soil (Zhao et al. 2011). In contrast, shrub planting and grazing exclusion in this region increased the number, density, coverage, and diversity of plant species, while also increasing total C and total nitrogen (N) in the soil and the resulting C/N ratio (Miao et al. 2015). Plant cover and aboveground biomass increased by 20.3 and from 12.1 times, respectively, after 26 years of grazing exclusion (Li et al. 2012a). C and N storage in the plant-soil system increased by 3.1 and 1.9 times, respectively, after 25 years of grazing exclusion (Li et al. 2012b).

Other research has shown that the sandy-land ecosystem is sensitive to changes in ambient environmental conditions. For example, a change towards a

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REGULAR PAPER

Effects of foliage litter of a pioneer shrub (*Artemisia halodendron*) on germination from the soil seedbank in a semi-arid sandy grassland in China

Yongqing Luo[1] · **Xueyong Zhao**[1] · **Yuqiang Li**[1] · **Tao Wang**[2,3]

Received: 8 January 2017 / Accepted: 27 April 2017

Abstract Vegetation recovery during succession is an important process for ecological restoration of the soil, especially in degraded sandy land. However, the driving mechanisms, such as how a pioneer species competes with other species, is uncertain. In China's Horqin Sandy Land, *Artemisia halodendron* is an important shrub that is common on semi-fixed dunes, where it replaces *Agriophyllum squarrosum* during succession, and is an important indicator species of the second stage of dune stabilization. However, how it outcompetes other species is still unclear. In this study, we conducted a seed bank germination experiment using soil from the native habitats of *A. halodendron* on semi-fixed dunes. We covered the soil with foliage litter of *A. halodendron* at a range of concentrations. Seed germination and seedling growth were strongly affected by the foliage litter. Seed germination and seedling growth were not harmed by a low concentration ($\leq$50 g m^{-2}) of the foliage litter but severely inhibited by high concentrations ($\geq$100 g m^{-2}). Strong allelopathy, indicated by decreased germination, increased seedling loss, and decreased plant biomass, appeared during the later stages of germination (after about 20 days of incubation). Our results suggest that as a pioneer shrub during the vegetation succession that occurs during dune stabilization, *A. halodendron* outcompeted other species through the allelopathic effect of its foliage litter. This helps to explain the patchy distribution and heterogeneity of vegetation communities in the Horqin Sandy Land.

Keywords Allelopathy · *Artemisia halodendron* · Degraded sandy grassland · Seed bank · Seedling growth · Vegetation recovery

Introduction

Much of the world's sandy land occurs in arid to semi-arid areas, where it has been subject to considerable degradation of the vegetation communities (Zhao et al. 2013; Zuo et al. 2012). As a result, it has high potential for carbon sequestration if the vegetation can recover. The ecosystems in sandy land cover large areas, and therefore have multiple effects in terrestrial ecosystem, such as livestock production from grazing (Zhao et al. 2003), sandstorm prevention (Li et al. 2004) and carbon sequestration (Li et al. 2012b). Large amounts of C are potentially stored in the soil of these ecosystems; soil storage may account for more than 80% of the C and N storage in some habitats of a degraded grassland ecosystem (Zuo et al. 2015). The resulting C and N storage ranges from 35.05 to 388.13 g m^{-2} and 1.09 to 16.06 g m^{-2}, respectively, to a depth of 60 cm in a desertified grassland (Li et al. 2006). Moreover, plants are the major source of C for soil, and the most important organisms for transforming C between organic and inorganic forms. Carbon dioxide captured by plants via photosynthesis is released by physiological activities including respiration, litterfall, root turnover, and release of root exudates. The net accumulation or emission of C by plants in sandy

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Effects of sand burial on the survival and growth of two shrubs dominant in different habitats of northern China

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Xiao-An Zuo · Shao-Kun Wang · Min Chen**

Received: 15 July 2016 / Accepted: 22 February 2017

Abstract Plants that grow in dune ecosystems always suffer from sand burial. Shrubs play implications on the healthy functioning of dune ecosystems due to control blowing sand. However, the survival and growth responses of shrubs to sand burial remain poorly understood. The survival rate and seedling height of two shrubs (*Artemisia halodendron* and *Lespedeza davurica*) along with the soil properties under different burial depths were examined in order to reveal the causing ecophysiological attributes of sand burial on shrubs in the desertified region. It was found that *A. halodendron* can survive a burial depth of 6 cm greater than its seedling height, which is a dominant shrub in mobile dunes with intense burial, whereas a burial depth equivalent to three fourths of its seedling height is detrimental to *L. davurica*, which is dominant in fixed dunes with less burial. The reasons for the shrub death under sand burial were associated with the physical barrier to vertical growth and the reduction in photosynthetic area. In conclusion, *A. halodendron* can facilitate the stabilization of mobile dunes because of their high tolerance to the frequent and intensive sand burial, while *L. davurica* can be beneficial for the recovery process because of their higher survival rates under shallow burial following restoration of mobile dunes.

Keywords Sand burial · Horqin Sandy Land · Survival rate · Seedling height · Dune shrubs

Introduction

Sand burial, a commonly recurring natural hazard in dune ecosystems, influences the different growth stages of plants (e.g., seeds, seedlings, and adult plants) in both coastal and inland dunes (Maun 1994, 1996; Brown 1997; Szczucinski 2012). Sand burial is not considered a primary stress but is a complex process that causes soil conditions to change (e.g., temperature, moisture, pH value, oxygen levels, bulk density and nutrient status), which in turn affects the survival and growth of dune plants included both vascular plants and cryptogams like lichen and moss (Poulson 1999; Jia et al. 2012, 2014). There are a large number of literatures focusing on seed germination and seedling emergence after sand burial (Maun 1996; Wang et al. 1998; Chen and Maun 1999; Benvenuti et al. 2001; Li et al. 2006). Gilbert et al. (2011) and Wang et al. (2016a) reported that the survival, growth, and reproduction of plants were positive to the shallow sand burial. It was reported that the moderate burial caused the leaf area to increase to compensate for the reduced photosynthetic rate (Martinez and Moreno–Casasola 1996; Gilbert et al. 2008) and the shoot, stem, and leaf petioles to elongate to promote

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PHYSIOLOGICAL RESPONSES OF TWO SHRUBS TO SAND BURIAL IN NORTHERN CHINA

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ABSTRACT

Sand activity is a common phenomenon that occurs in inland dune ecosystems. Plants that grow under these conditions inevitably suffer from sand burial. Shrubs are important for the healthy functioning of sand dune ecosystems because they control blowing sand. However, the survival mechanisms and physiological responses of shrubs relative to sand burial, particularly under different levels of sand dune stability, remain poorly understood. The seedlings of *Artemisia halodendron* and *Lespedeza davurica*, two shrubs that dominate different habitats of Horqin Sandy Land at different burial intensities, were selected for this study. The survival rate and physiological indices of these shrubs were studied. Results showed that *A. halodendron* seedlings survived burial depth beyond 6 cm, whereas *L. davurica* seedlings survived burial depth beyond 3/4 of their height. After sand burial, most of the antioxidant enzyme activity and osmotic substance content of *A. halodendron* increased, whereas no physiological index of *L. davurica* was observed to increase significantly after burial. Thus, compared with *L. davurica*, *A. halodendron* can more significantly reduce the damage caused by sand burial through increased antioxidant enzyme activity and osmotic substance content, such that it can tolerate deeper sand burial.

KEYWORDS :
Sand burial, Horqin sandy land, Survival rate, Antioxidant enzyme, Osmotic substance

INTRODUCTION

Sand burial, as a commonly recurring phenomenon in dune ecosystems, influences the different growth stages of plants (e.g., adult plants, seedlings and seeds) in both coastal and inland dunes [1-3]. Sand burial is not considered as a primary stress, but is rather a complex process that causes soil conditions to change (e.g., temperature, moisture, pH value, oxygen levels, bulk density and nutrient status), which in turn affects the survival and growth of dune plants [4]. The effects of sand burial on seed germination and seedling emergence have been an important research focus on which a large number of papers have been published [2, 5]. Several authors concluded that for seeds buried at the same depth, larger seeds easily germinate and emerge because they have greater energy reserves than smaller seeds [5]. Research on the survival, growth, or reproduction response of plants to sand burial has also been conducted, and plant responses were found to be positive with shallow burial. For instance, moderate burial increased leaf area to compensate for the reduced photosynthetic rate, elongated the stem and leaf petioles to promote vertical growth [2], increased production of flowers and seeds per plant to benefit reproduction [1], and produced adventitious roots for nutrient uptake [6]. However, plant burial beyond the tolerance limit is fatal because vertical growth is inhibited by the physical barrier presented by deep burial, as well as by the reduction in photosynthetic area and limited oxygen availability to the roots [1]. And the tolerance limit of plants under sand burial depth varies depending on species [2], some researchers found that species from habitats with intense burial can survive more than those from habitats with less burial under same burial stress [7,8].

However, the physiological responses of plants to sand burial have been rarely discussed in previous works. Few studies suggested that partial burial enhances chlorophyll content and increases carbon dioxide exchange rate and net photosynthetic rate [9]. Previous studies suggested that when plants subjected to environmental stresses like drought, freezing or high salt concentrations, the balance between generating and clearing reactive oxygen species (ROS) in plant cells could be destroyed, causing overproduction of reactive oxygen and lipid peroxidation, and resulting in the death of plants by inducing lipid peroxidation, membrane injuries, protein degradation, and enzyme inactivation [10]. And they suggested that plants have evolved special physiological mechanisms under environmental stress, including increase antioxidant enzyme activities and osmolyte contents to repair or resist damage caused by ROS [11,12]. Some researchers have recently explored the involvement of osmolyte contents and antioxidant protective enzymes of plants in the mechanisms of their resistance to sand burial [10].

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ORIGINAL RESEARCH
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Linking Changes to Intraspecific Trait Diversity to Community Functional Diversity and Biomass in Response to Snow and Nitrogen Addition Within an Inner Mongolian Grassland

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In recent years, both the intraspecific and interspecific functional diversity (FD) of plant communities have been studied with new approaches to improve an understanding about the mechanisms underlying plant species coexistence. Yet, little is known about how global change drivers will impact intraspecific FD and trait overlap among species, and in particular how this may scale to impacts on community level FD and ecosystem functioning. To address this uncertainty, we assessed the direct and indirect responses of specific leaf area (SLA) among both dominant annual and subordinate perennial species to the independent and interactive effects of nitrogen and snow addition within the Inner Mongnolian steppe. More specifically, we investigated the consequences for these responses on plant community FD, trait overlap and biomass. Nitrogen addition increased the biomass of the dominant annual species and as a result increased total community biomass. This occurred despite concurrent decreases in the biomass of subordinate perennial species. Nitrogen addition also increased intraspecific FD and trait overlap of both annual species and perennial species, and consequently increased the degree of trait overlap in SLA at the community level. However, snow addition did not significantly impact intraspecific FD and trait overlap of SLA for perennial species, but increased intraspecific FD and trait overlap of annual species, of which scaled to changes in community level FD. We found that the responses of the dominant annual species to nitrogen and snow additions were generally more sensitive than the subordinate perennial species within the inner Mongolian grassland communities of our study. As a consequence of this sensitivity, the responses of the dominant species largely drove impacts to community FD, trait overlap and community biomass. In total, our study demonstrates that the responses of dominant species in a community to environmental change may drive the initial trajectories of change to community FD and functioning.

Keywords: life history, community assembly, functional diversity, intraspecific variance, trait overlap

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ORIGINAL RESEARCH

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Contrasting effects of plant inter- and intraspecific variation on community trait responses to restoration of a sandy grassland ecosystem

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Abstract

Changes in plant community traits along an environmental gradient are caused by interspecific and intraspecific trait variation. However, little is known about the role of interspecific and intraspecific trait variation in plant community responses to the restoration of a sandy grassland ecosystem. We measured five functional traits of 34 species along a restoration gradient of sandy grassland (mobile dune, semi-fixed dune, fixed dune, and grassland) in Horqin Sand Land, northern China. We examined how community-level traits varied with habitat changes and soil gradients using both abundance-weighted and non-weighted averages of trait values. We quantified the relative contribution of inter- and intraspecific trait variation in specific leaf area (SLA), leaf dry matter content (LDMC), leaf carbon content (LCC), leaf nitrogen content (LNC), and plant height to the community response to habitat changes in the restoration of sandy grassland. We found that five weighted community-average traits varied significantly with habitat changes. Along the soil gradient in the restoration of sandy grassland, plant height, SLA, LDMC, and LCC increased, while LNC decreased. For all traits, there was a greater contribution of interspecific variation to community response in regard to habitat changes relative to that of intraspecific variation. The relative contribution of the interspecific variation effect of an abundance-weighted trait was greater than that of a non-weighted trait with regard to all traits except LDMC. A community-level trait response to habitat changes was due largely to species turnover. Though the intraspecific shift plays a small role in community trait response to habitat changes, it has an effect on plant coexistence and the maintenance of herbaceous plants in sandy grassland habitats. The context dependency of positive and negative covariation between inter- and intraspecific variation further suggests that both effects of inter- and intraspecific variation on a community trait should be considered when understanding a plant community response to environmental changes in sandy grassland ecosystems.

KEYWORDS

Community weighted traits, functional traits, interspecific and intraspecific variation, sandy grassland ecosystem, soil gradient, vegetation restoration

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ORIGINAL RESEARCH

A GDSL-motif esterase/acyltransferase/lipase is responsible for leaf water retention in barley

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Abstract

The hydrophobic cuticle covers the surface of the most aerial organs of land plants. The barley mutant *eceriferum-zv* (*cer-zv*), which is hypersensitive to drought, is unable to accumulate a sufficient quantity of cutin in its leaf cuticle. The mutated locus has been mapped to a 0.02 cM segment in the pericentromeric region of chromosome 4H. As a map-based cloning approach to isolate the gene was therefore considered unlikely to be feasible, a comparison was instead made between the transcriptomes of the mutant and the wild type. In conjunction with extant genomic information, on the basis of predicted functionality, only two genes were considered likely to encode a product associated with cutin formation. When eight independent *cer-zv* mutant alleles were resequenced with respect to the two candidate genes, it was confirmed that the gene underlying the mutation in each allele encodes a Gly-Asp-Ser-Leu (GDSL)-motif esterase/acyltransferase/lipase. The gene was transcribed in the epidermis, and its product was exclusively deposited in cell wall at the boundary of the cuticle in the leaf elongation zone, coinciding with the major site of cutin deposition. CER-ZV is speculated to function in the deposition of cutin polymer. Its homologs were found in green algae, moss, and euphyllophytes, indicating that it is highly conserved in plant kingdom.

KEYWORDS
abiotic stress, cell walls, cuticle/waxes, drought/water stress

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*These authors contributed equally to this work.

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RESEARCH ARTICLE

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

Chengchen Pan[1,2] · Qi Feng[1,2] · Jiliang Liu[1] · Yulin Li[1] · Yuqiang Li[1] · Xiaoya Yu[3]

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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; Pétillon 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

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sustainability

Article

Detecting Sustainability of Desertification Reversion: Vegetation Trend Analysis in Part of the Agro-Pastoral Transitional Zone in Inner Mongolia, China

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Abstract: Vegetation dynamics are an important topic in the field of global environment change, which is of great significance to monitor temporal–spatial variability of desertification at regional or global scales. Following the reported desertification reversion in the late 1990s in the Horqin Sandy Land, an issue was concerned for desertification control by decreased water availability. To detect the desertification process, MODIS Normalized Difference Vegetation Index (NDVI) sequences were investigated to analyze the effect on vegetation over the 2000–2015 growing season. Results showed that: (1) NDVI sequences exhibited a positive trend in most of the significant pixels (19.1%–44.7% of the total), particularly in the southeastern part of Horqin, while showing a negative trend of 2.2%–4.3%; (2) NDVI was weakly related to precipitation since 2000, because intensified anthropogenic activities have obscured the impacts of climate variables, with a rapid decrease in grassland, and increase in cropland and woodland; and (3) the improved NDVI was interpreted by expanding cropland and excessive groundwater irrigation, according to the positive effect of grain yield on NDVI all over the Horqin area. For persistent desertification reversion, a land use strategy should be more adaptive to the carrying capacity in this agro-pastoral transitional zone, particularly with respect to water capacity.

Keywords: MODIS Normalized Difference Vegetation Index (NDVI); desertification control; farming; sustainable restoration; path analysis; sustainable development goals (SDGs)

1. Introduction

Desertification is one of the major environmental issues, and seriously threatens water-constrained habitat covering 40% of the global land surface [1–3]. Building on earlier efforts, the United Nations Rio+20 have developed concrete sustainable development goals (SDGs) for worldwide prevention of desertification, as the Target 3 of Goal 15 mentions: "By 2020, combat desertification, restore degraded land and soil, including land affected by desertification, drought and floods, and strive to achieve a land-degradation-neutral world" [4]. Vegetation dynamics are an important aspect of the desertification process. However, it is controlled latitudinally and elevationally by global environmental change [5,6], or nutrient availability and rainfall seasonality at regional scales [7]. Changes in vegetation composition and structure influence ecosystem stabilization, and further the native access of ecosystem services [8], for

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Long-term grazing effects on vegetation characteristics and soil properties in a semiarid grassland, northern China

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Jie Lian · Xiyuan Yue**

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Abstract Understanding the responses of vegetation characteristics and soil properties to grazing disturbance is useful for grassland ecosystem restoration and management in semiarid areas. Here, we examined the effects of long-term grazing on vegetation characteristics, soil properties, and their relationships across four grassland types (meadow, *Stipa* steppe, scattered tree grassland, and sandy grassland) in the Horqin grassland, northern China. Our results showed that grazing greatly decreased vegetation cover, aboveground plant biomass, and root biomass in all four grassland types. Plant cover and aboveground biomass of perennials were decreased by grazing in all four grasslands, whereas grazing increased the cover and biomass of shrubs in *Stipa* steppe and of annuals in scattered tree grassland. Grazing decreased soil carbon and nitrogen content in *Stipa* steppe and scattered tree grassland, whereas soil bulk density showed the opposite trend. Long-term grazing significantly decreased soil pH and electrical conductivity (EC) in annual-dominated sandy grassland. Soil moisture in fenced and grazed grasslands decreased in the following order of meadow, *Stipa* steppe, scattered tree grassland, and sandy grassland. Correlation analyses showed that aboveground plant biomass was significantly positively associated with the soil carbon and nitrogen content in grazed and fenced grasslands. Species richness was significantly positively correlated with soil bulk density, moisture, EC, and pH in fenced grasslands, but no relationship was detected in grazed grasslands. These results suggest that the soil carbon and nitrogen content significantly maintains ecosystem function in both fenced and grazed grasslands. However, grazing may eliminate the association of species richness with soil properties in semiarid grasslands.

Keywords Horqin grassland · Vegetation characteristics · Soil properties · Grazing

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Introduction

Grassland is one of the most widespread biomes in China, accounting for 41% of the total national land area. Disturbance or unreasonable human activities lead to the degradation of the temperate grassland ecosystem (Li et al. 2007; Jiao et al. 2011; Limb et al. 2011) and subsequent desertification (Li et al. 2000; Reynolds et al. 2007). Grassland desertification characterized by vegetation and soil degradation is commonly caused by the continuous over-grazing (Golluscio et al. 2009; Zhou et al. 2010). Grazing affects semiarid and arid

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Trend shifts in satellite-derived vegetation growth in Central Eurasia, 1982–2013

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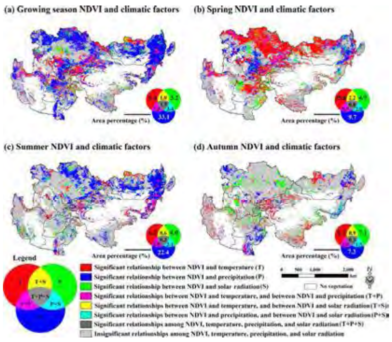
HIGHLIGHTS

- We associate climatic impacts on vegetation growth in Central Eurasia.
- Central Eurasian vegetation has a nonlinear response to changing climate.
- The response of vegetation to climatic factors varies in different seasons.
- The diverse vegetation responses to climate are related to different vegetation characteristics and climatic conditions.
- Ecosystem functions regulate the relationships between vegetation and climate.

GRAPHICAL ABSTRACT



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ABSTRACT

Central Eurasian vegetation is critical for the regional ecological security and the global carbon cycle. However, climatic impacts on vegetation growth in Central Eurasia are uncertain. The reason for this uncertainty lies in the fact that the response of vegetation to climate change showed nonlinearity, seasonality and differences among plant functional types. Based on remotely sensed vegetation index and in-situ meteorological data for the years 1982–2013, in conjunction with the latest land cover type product, we analyzed how vegetation growth trend varied across different seasons and evaluated vegetation response to climate variables at regional, biome and pixel scales. We found a persistent increase in the growing season NDVI over Central Eurasia during 1982–1994, whereas this greening trend has stalled since the mid-1990s in response to increased water deficit. The stalled trend in the growing season NDVI was largely attributed by summer and autumn NDVI changes. Enhanced spring vegetation growth after 2002 was caused by rapid spring warming. The response of vegetation to climatic factors varied in different seasons. Precipitation was the main climate driver for the growing season and summer vegetation growth. Changes in temperature and precipitation during winter and spring controlled the spring vegetation growth. Autumn vegetation growth was mainly dependent on the vegetation growth in summer. We found diverse responses of different vegetation types to climate drivers in Central Eurasia. Forests were more responsive to temperature than to precipitation. Grassland and desert vegetation responded more strongly to precipitation than to temperature in summer but more strongly to temperature than to precipitation in spring. In addition, the growth of desert vegetation was more dependent on winter precipitation than that of grasslands. This study has important implications for improving the performance of terrestrial ecosystem models to predict future vegetation response to climate change.

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ORIGINAL RESEARCH

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Effect of pollen and resource limitation on reproduction of *Zygophyllum xanthoxylum* in fragmented habitats

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Abstract

Limitations on pollen and resources may significantly affect plant reproduction in fragmented habitats. In this study, phenology and pollinator frequency and activity were investigated to estimate the role of pollinators in *Zygophyllum xanthoxylum* reproduction, and this species is ecologically important in northwest China. In addition, the relative impact of restrictive amounts of pollen and resources on the seed set per flower was evaluated. It was found that adding pollen boosted the size of the seed set per flower, but had no significant effect on the number of flowers. By contrast, the addition of resources increased flower numbers as well as had a slight impact on the seed set per flower. These results indicate the amount of available pollen is a limiting factor for reproductive success. Moreover, *Apis mellifera* was identified as the most effective pollinator of *Z. xanthoxylum*, and there were more overall pollinators and visitations in the control than in the fragmented habitats. Furthermore, the limitations in pollen were more restrictive in the fragmented area than in the control. This was due to increased pollinator visitations in the control that could ameliorate the effects of lower pollen levels. When there is a limited availability of suitable pollinators, self-pollination is critical in fragmented habitats. *Z. xanthoxylum* has reproductive strategies that aid in adapting to harsh environments, including protogyny and delayed selfing.

KEYWORDS
pollen limitation, pollinator behavior, pollinators, resource limitation, seed set

1 | INTRODUCTION

The sex allocation model has highly influenced the field of plant reproductive ecology (Goldman & Willson, 1986). This model is based on the observation that a significant proportion of flowers and ovules in a plant do not become fruit or seeds (Lloyd, 1980; Stephenson, 1981). Several hypotheses have been put forth concerning this phenomenon, including restriction of pollen and resources, that is, pollen limitation (Burd, 1994; Sutherland, 1987). Pollen limitation refers to pollen quantities or quality that hinders the reproductive success of plants (Aizen & Harder, 2007; Ashman et al., 2004). The most frequently studied example of this is insufficient pollinator service, which especially has an effect on selection for floral traits relating to the pollinator activity in animal-pollinated plants (Burd, 1994; Liao, Song, & Zhang, 2006; Suzuki, 2000; Yang, Sun, & Guo, 2005). In addition, the distance between plants can affect a number of pollination-related processes, such as attracting pollinators and breeding systems (Ashman & Morgan, 2004; Kearns, Inouye, & Waser, 1998). Restriction of pollen and resources is often encountered by plants influenced by natural pollination conditions and may lead to low reproductive output (Asikainen & Mutikainen, 2005; Knight et al., 2005). Many studies have suggested that it should be assumed plants are limited by resource availability if the reproductive output of an individual plant does not increase after supplemental hand pollination (Whigham, 1984; Zimmerman & Aide, 1989).

sustainability

MDPI

Article

Annual Precipitation Fluctuation and Spatial Differentiation Characteristics of the Horqin Region

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Abstract: Precipitation is the main water source for vegetation survival in arid and semi-arid areas. However, previous studies always focus on the effects of precipitation in different time scales, but ignore the effects of precipitation in different spatial scales. To further study the effects of precipitation fluctuation in different spatial scales, we used the wavelet analysis method to analyze its temporal and spatial change based on data from eighteen meteorological stations during 1961–2015 in Horqin region. Results showed that: (1) from the overall tendency of precipitation changes, the precipitation inter-annual variations in Horqin region had the tendency of gradually decreasing from the southeast (District IV) to the northwest; (2) the precipitation anomalies of District I–IV between 1960 and 1980 were small and approximate to the normal value; (3) in the time scale of 23–32 years, the cyclical fluctuations were very significant and the annual precipitation underwent two cyclical fluctuations from a period of low precipitation to a period of high precipitation; and (4) as results of analyzing the spatial wavelet variance of sub-region, the main cycle of precipitation in District I, District II and District III was between 10 and 11 years, while the main cycle of precipitation in District IV was 25 years. The main conclusions include the following. (1) This region tended to be arid, and the precipitation gradually decreased from the southeast (District IV) to northwest (District I). (2) The influence of spatial differentiation characteristics on precipitation fluctuation in this region was cyclical fluctuation, which gradually decreased from the southeast to the northwest. The length of the cyclical change period gradually shortened. In the first main cycle, whose annual precipitation changes were most significant, the changing characteristic was District IV and District I decreased from 25 years to 10 years. (3) Predicated from the cyclical changing law that the annual precipitation decreases from high to low, the Horqin region will remain in a period of low precipitation between 2016 and 2020.

Keywords: precipitation pulse; wavelet analysis; changing period; Horqin sandy land

1. Introduction

Precipitation is the main water source for vegetation survival in arid and semi-arid areas. It is also the main driving factor of various ecological processes of different ecological scales [1–5]. For a certain region, the precipitation fluctuation in different time scales usually takes place by pulse. The time for its occurrence, duration period, strength and other characteristic parameters are all greatly differentiated. These characteristics make the soil water content and the vegetation process fluctuate in a short time scale [6,7]. In current research, the abnormal fluctuation of precipitation in the context of global

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Effects of *Caragana microphylla* plantations on organic carbon sequestration in total and labile soil organic carbon fractions in the Horqin Sandy Land, northern China

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Abstract: Afforestation is conducive to soil carbon (C) sequestration in semi-arid regions. However, little is known about the effects of afforestation on sequestrations of total and labile soil organic carbon (SOC) fractions in semi-arid sandy lands. In the present study, we examined the effects of *Caragana microphylla* Lam. plantations with different ages (12- and 25-year-old) on sequestrations of total SOC as well as labile SOC fractions such as light fraction organic carbon (LFOC) and microbial biomass carbon (MBC). The analyzed samples were taken from soil depths of 0–5 and 5–15 cm under two shrub-related scenarios: under shrubs and between shrubs with moving sand dunes as control sites in the Horqin Sandy Land of northern China. The results showed that the concentrations and storages of total SOC at soil depths of 0–5 and 5–15 cm were higher in 12- and 25-year-old *C. microphylla* plantations than in moving sand dunes (i.e., control sites), with the highest value observed under shrubs in 25-year-old *C. microphylla* plantations. Furthermore, the concentrations and storages of LFOC and MBC showed similar patterns with those of total SOC at the same soil depth. The 12-year-old *C. microphylla* plantations had higher percentages of LFOC concentration to SOC concentration and MBC concentration to SOC concentration than the 25-year-old *C. microphylla* plantations and moving sand dunes at both soil depths. A significant positive correlation existed among SOC, LFOC, and MBC, implying that restoring the total and labile SOC fractions is possible by afforestation with *C. microphylla* shrubs in the Horqin Sandy Land. At soil depth of 0–15 cm, the accumulation rate of total SOC under shrubs was higher in young *C. microphylla* plantations (18.53 g C/(m^2•a); 0–12 years) than in old *C. microphylla* plantations (16.24 g C/(m^2•a); 12–25 years), and the accumulation rates of LFOC and MBC under shrubs and between shrubs were also higher in young *C. microphylla* plantations than in old *C. microphylla* plantations. It can be concluded that the establishment of *C. microphylla* in the Horqin Sandy Land may be a good mitigation strategy for SOC sequestration in the surface soils.

Keywords: *Caragana microphylla* plantation; soil organic carbon; light fraction organic carbon; microbial biomass carbon; carbon accumulation rate; Horqin Sandy Land

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ORIGINAL RESEARCH

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

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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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Adaptive evolution of *rbcL* in *Reaumuria soongarica* (Tamaricaceae)

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ABSTRACT

In the field of phylogenetic analyses, the *rbcL* gene encoded large subunit Ribulose-1,5-biphosphate carboxylase/oxygenase (Rubisco, EC4.1.1.39), which plays a crucial role in the process of photosynthesis for most terrestrial plants, has been considered to be conserved; however, recent controversy regarding *rbcL* conservation has appeared since it was proposed to be under natural selection within all principal lineages of land plants. In this study, by examining the variation of DNA and protein sequences among 17 species in the family Tamaricaceae, three nonsynonymous mutations were identified to be under positive selection. The favored sites were located in the alph-helix domains of Rubisco, with decreased hydrophobicity and increased entropy, which could facilitate CO_2 penetration into the active site of Rubisco. We also found that the expression level of *rbcL* in different genotypes of *Reaumuria soongarica* shifted in response to various stresses such as drought, temperature, salt, and light. This study not only sheds light on the functional/structural features of Rubisco in the evolution scenarios from C_3-like into C_4 in Tamaricaceae but also provides useful information on directing genetic performance to enhance photosynthesis efficiency of desert plants for sustaining fragile desert ecosystems; furthermore, it promotes the ability to cope with desert aridification and global warming.

Keywords: *rbcL* gene; *Reaumuria soongarica*; Tamaricaceae; adaptive evolution

1 Introduction

Photosynthesis is not only the most important chemical reaction to transform inorganic matter into organic matter through fixing solar energy on the earth but also the crucial source for plant carbon or biomass accumulation for growth and development. Its productivity is tightly linked to the delicate balance between carboxylation and oxygenation. As a bifunctional enzyme catalyzing both the carboxylation of D-ribulose-1,5-bisphosphate (RuBP) that initiates photosynthetic CO_2 fixation and the oxygenation of

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Intrastorm stemflow variability of a xerophytic shrub within a water-limited arid desert ecosystem of northern China

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ABSTRACT

An increasing number of studies in recent years has elucidated distinguishable effects of stemflow on hydrology and biogeochemistry within a variety of ecosystems. Nonetheless, no known studies have investigated the temporal variability of stemflow volume within discrete rainfall events for xerophytic shrubs. Here, stemflow was monitored at 5-min intervals using a tipping-bucket rain gage during the 2015 growing season for a xerophytic shrub (*Caragana korshinskii*) within a water-limited arid desert ecosystem of northern China. We characterized the stemflow temporal variability, along with rainfall, and found the temporal heterogeneity of rainfall clearly affected the timing of stemflow inputs into basal soil within discrete rainfall events. The rainfall threshold value for stemflow generation is not a constant value but a range (0.6~2.1 mm, with an average of 1.1 mm) across rainfall events and is closely associated with the antecedent dry period. Time lags existed between the onset of rainfall and the onset of stemflow, and between rainfall peaks and stemflow peaks. Our findings are expected to be helpful for an improved process-based understanding of the temporal stemflow yield of xerophytic shrubs within water-limited arid desert ecosystems.

Keywords: stemflow; temporal variability; xerophytic shrub; antecedent dry period; time lag

1 Introduction

Precipitation is partitioned into interception loss, stemflow, and throughfall by vegetation canopies (Crockford and Richardson, 2000; Llorens and Domingo, 2007); this pattern alters the horizontal and vertical distribution of precipitation within shrub communities, greatly increases the variability of soil-moisture recharge, and plays a pivotal role in vegetation survival and reproduction in water-limited desert ecosystems (*e.g.*, Martinez-Meza and Whitford, 1996; Johnson and Lehmann, 2006; Navar, 2011; Wang *et al.*, 2011; Li *et al.*, 2013; Zhang YF *et al.*, 2013, 2016a; Levia and Germer, 2015).

Stemflow is the portion of precipitation that is intercepted by leaves, twigs, and branches, and eventually delivered to the basal soil via trunks or stems. Stemflow has been reported to be a function of a suite of biotic and abiotic factors, including tree species and architecture (Levia and Frost, 2003; Barbier *et al.*, 2009; Zimmermann *et al.*, 2015; Zhang *et al.*, 2017); leaf shape, number, and angle (Staelens *et al.*, 2008; Levia *et al.*, 2013); branch angle (Herwitz, 1987; Martinez-Meza and Whitford, 1996; Park and Cameron, 2008); bark structure (Levia and Herwitz, 2005; Van Stan *et al.*, 2016); incident rainfall amount, intensity, duration, and angle (Crockford and Richardson, 2000; Dunkerley, 2014a; Zhang *et al.*, 2015); air temperature (Levia and Herwitz, 2000; Andre *et al.*, 2008); relative humidity (Andre *et al.*, 2008); wind

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The weak effects of fencing on ecosystem respiration, CH_4, and N_2O fluxes in a Tibetan alpine meadow during the growing season

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ABSTRACT

Fencing is the most common land-management practice to protect grassland degradation from livestock overgrazing on the Tibetan Plateau. However, it is unclear whether fencing reduces CO_2, CH_4, and N_2O emission. Here, we selected four vegetation types of alpine meadow (graminoid, shrub, forb, and sparse vegetation) to determine fencing effects on ecosystem respiration (Re), CH_4, and N_2O fluxes during the growing season. Despite increased average monthly ecosystem respiration (Re) for fenced graminoid vegetation at the end of the growing season, there was no significant difference between grazing and fencing across all vegetation types. Fencing significantly reduced average CH_4 uptake by about 50% in 2008 only for forb vegetation and increased average N_2O release for graminoid vegetation by 38% and 48% in 2008 and 2009, respectively. Temperature, moisture, total organic carbon, C/N, nitrate, ammonia, and/or bulk density of soil, as well as above- and belowground biomass, explained 19%~71% and 6%~33% of variation in daily and average Re and CH_4 fluxes across all vegetation types, while soil-bulk density explained 27% of variation in average N_2O fluxes. Stepwise regression showed that soil temperature and soil moisture controlled average Re, while soil moisture and bulk density controlled average CH_4 fluxes. These results indicate that abiotic factors control Re, CH_4, and N_2O fluxes; and grazing exclusion has little effect on reducing their emission—implying that climatic change rather than grazing may have a more important influence on the budgets of Re and CH_4 for the Tibetan alpine meadow during the growing season.

Keywords: fencing; ecosystem respiration; methane; nitrous oxide; Tibetan alpine meadow

1 Introduction

Livestock grazing is a dominant land-use activity on the Tibetan Plateau, which is very sensitive to anthropogenic perturbation (Yang *et al.*, 2013). Over past decades, overgrazing activity has led to severe

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ORIGINAL ARTICLE

Alpine soil carbon is vulnerable to rapid microbial decomposition under climate cooling

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As climate cooling is increasingly regarded as important natural variability of long-term global warming trends, there is a resurging interest in understanding its impact on biodiversity and ecosystem functioning. Here, we report a soil transplant experiment from lower to higher elevations in a Tibetan alpine grassland to simulate the impact of cooling on ecosystem community structure and function. Three years of cooling resulted in reduced plant productivity and microbial functional potential (for example, carbon respiration and nutrient cycling). Microbial genetic markers associated with chemically recalcitrant carbon decomposition remained unchanged despite a decrease in genes associated with chemically labile carbon decomposition. As a consequence, cooling-associated changes correlated with a decrease in soil organic carbon (SOC). Extrapolation of these results suggests that for every 1 °C decrease in annual average air temperature, 0.1 Pg (0.3%) of SOC would be lost from the Tibetan plateau. These results demonstrate that microbial feedbacks to cooling have the potential to differentially impact chemically labile and recalcitrant carbon turnover, which could lead to strong, adverse consequences on soil C storage. Our findings are alarming, considering the frequency of short-term cooling and its scale to disrupt ecosystems and biogeochemical cycling.

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Introduction

Global climate change science has predominantly targeted climate warming (Luo, 2007; Frey *et al.*, 2013; Nie *et al.*, 2013), but this focus is changing, as it is increasingly recognized that temporary, local cooling events are common amidst long-term global warming trends (Alley *et al.*, 2003; Ji *et al.*, 2014). There has been significant cooling in the Antarctic Peninsula as the late 1990s, arising from natural variability of the regional atmospheric circulation (Turner *et al.*, 2016). It has been projected that the climate in the 21st century is likely to produce periods as long as one or two decade(s) of cooling (Easterling and Wehner, 2009; Lyubushin and Klyashtorin, 2012), which is alarming because historic evidence shows that cooling may perturb ecosystems and biogeochemical cycling at a scale comparable to what is known for warming (McAnena *et al.*, 2013). For instance, cooling on the Antarctic continent between 1966 and 2000 led to a rapid decrease in the primary productivity of lakes (6–9% per year) as well as the number of soil invertebrates (more than 10% loss per year) (Doran *et al.*, 2002). Therefore, further understanding of the full range of possible climate change scenarios and

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ORIGINAL ARTICLE

Accumulation of heavy metals in native plants growing on mining-influenced sites in Jinchang: a typical industrial city (China)

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Abstract Such activities as mining, metal ore smelting and the discharging of mining wastes lead to heavy metal contamination. Phytoremediation, including phytoextraction and phytostabilization, has been considered for a long time to be effective in remediating metal-polluted soils. This research assessed the chance of 40 plants (35 species) distributing on mining-influenced sites for phytoremediation purposes. The results showed that total soil Ni, Cu, Cd, Cr and Co concentrations were in the ranges of 107–3045, 116–2580, 7.1–22.7, 115–897 and 23.2–144.3 mg kg^{-1}, respectively, whereas heavy metal contents in plants were in the ranges of 0.60–435.61, 2.41–298.31, 0.03–32.10, 0.08–88.20 and 0.11–28.52 mg kg^{-1}, respectively. Therefore, no species can be used for phytoextraction purposes because no hyperaccumulator was identified. *Salsola passerine*, *Stipa capillata*, *Cynanchum Chinense* and *Halogeton glomeratus* with translocation factor (TF) > 1 for all five metals were considered to be accumulators. All plants were observed to hold a bioconcentration factor (BCF) < 1, except for *Caragana korshinskii*, which had a BCF for Cd > 1, reflecting its low metal accumulation potential. Among the species studied, *Oxytropis aciphylla*, *Salix matsudana*, *Tamarix hispida*, *Robinia pseudoacacia*, *Picea crassifolia*, *Lycium barbarum* and *Phragmites communis* had both a BCF and TF < 1 for all five metals and were considered the most suitable for the phytostabilization of metal-polluted sites.

Keywords Heavy metals · Metal uptake · Mine tailings · Phytoremediation · Phytostabilization

Introduction

Such activities as mining, metal ore smelting and the discharging of mining wastes have all conduced accumulated heavy metal levels in the surroundings (Alloway 1994). Heavy metal toxicity leads to most environmental problems where, for example, containing land surfaces are destroyed and agricultural fields are polluted (Bhuiyan et al. 2010). Direct results include the loss of cultivated land, grazing land or forest and production, whereas indirect effects contain water and air pollution and river siltation, which eventually leads to loss of biodiversity, esthetic and economic benefit (Bradshaw 1993). In China, mining areas have eroded approximately 40,000 km^2 of land and simultaneously abandoned mining land is increasing by 330 km^2 annually (Zou et al. 2012).

Several technologies can be suitable for the restoration of soils that are polluted by heavy metals. Nevertheless, many of them may be high cost or rarely result in long-lasting or amenity effects (Mulligan et al. 2001; Cao et al.

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Effects of plant restoration on soil microbial biomass in an arid desert in northern China

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ABSTRACT

Soil microbial biomass acts as both a source and sink of organic carbon and available nutrients, consequently affecting plant growth and production. However, our understanding regarding the effects of plant restoration practices on the patterns of soil microbial biomass remains limited. In this study, we established a 54-year chronosequence comprising moving sand dunes and adjacent sites that had been stabilized through different periods (10, 20, 29, 46, and 54 years) of plant restoration in the southeastern fringe of the Tengger Desert, China. Microbial biomass carbon (MBC), microbial biomass nitrogen (MBN), and their relationship with soil physicochemical properties were analyzed. The results showed that plant restoration significantly increased MBC and MBN in the arid desert. In all stabilized sites, MBC and MBN decreased with increasing soil depth, while they increased along the chronosequence with decreasing plant cover and successional biological soil crusts. MBC and MBN in moving dunes remained lower than those in stabilized sites and slightly increased from topsoil to subsoil. Both MBC and MBN were positively correlated with silt and clay contents, soil organic carbon (SOC), total nitrogen (TN), and MBC/SOC and MBN/TN ratios, whereas they were negatively correlated with sand content. Higher MBC and MBC/SOC were found in the later successional stages, suggesting a great potential for carbon sequestration and higher nutrient turnover for stand biomass. This study indicated that plant restoration plays an important part in the recovery of the biological functioning of soil in an arid desert.

1. Introduction

Arid and semi-arid lands contain 16% of the global soil carbon pool. Over two-thirds of lands in arid and semi-arid regions have been destroyed by desertification, leading to carbon loss (Lal, 2001). Many measures have been taken to prevent environmental deterioration and restore degraded soil in arid and semi-arid lands (Luna et al., 2016; Yang et al., 2014; Xiao et al., 2016a). The availability of basic information on ecological processes that occur during the course of ecosystem recovery is critical for proper planning and management of rehabilitation programs in disturbed ecosystems (Liu et al., 2015; Garris et al., 2016).

Soil organic carbon (SOC) is a key factor in soil fertility and an important destination of atmospheric CO_2 fixed by plants (Lal, 2001). Evaluating the SOC can contribute to our understanding and prediction of the effects of changes in soil quality and management practices on soil biological conditions and the carbon cycle. Reasonable and efficient plant restoration measures have been reported to increase SOC stocks and improve soil quality in desert regions (Yu et al., 2016; Huang et al., 2012; Yang et al., 2014). However, restoration of degraded land through planting vegetation does not contribute more SOC than native forests, as shown by a meta-analysis of various factors such as plant species, site preparation, and study region on the basis of limited studies (Liao et al., 2010). Currently, the role of plant restoration on SOC remains unclear under different conditions. This emphasizes the necessity for more experimental studies on ecosystem carbon cycle for plantations.

Soil microbial biomass (SMB), the living component of soil organic matter, acts as the source and sink of carbon and available nutrients (Singh et al., 1989). SMB regulates biogeochemical

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Effect of biological soil crusts on microbial activity in soils of the Tengger Desert (China)

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ABSTRACT

Soil microbes, as an important biological component of soils, have a function in the formation of soils and soil-remediation processes. This paper aims to analyze effects of biocrusts on soil microbial activities in desert ecosystems. Two sets of samples were collected under biocrusts in April, July, October, 2013, and January, 2014, in natural and revegetated areas of the Tengger Desert. The results showed that biocrusts significantly improved soil physicochemical properties, basal respiration and the quantity of soil alkaline phosphatase, protease, and cellulose, and decreased qCO_2 in vegetated areas. Impact of biocrusts on soil microbial activities also varied, depending on the successional stage of crusts and the restoration age. Soil basal respiration and enzyme activity were obviously higher, but qCO_2 were significantly lower in moss-dominated crusts than those dominated by cyanobacteria-lichen. Soil basal respiration and enzyme activity positively correlated with the restoration age, but qCO_2 negatively correlated with the restoration age. Soil basal respiration and enzyme activity were the highest in summer, followed by autumn, and the lowest in spring and winter; whereas, qCO_2 displayed an opposite trend. The study suggests that biocrusts have the ability to improve soil quality and promote soil recovery in vegetated areas of the Tengger Desert.

1. Introduction

Arid and semiarid lands account for as much as 33–40% of Earth's terrestrial surface, and are expanding rapidly (Billings et al., 2003). Vegetation cover in these areas is patchy and discontinuous due to combined impacts of harsh environmental factors such as prolonged drought, high temperatures and high soil erosion rates. Nevertheless, biocrusts are able to adapt successfully to these adverse environments, colonize the bare disaggregated geological substrate (Li, 2012) and cover as much as 70% of the interspaces between the sparse vegetation in these areas (Steven et al., 2014). Numerous studies have examined the ecosystem functions of biocrusts in desert ecosystems, such as fixing of C and N, improving soil structure, enhancing soil stability, modifying soil temperature, moisture and local hydrology, reinforcing plant colonization and promoting soil invertebrate and microbial diversity (Belnap and Lange, 2003; Bowker et al., 2013; Darby et al., 2010; Liu et al., 2013; Neher et al., 2009).

Soil microbes, as an important biological component of soils, have a function in soil formation and soil remediation processes, through the decomposition of organic matter, formation of humus, and nutrient cycling. Soil basal respiration is mostly associated with activity of microbes, therefore it indicates the potential mineralization rate of soil organic matter by soil microbes from a desert ecosystem (Pell et al., 2006). The ratio of basal respiration to microbial biomass carbon (metabolic quotient: qCO_2), provides a method to relate both the amount and activity of soil microbes (Anderson and Domsch, 1990). Soil basal respiration, qCO_2 and enzyme activity provide a measure of microbial activity, which is a sensitive indicator of soil quality changes in response to

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植物固沙的生态－水文过程、机理及调控 *

项目承担单位：中国科学院寒区旱区环境与工程研究所（主持单位） 中国林业科学研究院荒漠化研究所
中国科学院沈阳应用生态研究所 兰州大学 中国科学院新疆生态与地理研究所
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中国的沙害造成直接经济损失每年超过 540 亿元，已成为制约中国北方社会经济、生态安全和可持续发展的重要因素。

植物固沙即是建立人工植被（图 1），是构建中国北方生态屏障的有效途径之一。到目前为止，全国荒漠化和沙化土地面积连续三个监测期保持“双减少”，但是治理效果，即人工植被固沙效益及其稳定可持续的维持，依然面临着巨大的挑战。要解决人工固沙植被大面积退化或死亡（图 2），就必须解决：①不同沙区土壤水来源和土壤水分植被承载力有多大？②固沙植被生态－水文过程是如何互馈互调的，作用机理是什么？③如何界定人工固沙植被稳定性的生态－水文阈值？固沙植被的稳定性和可持续性事关防沙治沙的成败，确定不同沙区人工植被稳定性维持的生态－水文阈值，是植物固沙研究和构建沙区生态屏障亟待解决的核心问题。

项目的主要研究进展：

（1）明确了主要固沙植物水分利用的来源，提出了不同气候带沙区土壤水的最大植被承载力，为沙区植物种选择、植被建设的合理规模提供理论依据

根据天然植被区土壤含水量的长期监测，计算出不同沙区可供人工植被利用的土壤储水量。结合茎干液流观测、稳定同位素技术与模型解析探明了我国主要固沙植物的水分利用来源。通过建立个体尺度沙区植被－水分关系模型，将年最大 LAI 的多年平均值作为植被承载力的特征指标，首次量化了土壤水的植被承载力，通过研究不同沙区植被承载力与环境要素的关系，建立了植被与环境要素的模型，进而对不同气候带沙区植被承载能力进行量化和预测。

（2）对典型固沙植被的水量平衡进行了量化研究，为确定不同沙区人工植被的类型和格局提供了理论支撑

针对不同气候区固沙植被－土壤系统水分传输的关键过程、固沙植被－土壤系统水分平衡关系的尺度效应两个关键科学问题，在个体、群落、景观尺度上解析了固沙植物吸水－输水－耗水关键过程及其调控机制，探究了不同尺度固沙植被水分平衡关系。在理论上，对个体、群落、景观尺度的水分平衡关系进行了解析，揭示了固沙植被－土壤系统水分平衡关系的尺度效应。实测证实，个体尺度水分平衡仅考虑目标植物，不能真实反映水分平衡关系，且群落尺度水分亏缺远大于景观尺度，固沙植被－土壤系统水分平衡实际上是景观尺度的水分平衡关系，从景观尺度量化了维持固沙植被稳定的水分平衡关系；探明了不同地貌单元间的水分传输是景观尺度水分平衡的关键过程，通过比较景观尺度和群落尺度的水分平衡差异，证实了半湿润区沙丘－丘间低地系统存在土壤水分运移，而干旱区不存在土壤水分运移，阐明了景观尺度水分平衡要素的区域差异。

（3）揭示了固沙植物在不同水平上对水分胁迫的适应机制

发现不同固沙植物响应干旱胁迫的渗透调节分子不同，说明固沙植物以代谢多样性来适应干旱环境。包括沙拐枣与油蒿、柠条、柽柳、红砂、沙米等。以叶片形态结构特征为基础，分析了自然生境下锦鸡儿属主要固沙种的抗旱适应能力，为同属内不同固沙物种的筛选奠定了基础；

揭示了固沙植物响应水分胁迫的生理生态机制，阐释了不同气候带典型沙生植物光合作用特征。水分胁迫下，不同植物在光合色素含量和光合作用能力各不相同，渗透调节物质及酶类物质的积累各有侧重，反映了生理性耐旱机理的多样性。建立了固沙植物叶片抗旱性综合

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长期生态学研究引领中国沙区的生态重建与恢复*

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摘要　长期生态学研究揭示了干旱沙区土壤水循环的植被调控机理，解决了降水小于200 mm沙区植被建设的关键技术，提出了生态恢复的技术体系及其应用模式；引领了荒漠生物土壤结皮的研究，探明了人工植被稳定性维持的机理，拓展了荒漠系统生态恢复的生态水文学理论基础，推动了干旱逆境生理生态学的研究，在国内外产生了重要影响，为我国风沙危害治理和沙区生态重建与恢复提供了基础理论和技术支撑。

关键词　风沙治理，荒漠生态系统，长期定位监测研究，人工植被，生态水文

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退化系统的恢复和重建是人类生存与可持续发展所面临的严峻挑战。我国的生态退化十分严重，已呈现出由结构性破坏向功能性紊乱演变的发展趋势，退化生态系统面积约占国土总面积的1/4。其中，沙化土地占国土总面积的17.93%，因荒漠化造成的直接经济损失约540亿元/年。新中国成立以来，党和国家十分重视沙化土地的治理和沙区生态重建工作。自2000年以来，全国荒漠化和沙化土地面积连续3个监测期保持“双减少”，沙化土地面积由20世纪末年均扩展3 436 km^2转变为目前的年均缩减1 980 km^2，实现了由“沙进人退”到“人进沙退”的历史性转变。2015年中央出台的《关于加快推进生态文明建设的意见》中明确提出，到2020年我国50%以上可治理的沙化土地要得到有效治理。中科院沙坡头沙漠试验站作为我国最早建立的沙漠研究治理生态站，60余年的长期生态学研究为沙化土地治理和沙区生态重建与恢复提供了重要理论和技术支撑，为中国的防沙治沙作出了贡献。

1 解决了降水小于200 mm的干旱沙漠地区植被建设的关键技术，证实了区域生态恢复的可行性

在成功地解决了包兰铁路沿线流动沙丘固定的基础上，对干旱沙漠地区无灌溉人工植被建立的理论范式和技术体系进行了长期的定位研究。明确了以建立覆盖度小于15%的旱

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生物土壤结皮对一年生植物影响研究进展

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摘要： 生物土壤结皮在荒漠地区广泛分布，它的形成和演替深刻地改变了土壤表层的结构特征和理化性质，进而影响了荒漠地区一年生植物的种子传播、萌发、幼苗存活及生长过程。本文回顾了国内外有关生物土壤结皮对一年生植物影响的研究，综述了生物土壤结皮对一年生植物的土壤种子库、种子萌发、幼苗存活及生长过程的影响，分析了各研究结论中存在争议的原因，总结了生物土壤结皮对一年生植物种子传播、萌发、幼苗存活及生长影响的内在机理，指出了生物土壤结皮对荒漠地区植被组成的筛选作用，并对进一步的研究进行了展望。

关键词： 生物土壤结皮；一年生植物；土壤种子库；萌发；幼苗存活

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0 引言

生物土壤结皮(BSCs)是干旱、半干旱地区特殊环境的产物，是由隐花植物如蓝藻、荒漠藻、地衣、苔藓和土壤中微生物，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[1-3]。BSCs有着独特的生理生态过程和较强的逆境适应能力，广泛分布在各种荒漠生境，覆盖度占荒漠地表活体覆盖的40%以上，是荒漠地区最具特色的微自然景观[3-5]。BSCs中的藻类、地衣和藓类等生物组分不仅能够克服荒漠地区的恶劣环境，还能通过自身的诸如共代谢等方式潜移默化地影响并改变着周围的生境[6]。它的形成和发育使土壤表层在物理、化学和生物学特性上明显不同于松散的沙土，具有较强的抗风蚀、水蚀功能和重要的生态及地学效应，是荒漠地区植被演替的重要基础[3,7-8]。

BSCs对荒漠生态系统的影响主要体现在以下几个方面：(1) BSCs中的细菌、真菌、地衣和苔藓植物的地下菌丝和假根能够黏结沙粒，增强了土壤抵抗侵蚀的能力，增加了土壤稳定性，改变了土壤表层结构特征，并且从大气中捕获大量降尘，促进沙区土壤形成过程[9-11]。(2) BSCs中的一些藻类具有从大气中固定N素的功能，BSCs中的生物体还可以通过光合、呼吸、分解和矿化作用，为贫瘠的荒漠系统输入大量的生命元素，改善了土壤的理化性质，增加了土壤有机质的含量[12-15]。(3) BSCs通过改变降水入渗、地表径流、蒸发和凝结水捕获等方式重新分配了土壤水分[16-18]。来自温带荒漠的研究表明[19-20]，BSCs对降水起到了显著的拦截作用，阻止了水分向土壤深层的入渗，使土壤水分浅层化。这种改变驱动了固沙植被在组成、结构和功能上的响应，即深根系的木本植物减少，浅根系的草本植物增加。

BSCs的形成和演替深刻地改变了土壤表层的形态特征和理化性质，进而影响荒漠地区一年生植物的种子传播、萌发、幼苗存活及生长过程[3,8,21]。BSCs作为生态系统初级演替的拓殖者，研究其对一年生植物的影响作用能够加深我们对荒漠地区的生态恢复过程与植被演替规律的认识，对荒漠生态系统管理与资源可持续利用也有着重要意义。目前，BSCs对一年生植物的影响已引起了众多学者的关注，成为荒漠生态系统十分有趣且重要的科学问题，国内外的许多学者就这一问题开展了大量研究，然而两者之间的关系是复杂的，影响和作用是多方面的，许多研究结论相互矛盾，存在着广泛的争议[7]。尽管目前关于BSCs对一年生植物影响的研究在各方面均有涉及，但许多研究不够深入，BSCs对一年生植物影响的机理性研究较少，许多研究仅仅探究了BSCs对几种植物生活周期的一些特定阶段的影响，严重缺乏连续性和系统性，且缺乏横向的对比和

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陈孟晨,张景光,冯丽,滕嘉玲.沙坡头地区生物结皮覆盖区土壤种子库组成及垂直分布特征.生态学报,2017,37(22):7614-7623.

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沙坡头地区生物结皮覆盖区土壤种子库组成及垂直分布特征

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摘要: 采用野外随机取样和室内萌发试验相结合的方法,对沙坡头人工植被区的藓类结皮、地衣结皮和裸沙覆盖区土壤种子库的组成及垂直分布特征进行了研究。结果表明: 1) 人工植被区土壤种子库的物种组成简单,以 1 年生草本为主,相较于裸沙,两种生物结皮的存在显著增加了土壤种子库的密度($P < 0.01$),但降低了土壤种子库的物种多样性及其与地上植被的相似性; 2) 两种生物结皮覆盖区土壤种子库的总密度虽无显著差异,但在 0—2 cm 土层中,地衣结皮土壤种子库的密度显著高于藓类结皮($P < 0.05$),而在 2—5 cm 和 5—10 cm 土层中,藓类结皮土壤种子库的密度高于地衣结皮,但差异不显著; 3) 不同生物结皮覆盖区土壤种子库的垂直分布特征存在差异,藓类结皮覆盖土壤中有活力的种子主要分布在 0—5 cm 土层中,而地衣结皮和裸沙覆盖土壤中有活力的种子主要分布在 0—2 cm 土层中,且随着深度的增加,土壤中有活力的种子急剧减少。该研究表明,相较于裸沙,生物结皮的存在不仅增加了土壤种子库的大小,还改变了土壤种子库的垂直分布格局。生物结皮层下仍有相当比例有活力的小种子,这些种子欠缺萌发条件,对地上植被的贡献作用较小,但它们的存在对荒漠生态系统健康及可持续发展具有重要意义。

关键词: 生物结皮; 土壤种子库; 垂直分布; 物种多样性

The composition and vertical distribution characteristics of soil seed banks in soil coverage with biocrusts in the Shapotou Region

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Abstract: Using random sampling in the field and observing the emergence of seedlings, we studied the structure, the density and vertical distribution of soil seed banks in moss crusts, lichen crusts, and bare sands in the artificially re-vegetated region of Shapotou. We found that the soil seed banks of this region were mainly composed of annual herbs and had a simple species composition and a significantly higher seed density in soil covered by biocrusts than in bare sands ($P < 0.01$). However, the existence of biocrusts decreased the species diversity of soil seed banks and the similarity of soil seed banks with corresponding ground vegetation. Furthermore, although the total density of soil seed was not significantly different between the two types of crusts, there were differences in the distribution within the different soil layers. Specifically, the soil seed density in the 0—2 cm soil layer of lichen crusts was significantly higher than in the

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人工固沙区土壤碳分布及其与土壤属性的关系

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摘要：选择腾格里沙漠东南缘沙坡头地区不同年代建立的人工固沙林（1964、1981、1990年）及临近的流动沙丘，对0～3.0 m剖面上的土壤进行取样和分析，以探讨固沙植被的建立和发展对土壤碳（有机碳和无机碳）分布的影响及其与土壤属性的关系。结果表明：在流动沙丘建立人工固沙植被近50年后，表层（0～0.1 m）土壤有机碳和无机碳含量均明显增加，土壤有机碳含量为1.95 $g \cdot kg^{-1}$，是流动沙丘的6.67倍，无机碳含量为4.19 $g \cdot kg^{-1}$，是流动沙丘的1.46倍。将土壤剖面划分为3层后（0～0.4，0.4～1.0、1.0～3.0 m）分析显示，从流动沙丘到1964年固沙区，土壤有机碳密度显著增加（0.18 $kg \cdot m^{-2}$到0.52 $kg \cdot m^{-2}$），且浅层（0～0.4 m）的增加快于深层（1.0～3.0 m）；同时，浅层有机碳密度在整个剖面中所占比例显著增加（14.3%到30.4%），而深层减少（64.8%到51.6%）。浅层和深层无机碳密度均有增加趋势，但差异不显著。冗余分析显示，土壤细颗粒含量、水分有效性、总氮含量、总磷含量、pH值和电导率与土壤碳密度关系密切，解释了土壤碳密度86.2%的变异。土壤有机碳密度与土壤细颗粒、总氮总磷含量及水分有效性、电导率极显著正相关（$P<0.001$）；土壤无机碳密度与土壤细颗粒、总磷含量及水分有效性、总氮含量显著正相关（$P<0.05$）。在1.0～3.0 m和0～3.0 m剖面上，土壤有机碳密度与土壤水分含量分别存在显著和极显著的负相关关系（$P<0.05$和$P<0.01$）。

关键词：流动沙丘；固沙植被；有机碳；无机碳；土壤性质

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0 引言

以温室气体增加和全球变暖为主要特征的全球气候变化已成为无可争议的事实，也是中国以及国际社会面临的严峻挑战，温室气体减排和增汇是当前缓解此变化的首要任务[1-2]。土壤是连接大气圈、水圈、生物圈和岩石圈的核心纽带，在全球生物地球化学循环中占据着至关重要的地位。据估计，全球陆地土壤有机碳库的容量（1 m深度）约为1 500 Pg，无机碳库约为1 000 Pg，总土壤碳库的容量是大气碳库的3倍和植被碳库的4.5倍。研究认为，通过土壤固碳（包括增加土壤有机碳和无机碳），土壤碳库的潜在容量足以抵消排放到大气中的CO_2[3]。因此，土壤碳库的变化及其对大气CO_2的调控作用值得深入研究。

长期以来，对土壤固碳的研究重点集中于土壤有机碳，大量研究证实土壤有机碳的动态变化与土地利用方式密切相关，如林地、农田和草地面积的消涨和相互之间的转换等[4-8]。土壤无机碳在土壤固碳的相关研究中往往不受重视，甚至被忽略，而事实上无机碳在干旱半干旱地区的分布和储量多于有机碳[9-11]。中国总无机碳库接近60 Pg[12-13]，其中71.8%左右分布于降水小于400 mm的地区，该部分地区仅占国土面积的41.4%[14]。另一方面，相对于土壤有机碳，无机碳的更新时间更长，作为干旱半干旱地区重要的碳储存形式对于削减大气CO_2浓度的长期效应不可忽视[9,13]。在大多数涉及土壤碳库估算的研究中，均默认固定取样深度为1 m[15]，部分研究取样深度甚至更小[16-17]，从而影响研究的准确性和对深层土壤碳分布规律的准确认知[18]。虽然大部分土壤类型中土壤碳的分布与深度有较好的相关关系[19]，可以据此方便、快捷地推测深层土壤碳的含量，但深层土壤碳的实测资料仍不可或缺[20]。在特定的气候和植被类型下，土壤碳的分布和固存除受制于成土母质和地形的影响外，还与其他土壤特性紧密相关，如土壤粒径组成、土壤氮磷含量和pH值等[15,21-24]。

建立人工固沙植被是干旱半干旱荒漠地区生态

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1961—2014年张掖市降水变化趋势

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摘要：选取张掖气象站1961—2014年逐日降水观测资料，采用线性趋势分析和Mann-kendall检验等方法分析了张掖市年降水量、年最大降水量、冬季降水量和其他季节降水量的变化趋势和突变特征。结果表明：1961—2014年张掖市年降水量总体呈增加趋势，其中1982—1984、1995—1996、2007—2013年降水量增加趋势显著。年最大降水量和冬季降水量增加趋势明显，分别发生了6次和1次突变，其中年最大降水量突变点分别发生在1963年、1980年、1982年、1984年、1987年和1991年；冬季降水量1964年后呈显著增加趋势，1969年降水量突变增加。而其他季节降水量呈波动增加趋势，突变增加分别在1963年、1967年和1969年发生。

关键词：降水趋势；突变分析；Mann-kendall检验；张掖市；干旱地区

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0 引言

水分是干旱半干旱地区最关键的生态要素[1-4]，而降水变化是自然条件下导致干旱区景观变化的重要原因[5]。降水的变化对中国西北地区荒漠植被格局及生态环境有着深刻的影响，是该区生态环境建设和社会经济发展首要制约因素。

目前，中国西部大开发战略的实施使水资源需求量增大，如何根据降水的时空格局合理分配和利用水资源，对西部大开发战略的实施意义重大[6]。中国西部干旱地区降水变化演变趋势已经成为国内外学者关注的热点[7-13]。一方面，受研究时段与站点资料限制，以往对西北干旱区降水量变化的研究所用资料序列大多仅到20世纪末甚至更短[2]，并且大多数学者关注的是极端降水时间特征及其变化趋势[14]。另一方面，尽管对于降水的年、季和月等时间尺度的平均状况研究较多，但对长时间序列降水趋势的研究报道相对较少。

本文拟采用线性趋势分析和非参数Mann-kendall趋势检验法对张掖市1961—2014年的降水量资料进行统计分析，揭示降水的动态特征和变化趋势，为水资源合理利用和生态环境建设提供科学依据。

1 材料与方法

1.1 研究区概况

张掖（37°28′—39°57′N，97°20′—102°12′E）位于甘肃省西北部、河西走廊中段，南枕祁连山，北依合黎山、龙首山，平均海拔1 770 m，大部分属于河西走廊冲积洪积平原[15-18]。植被包括荒漠灌丛、高山草甸、山地草原、高山草原、高山灌丛和针叶林等6种类型[17]，形成了特有的荒漠绿洲景观。属温带大陆性气候，干旱少雨，1月最冷，7月最热；年平均气温7 ℃，年降水量198 mm，年蒸发量2 002.5 mm，干旱指数为15。雪极少，春季风沙大、降水稀少，夏季凉爽、降水集中[13]。全市人均占有水量为1 250 m^3，单位面积平均7 665 $m^3 \cdot hm^{-2}$，分别为全国平均水平的57%和29%，属于典型的资源型缺水区[19]。黑河贯穿全境。多年平均天然径流量24.75 $\times 10^8$ m^3。

1.2 数据

数据来源于中国地面气候资料日值数据集，选取张掖气象站数据，时段为1961年1月1日至2014年9月30日，除2014年外，其他年份观测资料都较完整。按照气象学方法划分季节，即前一年

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腾格里沙漠东南缘生物结皮土壤呼吸对水热因子变化的响应

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摘　要　生物结皮土壤呼吸是干旱区碳循环的重要参与者, 是了解荒漠生态系统碳循环的重要过程之一, 但有关生物结皮土壤呼吸对水热因子的响应还存在许多不确定性, 难以在区域尺度上准确评估生物结皮土壤系统碳排放对水热因子变化的响应及反馈方向和程度。该文以腾格里沙漠东南缘天然植被区藓类和藻-地衣结皮土壤为研究对象, 利用开顶式生长室模拟增温, 采用全自动土壤碳通量测定系统研究了模拟增温及降水格局变化对不同类型生物结皮土壤呼吸的影响。结果表明: 观测期间(2016年4月1日到7月31日), 不同自然降水事件下(降水量在0.3–30.0 mm间), 藓类结皮土壤呼吸速率在–0.16–4.69 $\mu mol \cdot m^{-2} \cdot s^{-1}$之间变动, 藻-地衣结皮土壤呼吸速率在–0.21–5.72 $\mu mol \cdot m^{-2} \cdot s^{-1}$之间变动。藓类结皮土壤呼吸速率平均为1.09 $\mu mol \cdot m^{-2} \cdot s^{-1}$, 高于藻-地衣结皮土壤呼吸速率的0.94 $\mu mol \cdot m^{-2} \cdot s^{-1}$, 是藻-地衣结皮土壤呼吸速率的1.2倍。生物结皮土壤呼吸在不同的降水事件下具有明显的时空异质性, 且生物结皮土壤呼吸速率与降水量有显著正相关关系。对照下两类结皮土壤呼吸速率平均为1.24 $\mu mol \cdot m^{-2} \cdot s^{-1}$, 增温条件下为0.79 $\mu mol \cdot m^{-2} \cdot s^{-1}$, 增温显著降低了其呼吸速率, 增温主要是通过加速土壤水分的散失而降低两类结皮土壤呼吸。大多数情况下, 土壤温度和生物结皮土壤呼吸呈现类似的单峰曲线, 但土壤温度峰值出现的时间滞后于生物结皮土壤呼吸峰值出现的时间, 滞后时间一般为2 h。

关键词　呼吸作用; 生物结皮; 降水格局; 模拟增温

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Responses of soil respiration with biocrust cover to water and temperature in the southeastern edge of Tengger Desert, Northwest China

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Abstract

Aims　Soil respiration of the lands covered by biocrusts is an important component in the carbon cycle of arid, semi-arid and dry-subhumid ecosystems (drylands hereafter), and one of the key processes in the carbon cycle of drylands. However, the responses of the rate of soil respiration with biocrusts to water and temperature are uncertain in the investigations of the effects of experimental warming and precipitation patterns on CO_2 fluxes in biocrust dominated ecosystems. The objectives of this study were to investigate the relationships of carbon release from the biocrust-soil systems with water and temperature in drylands.

Methods　Intact soil columns with two types of biocrusts, including moss and algae-lichen crusts, were collected in a natural vegetation area in the southeastern fringe of the Tengger Desert. Open top chambers were used to simulate climate warming, and the soil respiration rate was measured under warming and non-warming treatments using an automated soil respiration system (LI-8150).

Important findings　Over the whole observational period (from April 2016 to July 2016), soil respiration rates varied from −0.16 to 4.69 $\mu mol \cdot m^{-2} \cdot s^{-1}$ for the moss crust-covered soils and from −0.21 to 5.72 $\mu mol \cdot m^{-2} \cdot s^{-1}$ for the algae-lichen crust-covered soils, respectively, under different rainfall events (the precipitations between 0.3–30.0 mm). The mean soil respiration rate of the moss crust-covered soils is 1.09 $\mu mol \cdot m^{-2} \cdot s^{-1}$, which is higher than that of the algae-lichen crust-covered soils of 0.94 $\mu mol \cdot m^{-2} \cdot s^{-1}$. The soil respiration rate of the two types of biocrust-covered soils showed different dynamics and spatial heterogeneities with rainfall events, and were

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极端降雨事件下生物结皮-土壤呼吸对温度的响应

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摘　要： 以腾格里沙漠东南缘天然植被区藓类结皮和藻-地衣结皮-土壤为研究对象，利用开顶式生长室，采用Li-8150系统连续测定一次极端降雨事件下生物结皮-土壤呼吸的变化，分析温度对生物结皮-土壤呼吸的影响．结果表明：两种类型生物结皮-土壤呼吸的日变化均呈现为单峰曲线，生物结皮-土壤呼吸速率的最大值出现在12:00–14:00，最小值出现在00:00–2:00．增温对两种类型生物结皮-土壤呼吸具有抑制作用．极端降雨事件下，采用日平均值拟合土壤温度与生物结皮-土壤呼吸间的关系不能正确反映二者间的关系，采用小时平均值拟合土壤温度与生物结皮-土壤呼吸间的关系更为恰当，二者呈显著的线性正相关关系．

关键词： 呼吸作用；生物结皮；温度；极端降雨事件

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Effects of temperature on the respiration of biocrusts-dominated soils under extreme rainfall events

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Abstract: To study the effects of temperature on the respiration of biocrust-dominated soil, intact soil columns with two types of biocrusts (moss and algae-lichen crusts) were collected in a natural vegetation area in the southeast fringe of the Tengger Desert. Automated soil respiration system (Li-8150) was used to measure the respiration rates of biocrust-dominated soils under warming (by placing them in an open top chamber) and non-warming treatments during an extreme rainfall event. The results showed that diurnal variation of the respiration of two types of biocrust-dominated soil showed a single peak at 12:00-14:00, after which it began to decrease, reaching a minimum value at 00:00-2:00. During the whole observation period, imitated climate warming impeded respiration rates of the two biocrust-dominated soils. Under an extreme rainfall event, the relationship between the daily mean respiration rate of biocrust-dominated soil and soil temperature could not correctly reflect their relationship. But the diurnal variations of the respiration rate of biocrust-dominated soil could properly reflect their relationship, and the respiration rates of biocrust-dominated soil showed significantly positive linear correlations with soil temperature.

Key words: respiration; biocrust; temperature; extreme rainfall event

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沙区生物土壤结皮对外来植物种子萌发的影响

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摘　要: 以沙坡头包兰铁路以北的人工固沙植被区生物土壤结皮为研究对象, 分析了在不同干扰生物土壤结皮存在条件下, 归化物种狗尾草与相邻荒漠草原区地带性优势物种驼绒藜种子萌发情况. 结果表明: 完整的地衣结皮和藻类结皮均抑制了两种外来植物种子的萌发; 生物结皮对外来植物种子萌发的抑制程度还取决于种子的大小和形态特征. 认为干旱沙区生物土壤结皮的存在能有效降低外来植物种子进入土壤, 降低外来植物的种子传播与定居, 降低外来植物入侵对沙区生态系统的威胁.

关键词: 干旱区; 植物入侵; 生物土壤结皮; 外来植物; 种子萌发
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Physical effect of biological soil crusts on germination of exotic species in the desert

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Abstract: The influence of biological soil crusts on two exotic plant species, *Setaria viridis* and *Ceratoides latens* in the re-vegetation region at the north of the Baotou-Lanzhou Railway was analyzed and the results showed that intact algal and lichen crust inhibited seed germination of *Setaria viridis* and *Ceratoides latens*, but once algal and lichen crust were disturbed, the germination of the two exotic plants increased significantly. The size and morphological characteristics of the seeds also determined the inhibition degree of biological soil crust on seed germination of the exotic plants. It was concluded that the presence of biological soil crusts might effectively reduce the exotic plant seeds in the soil and resist establishment and threats of exotic plant in desert ecosystem.

Key words: arid area; plant invasion; biological soil crust; exotic plant; seed germination

干旱区是生态环境最严酷和脆弱的地区之一, 约占中国陆地面积的1/4, 主要的生态问题是风沙危害[1]. 为有效遏制风沙危害, 中国从20世纪50年代开始启动了一系列以人工植被建设为主的生态建设工程[2], 取得了举世瞩目的成就. 其中包兰铁路沙坡头地区植被防护体系模式是最成功的

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沙埋对干旱沙区真藓结皮层细菌群落结构和多样性的影响

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摘要:作为干旱沙区常见干扰之一的沙埋显著影响着生物结皮的结构和功能,但其内在的生物学机理还不清楚。利用高通量测序技术,通过对 0(对照)、0.5(浅层)、2 和 10 mm(深层)沙埋处理后的腾格里沙漠东南缘沙坡头地区真藓(*Bryum argenteum*)结皮层细菌群落物种组成与丰度的测定,研究了沙埋对真藓结皮层细菌群落结构和多样性的影响。结果表明:(1) 共检测到沙坡头地区真藓结皮层细菌 38 门 106 纲 181 属,以放线菌、变形菌、蓝藻、浮霉菌、拟杆菌和酸杆菌等为主(占细菌群落的 78.4%—83.0%);(2) PCA 分析表明沙埋导致该地区真藓结皮层细菌群落结构组成发生明显改变。无沙埋时,真藓结皮层细菌群落中相对丰度最高的是蓝藻(18.6%),随着沙埋厚度的增加,依次变为变形菌(21.5%, 沙埋厚度 0.5 mm)、浮霉菌(21.5%, 沙埋厚度 2 mm)和放线菌(23.3%, 沙埋厚度 10 mm);浅层沙埋显著增加了真藓结皮层细菌群落中光合菌、固氮菌和产菌丝体细菌等关键功能菌的丰度,但深层沙埋降低了它们的丰度;(3) 沙埋显著增加了真藓结皮层细菌群落多样性($P<0.05$)和物种丰富度($P<0.05$),0.5 mm 沙埋后的细菌群落丰富度指数最高,2 mm 沙埋后的结皮层细菌群落多样性指数最高。揭示了沙埋对干旱沙区真藓结皮层细菌群落结构与多样性的影响,为深入理解沙埋对沙区生物结皮结构和生态功能影响的生物学机制提供了一定的理论依据。

关键词:真藓结皮; 高通量测序技术; 沙埋; 细菌; 群落结构和多样性

Impact of sand burial on bacterial community structure and diversity within biocrusts dominated by *Bryum argenteum*

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Abstract: Bacteria, as a key component of biocrusts, which constitute up to or more than 70% of the living cover in arid and semiarid lands worldwide, play the primary role in carbon and nitrogen inputs in deserts. Thus, changes in bacterial community structure and diversity can significantly alter their ecological processes and the functions of biocrusts. Sand burial is a common environmental stress of the biocrusts in arid and semiarid areas, yet little information is available regarding the effects of sand burial on bacterial community structure and diversity within biocrusts. Therefore, we adopted the high-throughput sequencing techniques to investigate the effects of sand burial on bacterial community structure and diversity of biocrusts dominated by *Bryum argenteum* following sand burial of

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谢敏,回嵘,刘立超,高艳红,李刚,王艳莉,魏文斐.降雪对荒漠地区藓类结皮中真藓生理生化的影响.生态学报,2017,37(3):915-921.

Xie M, Hui R, Liu L C, Gao Y H, Li G, Wang Y L, Wei W F.Effects of snowfall on physiological and biochemical characteristics of *Bryum argenteum* distributed in desert moss crusts.Acta Ecologica Sinica,2017,37(3):915-921.

降雪对荒漠地区藓类结皮中真藓生理生化的影响

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摘要: 生物土壤结皮的生存环境是地球上自养生物生存最为极端的生境之一,真藓是荒漠结皮中最为重要的组分之一。很少有研究涉及冬季降雪对结皮层生物体的影响。以宁夏沙坡头人工植被区内发育良好、长势均匀的真藓结皮为研究对象,系统研究降雪影响下荒漠地区藓类结皮层真藓的光合色素含量、可溶性糖含量、可溶性蛋白含量、丙二醛(MDA)含量以及脯氨酸含量的变化,并探讨其对降雪的生理生化响应。采用了 4 个降雪处理,分别是无降雪、0.5 倍降雪、1 倍降雪、2 倍降雪。结果表明:随着降雪量的增加,其光合色素含量和可溶性蛋白含量显著增加;而可溶性糖含量、游离脯氨酸含量以及 MDA 含量均呈下降趋势。研究结果表明,作为生物土壤结皮重要水源之一的冬季降雪,能够为结皮层生物体提供适宜的水分条件以激发其生理生化活性,对维持荒漠生态系统的稳定性具有重要作用。

关键词: 降雪;真藓结皮;光合色素;渗透调节;丙二醛

Effects of snowfall on physiological and biochemical characteristics of *Bryum argenteum* distributed in desert moss crusts

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Abstract: Biological soil crusts (BSCs) endure the most extreme habitats in the world. They grow on the soil surface in desert regions and withstand extreme temperature, drought and intense radiation. BSCs comprise many kinds of micro-organisms, such as bacteria, algae, lichen and moss. Water is the main limiting factor in the growth of BSCs, and winter snowfall is likely to be one of their important water resources. However, few studies have explored the effects of snowfall on BSCs untill now. In this study, moss crust (*Bryum argenteum*) was sampled from a revegetated area in Shapotou, at the southeastern fringe of the Tengger Desert. The effects of snowfall on the content of photosynthetic pigment, water-soluble sugar, water-soluble protein, proline and malondialdehyde (MDA) in *B. argenteum* were measured. Four snowfall treatments were applied: non-snowfall (control, 0S), half of the ambient conditions (0.5S), ambient snowfall (1S), and double ambient conditions (2S). The 0S samples were each covered with a euphotic plastic disc of 10 cm diameter to exclude all snowfall. The remaining treatments accepted natural snowfall, then half of the natural snowfall was removed from 0.5S samples and an additional mass of snowfall equivalent to natural snowfall was added to the 2S samples. The results

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沙漠生物土壤结皮中真藓(*Bryum argenteum*)和土生对齿藓(*Didymodon vinealis*)对降雪的生理响应

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摘要：以腾格里沙漠东南缘人工固沙植被区藓类结皮优势种真藓（*Bryum argenteum*）和土生对齿藓（*Didymodon vinealis*）为研究对象，在野外条件下设置4个降雪处理，分别是无降雪（对照）、1/2降雪、1倍降雪、2倍降雪，降雪后测定植株光合色素含量、脯氨酸含量、可溶性糖含量、可溶性蛋白含量以及丙二醛（MDA）含量，研究结皮层2种藓类植物对降雪的生理生态响应及其差异性。结果表明：随降雪量增加，真藓和土生对齿藓光合色素含量和可溶性蛋白含量均升高，且土生对齿藓含量上升趋势更明显；随降雪量增加，2物种脯氨酸含量、可溶性糖含量及丙二醛（MDA）含量均降低，且土生对齿藓可溶性糖含量与MDA含量下降趋势更明显。冬季降雪能够对结皮层藓类植物光合作用和生理活性起到一定促进作用；土生对齿藓对降雪的响应更明显。降雪量增加可能会改变藓类结皮层物种组成和结构，并对维持荒漠生态系统健康产生重要影响。

关键词：降雪；真藓（*Bryum argenteum*）；土生对齿藓（*Didymodon vinealis*）；生理响应；差异

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0 引言

在中国广大荒漠地区，降雪是全年降水量的重要组成部分[1]。气候变化会引起降雪频率、降雪量、积雪厚度及覆盖时间的深刻改变[2-3]。在全球变化背景下，中国北方荒漠区雪季长度有缩短趋势，但降雪量并没有明显减小，部分地区降雪量和降雪次数甚至有增加趋势[4]。冬季降雪和积雪覆盖通过改变温度、土壤水分和养分条件影响生态系统的物种组成、群落结构及其生长发育[5-7]。吕金岭等[8]研究表明，冬季降雪能够显著改善荒漠地区土壤水分环境，并且是荒漠灌木和草本春季生长发育的重要水源。在新疆地区，冬季覆雪和春季融雪水对古尔班通古特沙漠地区高植被覆盖度的形成、生物多样性的发育以及荒漠生态系统稳定性的保持具有重要作用[9-11]；荒漠灌木的分布、形态塑造、丰富度、水势以及进行光合作用的能力与积雪厚度、融雪时间等有密切关系[12-13]。因此，系统研究降雪对荒漠生态系统的影响具有重要意义。

生物土壤结皮（BSCs）是荒漠生态系统的重要组成部分，由细菌、蓝藻、地衣、藓类植物等结皮生物体和土壤颗粒胶结形成[14]。这些结皮生物体大部分属于典型的变水植物，对水分变化极为敏感，少量水分就能够激发其光合生理活性。到目前为止，有大量研究涉及了夏季降水对生物结皮的分布、演替特征、生理特征及其对土壤碳氮循环的影响[15-18]，但有关结皮生物对冬季降雪的响应研究相对较少。由于结皮生物体紧贴地表生长，积雪对灌木、草本等荒漠植物覆盖程度较低，而对结皮生物能够完全覆盖，因此，降雪对结皮生物的影响更为深远[19-20]。考虑到结皮生物极强的逆境适应特性及自身形态特征[21-23]，冬季降雪对结皮生物的影响可能会体现在两方面：①冬季降雪作为荒漠地区水分的重要来源之一，通过润湿作用，为结皮生物过程提供适宜的水

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赵芸，贾荣亮，滕嘉玲.贾文雄，高艳红.腾格里沙漠人工固沙植被演替生物土壤结皮盖度对沙埋的响应.生态学报，2017，37(18)：6138-6148.

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腾格里沙漠人工固沙植被演替生物土壤结皮盖度对沙埋的响应

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摘要：生物土壤结皮（简称结皮）的形成与发展是沙区固沙植被建设成功的重要标志之一，其盖度随固沙植被演替的变化趋势是表征该植被系统地表稳定性的一个直观性生态学指标。利用空间代时间的方法，以腾格里沙漠不同始植年代（1956、1973、1981 和 1987 年）固沙植被区发育的 4 种优势结皮-真藓（*Bryum argenteum* Hedw.）结皮、土生对齿藓（*Didymodon vinealis*（Brid.）Zand.）结皮、齿肋赤藓（*Syntrichia caninervis* Mitt.）结皮和藻-地衣-藓类混生结皮（Mixed crust）为研究对象，在测定结皮盖度、高度以及粗糙度随沙埋厚度逐渐增加变化的基础上，计算了使结皮盖度（从 99.99%）开始降低的初始沙埋厚度（*D*1）和盖度降低为 0%的临界沙埋厚度（*D*2），研究了该区固沙植被演替过程中结皮盖度对沙埋厚度增加的响应特征及其相关机制。结果显示：（1）4 种结皮的盖度随沙埋厚度的增加呈 logistic 曲线逐渐降低。（2）在同一年代固沙区不同种间比较，混生结皮的 *D*1 值最小，*D*2 值最大；真藓结皮的 *D*1 和 *D*2 值均小于其他两种藓类结皮；土生对齿藓结皮和齿肋赤藓结皮因固沙年限的不同而不同，在 1956 年固沙区，土生对齿藓结皮<齿肋赤藓结皮，而在 1973 年固沙区和 1981 年固沙区，齿肋赤藓结皮<土生对齿藓结皮。（3）随固沙植被演替，4 种结皮盖度随沙埋厚度增加的降低速率逐渐减小，*D*1 和 *D*2 值逐渐增大。（4）结皮总盖度随沙埋厚度增加的降低速率逐渐减小，表明随固沙植被演替，结皮对沙埋的抵御能力逐渐增强，固沙区植被系统地表稳定性增加。（5）结皮的粗糙度和高度随固沙植被演替逐渐增加，并显著影响了 4 种结皮盖度随沙埋厚度增加的降低速率、*D*1 及 *D*2 值。研究为全面评估沙埋对沙区结皮结构、功能的影响乃至固沙植被稳定性提供了参考。

关键词：植被演替；生物土壤结皮；沙埋；盖度；粗糙度

Response of biological soil crust coverage to wind-blown sand burial during the succession of artificial sand-fixing vegetation in the Tengger Desert，Northern China

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Abstract: In artificially constructed desert ecosystems，the formation and development of biological soil crust（hereafter crust）is one of the key indicators of successful construction of artificial sand-fixing vegetation. Importantly，with the

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腾格里沙漠人工固沙植被演替过程中生物土壤结皮归一化植被指数的变化特征

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摘 要 生物土壤结皮(简称结皮)影响干旱沙区生态系统归一化植被指数(*NDVI*)。该文基于空间代时间的方法, 利用地物光谱仪采集腾格里沙漠不同始植年代(1956、1964和1973年)固沙植被区发育的5种优势结皮的*NDVI*数据, 分析了固沙植被演替过程中结皮*NDVI*的变化特征及其对降水和温度变化的响应规律, 并通过与固沙区主要地物进行比较, 评估了结皮*NDVI*在该沙区生态系统*NDVI*中的作用。结果表明: 1)随着固沙植被演替, 结皮*NDVI*逐渐增加。不同种类结皮*NDVI*相比较, 土生对齿藓(*Didymodon vinealis*)结皮>真藓(*Bryum argenteum*)结皮>混生结皮>地衣结皮>藻结皮。2)结皮*NDVI*受降水量、气温及二者间的交互作用影响显著, 且具有明显的季节差异。结皮*NDVI*与降水量及其覆盖土壤浅层含水量均呈显著线性正相关关系, 并且结皮*NDVI*对水分的敏感性随固沙植被演替而逐渐增加。结皮*NDVI*总体与日平均气温呈显著线性负相关关系, 而与结皮表面温度呈显著指数负相关关系, 并且结皮*NDVI*对温度的敏感性随固沙植被演替逐渐增加。结皮*NDVI*对温度变化的敏感性春季高于夏季, 对水分变化的敏感性夏季高于春季。3)春季降水后, 藓类结皮*NDVI*显著高于油蒿(*Artemisia ordosica*)、花棒(*Hedysarum scoparium*)、柠条(*Caragana korshinskii*)等灌木及裸沙; 夏季降水后, 结皮*NDVI*显著低于灌木。若考虑结皮较高的盖度, 春、夏季结皮*NDVI*对固沙区系统*NDVI*的贡献率分别为90.01%和82.53%, 均超过灌木(春季9.99%和夏季17.47%), 并且结皮对固沙区系统*NDVI*的贡献率随着固沙植被演替而逐渐增加, 而灌木的贡献率逐渐降低。该研究证明了在区域尺度上利用结皮*NDVI*并结合气象资料区分结皮演替阶段的可行性, 并为干旱沙区在区域尺度上地表生态参量遥感估算的误差分析及结皮遥感监测的时相选择提供了数据基础。

关键词 归一化植被指数; 生物土壤结皮; 植被演替; 降水; 温度

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Characteristics of normalized difference vegetation index of biological soil crust during the succession process of artificial sand-fixing vegetation in the Tengger Desert, Northern China

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Abstract

Aims Biological soil crust (hereafter crust) affects normalized difference vegetation index (*NDVI*) values in arid desert ecosystems. This study aimed to demonstrate the feasibility of combining crust *NDVI* values with meteorological data to distinguish the crust successional stage at the regional scale. Meanwhile, the characteristics of crust *NDVI* could provide the basis for the error analysis of *NDVI*-based surface ecological parameters estimation in desert ecosystems. We also suggested the optimum periods for crust observation based on the multi-temporal remote sensing images.

Methods *NDVI* values of five types of dominant crusts, three typical sand-fixing shrubs and bare sand were collected by spectrometer in the field. Crusts and shrubs were randomly selected in revegetated areas established in 1956, 1964, and 1973 at Shapotou, which is on the southeastern edge of the Tengger Desert. We used the space-for-time method to study the characteristics of crust *NDVI* values and their responses to precipitation and temperature during the succession process of artificial sand-fixing vegetation. Additionally, we evaluated the contribution of crust *NDVI* values to the whole ecosystem *NDVI* values by comparing the *NDVI* values of crusts, shrubs and bare sand.

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生态水文阈值在中国沙区人工植被生态系统管理中的意义

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摘要：中国北方风沙区是全球沙漠化发展和生态退化最为严重的地区之一。利用植被固沙是遏制沙化土地扩张和生态重建与恢复的主要途径，但人工植被的稳定维持是可持续性风沙治理所长期面临的挑战。作为人工植被生态系统管理的依据，对生态水文阈值的认识及界定具有重要的理论和实践意义。本文以固沙植被中人工种植的灌木和乔木（仅限东部沙区）的盖度与深层土壤水分含量互馈互调作用的长期变化为依据，基于对中国不同气候带沙区典型人工植被系统生态和水文过程的模拟，通过建立生态水文模型初步界定了不同沙区适宜于人工植被生态系统管理的生态水文阈值，对现有沙区固沙植被的生态系统管理和未来风沙区植被建设具有一定的借鉴意义。

关键词：中国北方风沙区；人工固沙植被；水分平衡；固沙植被稳定性；生态水文阈值；生态重建

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0 引言

中国北方风沙区主要包括贺兰山以东的沙地、农牧交错带和以西的沙漠与绿洲、沙漠与荒漠草原的过渡区，约 3.2×10^5 km^2。利用植物固沙，建立固沙植被是遏制风沙危害、控制沙漠化和区域生态重建恢复的重要手段与途径。60年来，中国在北方风沙区累计营建以防沙固沙为主的人工植被达600万 hm^2[1]，构建了重要生态屏障，有效地控制了风沙危害，促进了沙化土地的恢复，取得了举世瞩目的成就[1-5]。然而，实践中也出现了很多问题，固沙植被建立几十年，后一些沙区的植被大面积退化，地下水位下降，甚至在原来的固沙区出现了新的沙化。如何维持植被的稳定性和防风固沙效益的可持续性成为沙区生态重建与恢复所面临的巨大挑战[1,6-7]。

人工植被有别于天然植被。后者是长期适应区域或局地气候条件和土壤环境的产物，在干扰较小的情况下具有较高的稳定性[8]，而人工植被是人为建立并具有明确的目的和用途，其稳定性需要通过适宜的人为调控或生态系统管理才能实现[3]，而阈值是生态系统管理或调控必需面对的一个客观实际需求，即必须了解在什么样的阈值范围人工植被是稳定的。反之，植被会发生退化或演变，系统向另外一种状态发生转移[9]。在区域气候不发生显著变化的情景下，突破阈值下限引发的状态转移往往会导致植被的防风固沙效益不可持续[10]。因此，探讨一个能够表征固沙植被演变规律及准确刻画其演变机理，且能够量化的阈值是人工植被系统管理和调控的重要前提和实践需求[3]。

传统的阈值是指阈值点或阈值区间，用来描述系统从一个状态到另一个状态的转变[11]。生态阈值常被定义为一个关键点，在此点处生态系统将发生状态转移，这些阈值点往往预示着生态系统的突变。生态阈值也被定义为生态系统发生改变过程中的一个过渡性的区间或者区域[12-14]。生态阈值在生物多样性保育[15]和自然生态系统演替理论研究[16]，以及自然保护区划分等实践中发挥了重要的作用[9,17]，然而针对特定的生态系统和所涉及的科学问题和实践需求，如人工植被稳定性的调控管理，生态阈值不能准确反映人工植被在沙区独特的生态过程和水文过程，特别是水文过程对生态过程的影响，以及互馈互调机理在植被稳定性上的体现。因此，探讨并提出固沙植被生态系统管理的阈值，不仅在理论而且在实践中都十分必要，对未来风沙区植被建设及其固沙效应稳定性维持具有重要的指导意义。

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环境因子对沙坡头人工植被区碳通量的影响

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摘　要: 基于腾格里沙漠东南缘沙坡头人工植被区涡度相关通量观测数据, 对人工植被区碳通量及环境因子进行分析. 研究表明: 碳通量的月均日变化和季节变化趋势明显. 该生态系统在生长季(4–10月)各月均为碳汇, 6月份碳吸收最多, 日吸收量最大值也出现在6月份. 由于遭遇严重干旱、持续高温、强辐射和大饱和水汽压差, 使叶片的气孔阻力较大, 抑制了植物的光合作用, 盛夏7月净生态系统CO_2交换量较相邻月份小. 采用通径分析方法解析了光量子通量密度、净辐射、饱和水汽压差、空气温度、空气相对湿度、5 cm土壤温度、5 cm土壤含水量和风速等环境因子与碳通量的关联性, 结果发现白天碳通量的影响因子以光量子通量密度和饱和水汽压差为主, 光量子通量密度是影响净生态系统CO_2交换量的最主要因子, 饱和水汽压差次之. 光量子通量密度与碳通量呈直角双曲线的关系, 净生态系统CO_2交换量随光量子通量密度的增加而减小, 但当饱和水汽压差大于1.5 kPa时, 这种减小关系的程度有所减弱. 不同月份的光响应模型参数光饱和时的最大光合速率、表观初始光能利用率和白天生态系统暗呼吸速率不同, 三者的最大值都出现在6月份. 夜间生态系统呼吸的主导因子为空气温度, 次要因子为5 cm土壤含水量. 当土壤干旱(土壤含水量小于3.5%)时空气温度超过21.25 ℃后会降低夜间生态系统呼吸速率.

关键词: 人工植被; 碳通量; 涡度相关; 通径分析; 光量子通量密度; 饱和水汽压差; 土壤含水量
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Effects of environment factors on the carbon flux of artificial vegetation in Shapotou

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Abstract: Based on the eddy covariance data of artificial vegetation in the southeastern margin of the Tengger desert, the carbon flux and environmental factors in the artificial vegetation area were analyzed. The results indicated that the daily diurnal and seasonal variations of carbon flux were significant. From April to October, this ecosystem was mainly of carbon sink, and the carbon absorption in June was highest. The highest daily absorption also happened in June. Net ecosystem exchange in July, compared with the adjacent month, was smaller, due to the fact that, in this period, the temperature, radiation and vapor

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红砂(*Reaumuria soongorica*)响应干旱和UV-B辐射双重胁迫的基因转录表达

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摘要：荒漠植物在自然生境中同时遭受多种环境因子的胁迫，但植物对多重胁迫因子的应答响应机理目前仍然未知。利用数字基因表达谱技术分析了荒漠植物红砂(*Reaumuria soongorica*)在干旱、UV-B辐射以及干旱和UV-B辐射共胁迫下基因在转录水平的表达响应。结果显示：胁迫处理的材料与对照材料相比，差异表达的基因有上调表达基因和下调表达基因，且不同胁迫中下调表达基因总数多于上调的。双重胁迫与单因子胁迫相比，差异表达基因数量明显增加，且上调表达基因的数量增多，单因子胁迫之间的表达谱比双重胁迫与单因子之间的更为相似。双重胁迫诱导了356个上调和248个下调的特异表达基因。从诱导基因的差异表达量来看，多数基因的差异表达量集中在2～5倍，同时也诱导了少数基因的高度表达(高于100倍)。差异表达基因的GO(Gene Ontology)功能富集显著性分析和KEGG(Kyoto Encyclopedia of Genes and Genomes)代谢通路分析表明，双重胁迫相比单因子胁迫，固碳作用等生物过程的表达显著性富集，且不同的代谢途径对不同的胁迫处理表现出不同程度的响应。这说明植物在基因转录水平对单因子胁迫和双重胁迫的响应机理在很大程度上存在差异。

关键词：红砂(*Reaumuria soongorica*)；干旱胁迫；UV-B辐射；双重胁迫；数字基因表达谱

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0 引言

植物对单一环境胁迫因子的适应性研究目前较多，但对接近于自然条件下的多重胁迫的适应机理还知之甚少。增强的UV-B辐射和干旱复合胁迫对滇杨(*Populus yunnanensis*)造成的伤害程度小于UV-B单一胁迫下的伤害[1]；生长在增强UV-B辐射下的拟南芥(*Arabidopsis thaliana*)由于脯氨酸含量的增加和气孔导度的下降，对于干旱胁迫有更高的耐性[2]；豌豆(*Pisum sativum*)与小麦(*Triticum aestivum*)在增强的UV-B辐射和干旱协同诱导时植物抗氧化酶活性升高，从而降低植物自身所受的伤害[3]；拟南芥在增强的UV-B辐射和干旱胁迫下的基因表达具有高度的相似性[4]；拟南芥叶片含水量的维持在增强的UV-B辐射和干旱复合胁迫下有所改善[5]；当增强的UV-B辐射和干旱胁迫同时发生时，由于UV-B辐射诱导的抗氧化酶活性增强和干旱诱导的渗透调节物质含量增加产生叠加作用，增强了烟草(*Nicotiana tabacum*)植株的抗氧化能力，氧化损伤程度低于单因子胁迫或处于两种单因子胁迫之间[6]。近些年对于植物复合胁迫的转录组学[7]和蛋白质组学[8]研究已有报道。但这些复合胁迫的研究主要集中在水稻、玉米等作物以及部分蔬菜和果树方面[9]，而对长期遭受高强度多重胁迫的荒漠植物报道较少。

自然生境中的荒漠植物，往往受到多重环境因子的同时胁迫，如UV-B辐射、干旱、高盐碱、极端温度、矿质营养匮乏等。特别是在夏季，干旱和高强度UV-B辐射是限制植物生长的主要因素[10-11]。本研究拟通过数字基因表达谱技术对比研究增强的UV-B辐射、干旱及二者复合胁迫下荒漠植物红砂(*Reaumuria soongorica*)的基因表达差异性，深入探讨红砂响应单因子胁迫和复合胁迫的基因转录水平适应机理。

1 材料与方法

1.1 材料与方法

红砂苗取自兰州市南北两山红砂繁育基地(36°

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干旱区生态系统跃变:以输沙势为外部驱动力

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摘要:生态系统靠近跃变点时可能发生跃变,骤然从一种稳定状态跃变到另外一种稳定态。然而以往关于干旱区的系统跃变的研究主要集中于水文过程,对其他过程(如风积过程)关注不够,并且很少考虑外部驱动力与系统状态之间的交互作用。我们以输沙势(风积过程)为系统跃变的外部驱动力,利用空间隐式模型,研究干旱区生态系统的跃变动态,并考虑输沙势与系统状态之间的交互作用对系统跃变动态的影响。结果表明:当输沙势较低(<93 VU)或较高(>230 VU)时植被态和裸地态分别是唯一的稳定态,而当输沙势为93~230 VU时,植被态和裸地态都可稳定存在。考虑交互作用使系统退化(恢复)时的跃变点从无交互作用的230 VU(93 VU)推移到了高强度交互作用的337 VU(213 VU),在研究干旱区生态系统的系统跃变时,可以以输沙势为外部驱动力,并考虑输沙势与系统状态之间交互作用。

关键词:系统跃变;荒漠化;输沙势;外部驱动力;干旱区;生态系统

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0 引言

干旱区约占全球陆地面积的41%,养育着全球约38%的人口,其中10%~20%的干旱区已经发生各种形式的荒漠化,直接影响到约2.5亿人的生存与发展[1-2]。尤其是在全球气候变化的背景下,随着人类活动范围和强度的不断增大,荒漠化问题更加突出[1]。

在环境条件即使发生线性变化的情况下,生态系统也可能会表现出非线性响应(图1),在分叉点(fold-bifurcation point或者tipping point)附近从一种稳定态(如典型草原)跃变到另外一种截然不同的稳定状态(如裸地),这种现象称为系统跃变(regime shift)[3]。系统跃变的发生一般比较急剧,很难预测并且无法或者很难恢复到原稳定态。因此荒漠化作为发生于干旱区生态系统的一种系统跃变,系统跃变的这些特征加剧了荒漠化的潜在影响[4-6]。为了维持生态系统的功能与服务,更好地理解系统跃变显得尤为重要[7-8]。

干旱区土地荒漠化的两个主要直接因素是风积过程(土壤风蚀)和水文过程(水土流失),两者造成的退化分别占到总退化面积的42%[9-10],然而以往的研究较多地倾向于从水土流失等水文过程角度出发,风蚀的重要性没有得到充分认识[10-11]。研究表明在降水较少的地区,尤其是在沙质土地上,风蚀等风沙过程起着主导作用,这是因为降水少时水文过程的侵蚀强度较弱,再者沙质土地水分入渗快,无法形成地表径流[10-12]。尽管土壤风蚀在风沙物理学方面得到较为细致的研究[13-15],然而在生态学中的研究较少,主要集中于种群和群落生态学方面[16-18],在系统水平更加薄弱[19]。Tsoar[12]提出用以风速为唯一影响因子的输沙势(DP)作为风蚀强度的指标,从系统水平研究生态系统的动态变化。Yizhaq等[20]发现当输沙势为139~2 828 VU时,生态系统存在双稳态-植被态和裸地态;当输沙势低于139 VU和高于2 828 VU时,植被态和裸地态分别是唯一稳定态。

在系统跃变的研究中,大部分有一个明确或者潜在的假设:外部驱动力不会随系统状态变化而变化,即外部驱动力与系统状态之间无交互作用[3-4,21-22]。这个假设在很多情况下或很大程度上是成立的,如浅水湖泊的营养物质输入量-外部驱动力不会因为湖泊中藻类(或潜水植被)的多少而发生变化[21-23]。然而这个假设在热带雨林和西非荒漠草原的研究中受到了质疑,研究表明系统状态与降

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腾格里沙漠东南缘不同生境油蒿种群的数量动态

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摘要：对腾格里沙漠东南缘不同的生境条件(包括始建于1964年的人工植被区和天然植被区)下油蒿(*Artemisia ordosica*)种群调查取样，按照植株的体积大小分为7个龄级(Ⅰ，0～2 $\mathrm{cm^3}$；Ⅱ，2～5 $\mathrm{cm^3}$；Ⅲ，5～10 $\mathrm{cm^3}$；Ⅳ，10～15 $\mathrm{cm^3}$；Ⅴ，15～20 $\mathrm{cm^3}$；Ⅵ，20～30 $\mathrm{cm^3}$；Ⅶ，>30 $\mathrm{cm^3}$)，分析了种群的组成、静态生命表和存活曲线。结果表明：人工植被区油蒿种群的总体规模大于天然植被区，幼龄个体占有很高的比例；天然植被区油蒿的死亡率低于人工植被区，天然植被区Ⅰ和Ⅱ龄级油蒿种群的死亡率最高，人工植被区Ⅴ～Ⅶ龄级的油蒿种群死亡率最高；天然植被区油蒿种群的稳定性维持主要通过幼苗的更新，而人工植被区可通过幼苗的自我更新和大龄植株的自疏作用；Ⅴ龄级的油蒿个体是种群中的生存质量最佳的个体；两种生境下油蒿种群均符合Deevey Ⅱ型存活曲线。

关键词：油蒿(*Artemisia.ordosica*)；种群生命表；存活曲线；腾格里沙漠

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0　引言

植物种群的结构和数量动态是种群生态学研究的重要内容[1-4]。种群的结构不仅反映不同龄级的个体在种群中的配置情况和种群的数量动态，也可为预测种群的演替及发展趋势提供重要的科学依据。生命表是研究种群结构及动态变化的重要工具[5-6]，也是解释种群变化的前提，它能反映种群中各龄级的个体的实际生存个数、死亡个数以及存活趋势[7]。存活曲线是其中最常见和最直观的分析方法，生命表和存活曲线相结合是进行种群统计和分析种群动态的有效手段[5,8]。

油蒿(*Artemisa ordosica*)是菊科蒿属、半灌木、沙生植物，广泛分布于中国北方内蒙古、宁夏、陕西、甘肃等省区的草原、半荒漠和荒漠中，主要生长在固定沙丘、半固定沙丘、沙地和覆沙土壤上[9-12]。作为优良的固沙树种，油蒿具有耐旱、耐沙埋、抗风蚀、耐贫瘠、分枝和结实性能好的生物生态学特性[13]，在中国北方沙漠化治理中被大量栽植[14-15]。在分布区内，油蒿在自然和人工固沙植被区占有非常重要的地位，常是群落中或群落演替过程中某个阶段的建群种或优势种[9,12,16-17]。为了确保逾40 km包兰铁路沙坡头段畅通无阻，中国科学院和铁路相关单位于1956年开始相继设计和逐步建立了“以固为主、固阻结合”防沙固沙体系[18]。在无灌溉条件下栽植柠条(*Caragana korshinskii*)、油蒿、花棒(*Hedysarum scoparium*)、小叶锦鸡儿(*Caragana microphylla*)、沙拐枣(*Calligonum arborescens*)和沙木蓼(*Atraphaxis bracteata*)等旱生灌木[19]。分别于1956、1964、1973、1981、1991年在沿铁路两侧的区域(全长16 km)进行植物固沙。在沿包兰铁路两侧形成了北侧宽500 m，南侧宽200 m的人工固沙植被防护体系。随着植被的演替，其他灌木如沙拐枣、沙木蓼等逐渐退出固沙植被系统，而油蒿、一年生草本植物与隐花植物则大量繁衍[20-21]。自植被建立约10年后至今，油蒿一直是该地区天然和人工固沙植被生态系统的优势种[9,22-23]，在群落稳定性和多样性、生态系统格局和过程、防风固沙等方面发挥着至关重要的作用[9,14,23]。

腾格里沙漠东南缘固沙植被自建成之日起，其群落的结构和演替方向是众多学者和国内外媒体关注的焦点，因其不但关系到固沙体系的成败[9]，也是中国干旱半干旱地区生态重建所面临的重大科学问题之一。本文通过分析腾格里沙漠南缘人工固沙植被区和天然固沙植被区油蒿种群的组成结构、生命表和存活曲线，研究该地区不同生境下油蒿种群的

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生物土壤结皮对荒漠区土壤微生物数量和活性的影响

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摘要：生物土壤结皮对荒漠生态系统的维持与改良发挥着重要作用。土壤微生物可敏感地指示土壤质量，是衡量荒漠区生态健康程度的重要生物学特征，而对荒漠区生物土壤结皮与土壤微生物关系知之甚少。本研究设计了两组对比试验。一组以腾格里沙漠东南缘的1956、1964、1981、1991年的植被固沙区结皮下的沙丘土壤为对象，以流沙区和天然植被区为对照。另一组以植被固沙区人为干扰生物土壤结皮下的沙丘土壤为研究对象，以未干扰结皮下的沙丘土壤为对照。结果表明：腾格里沙漠东南缘植被固沙区的藻-地衣和藓类结皮均可显著提高土壤可培养微生物的数量和基础呼吸（$P<0.05$）；适度人为干扰生物土壤结皮不会显著影响土壤可培养微生物的数量和基础呼吸，而严重人为干扰结皮可显著降低土壤可培养微生物的数量和基础呼吸，指示严重人为干扰结皮可导致荒漠区土壤质量下降；土壤可培养微生物的数量和基础呼吸也因结皮演替阶段的不同而有所不同，演替晚期的藓类结皮下土壤微生物数量和基础呼吸显著高于演替早期的藻-地衣结皮（$P<0.05$）；土壤可培养微生物的数量和土壤基础呼吸与固沙年限均存在显著的正相关关系，随着沙丘固沙年限的增加，结皮层增厚，结皮下土壤微生物数量及基础呼吸显著增加（$P<0.05$）；生物土壤结皮下土壤可培养微生物数量和基础呼吸呈现显著的季节变化，表现为夏季＞秋季和春季＞冬季。因此，腾格里沙漠东南缘植被固沙区的生物土壤结皮提高了土壤微生物数量和活性，表明生物土壤结皮有利于荒漠区土壤及荒漠生态系统的恢复。

关键词：生物土壤结皮；土壤微生物；人为干扰；结皮演替阶段；固沙年限

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0　引言

生物土壤结皮是由隐花植物和土壤微生物及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复合体，是占全世界陆地面积40%的荒漠地区地表景观的重要组分[1-3]。受水分、极端温度和光照、高pH值等因素的限制，干旱半干旱荒漠地区高等植物种类少且稀疏，呈现斑块状的分布格局，为生物土壤结皮的定殖和覆盖创造了合适的生态位，该地区生物土壤结皮的覆盖占生物覆盖面积的70%以上。这种生态地位已引起了研究者的广泛重视[4-5]。生物土壤结皮在土壤生态水文过程、土壤生物过程、地球化学循环过程、荒漠景观形成过程和荒漠区生态修复过程中发挥着重要作用，研究生物土壤结皮是实现荒漠生态系统管理与修复的重要前提[3,6]。

土壤微生物作为土壤生物相中最活跃的成员之一，参与土壤有机质分解、腐殖质形成、养分转化和循环等一系列土壤形成和改良过程，其变化可敏感地反映土壤质量。土壤基础呼吸主要来自土壤中的微生物，其变化可指示土壤微生物活性，因此，土壤微生物数量和基础呼吸作为土壤生物中的重要指标，可敏感地预示土壤质量变化，可判别退化生态系统的修复程度[7-11]。当前，对于生物土壤结皮的研究主要集中在生物土壤结皮与土壤稳定性和肥力[12]、土壤理化性质[13]、土壤水文过程[2]、维管植物[14]和土壤动物多样性的关系[15]及一些干扰因子对结皮的影响[16-17]，而关于生物土壤结皮与土壤微生物数量和土壤基础呼吸的研究还相对较少。Belnap等[3]及边丹丹[18]指出，生物土壤结皮不仅可增

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•研究报告•

基于人工地物时空变化的自然保护区空间近邻效应评估：以沙坡头国家级自然保护区为例

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摘要: 已有研究表明, 建立自然保护区会对其周边生态环境产生影响, 即自然保护区的空间近邻效应。当前, 一些自然保护区的周边区域生态环境发生了较大变化, 尤其体现在人工地物的时空变化上。研究基于人工地物时空变化的自然保护区空间近邻效应, 关系到自然保护区及其保护对象长久的生存和安全。为研究空间近邻效应的变化区间和作用距离, 识别驱动因子, 本文以宁夏沙坡头国家级自然保护区为例, 对自然保护区周边20 km范围内的空间进行分割, 结合1990–2015年遥感影像解译和人工地物提取, 利用Mann-Kendall趋势分析法和驱动因子的相关性检验分析, 提出了基于人工地物时空变化的空间近邻效应评估技术。结果表明: (1)随着时间的推移, 研究区域内人工地物面积及景观格局不断扩大和扩张, 人为活动影响在增强。(2)人工地物的空间近邻效应随时间的推移而增强, 随距离尺度的增加而下降。(3)空间近邻效应的变化趋势在各区间内的显著性和驱动力因子为: 第一区间(1–5 km)的下降趋势偶见显著性, 驱动力来自防护林; 第二区间(6–10 km)的下降趋势具有显著性, 驱动力来自城镇用地; 第三区间(11–20 km)的下降趋势具有极显著性, 驱动力来自农田。沙坡头国家级自然保护区建立以来, 周边土地利用变化受人为作用影响明显, 须引起关注。

关键词: 自然保护区; 空间近邻效应; 溢出; 泄露; 趋势分析

Assessment of the space neighborhood effect on nature reserves based on temporal and spatial changes of artificial objects: a case study on Shapotou National Nature Reserve

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Abstract: It has been shown that the established nature reserves will affect the surrounding ecological environment, that is, the space neighborhood effect on nature reserves. At present, the ecological environment of the surrounding areas of some nature reserves has changed greatly, especially in the temporal and spatial changes of artificial objects. To study the space neighborhood effect on nature reserves based on temporal and spatial changes of artificial objects will do significant help to maintain the survival and safety of nature reserve and its protected objects. To analyze the variation intervals of the space neighborhood effect and the distance scale, and to identify the driving factors, we chose Ningxia Shapotou National Nature Reserve as a case study. We divided the study area within a range of 20 km around the nature reserve, extracted the artificial objects from the remote image analysis between 1990 and 2015, and used Mann-Kendall trend analysis and driving factor correlation test analysis, to assess the space neighborhood effect of nature reserves based on temporal and spatial changes in artificial objects. Results showed that the areas and patterns of artificial objects were expanding, which meant the impacts of human activities were increasing over time. In addition,

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罗永清，赵学勇，王涛，李玉强．沙地植物根系特征及其与土壤有机碳和总氮的关系．草业学报，2017，26(8)：200 206．

LUO Yong Qing，ZHAO Xue Yong，WANG Tao，LI Yu Qiang．Characteristics of the plant root system and its relationships with soil organic carbon and total nitrogen in a degraded sandy grassland．Acta Prataculturae Sinica，2017，26(8)：200 206．

沙地植物根系特征及其与土壤有机碳和总氮的关系

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摘要：以位于风沙活动剧烈的科尔沁沙地为研究区，通过对不同恢复阶段的流动沙丘、半固定沙丘、固定沙丘和封育草地 4 种生境的植物特征和土壤总有机碳（SOC）和总氮（TN）含量进行调查，分析了沙地不同恢复阶段土壤碳氮特征与植物的关系。结果表明，1）植物地上和地下生物量的变化随沙地恢复过程呈现不同的特征，地上生物量随沙地恢复表现为先增加后减小的趋势，地下生物量则为指数增加的特征，封育草地植物的根冠比显著高于其他恢复阶段；2）与生物量类似，根系长度和根表面积均随沙地恢复逐渐增加，生境间差异极显著，而根体积虽存在生境间差异，但随沙地恢复梯度的规律性不明显；3）SOC 和 TN 的含量与储量均随沙地恢复逐渐增加，0～10 cm 层 SOC 和 TN 含量高于 10～20 cm 层，但随沙地恢复过程，10～20 cm 层的增幅高于 0～10 cm 层；4）地上生物量和地下生物量均与 SOC 和 TN 储量呈显著的线性回归关系，地下生物量与 SOC 和 TN 储量的回归系数均高于地上生物量；5）根系长度和根表面积与土壤碳氮的回归系数均高于生物量和体积。本研究表明，在风沙活动剧烈的沙地生境，植物根系与土壤碳氮的关系较地上部分更为紧密，根系活动可能是影响土壤碳氮积累的重要因素之一。

关键词：沙地恢复；植物；生物量；根系形态；土壤有机碳；总氮

Characteristics of the plant-root system and its relationships with soil organic carbon and total nitrogen in a degraded sandy grassland

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Abstract：Plants are the key component of ecosystems in terms of matter exchange and energy flux. The aboveground and belowground biomasses affect carbon and nitrogen feedback processes differently in the plant-soil system. In this study，the plant characteristics，soil organic carbon (SOC)，soil total nitrogen (TN)，and their relationships were investigated in four different habitats in the Horqin Sandy Land：mobile dune，semi-fixed dune，fixed dune，and fenced grassland. These four habitats represent four consecutive stages of the restoration process. The results showed that plant aboveground biomass and belowground biomass varied among the habitats. Aboveground biomass initially increased and then decreased during the restoration process，while the belowground biomass showed an exponential increase during restoration. The root to shoot ratio was significantly higher in fenced grassland than in the other three habitats. Similarly to biomass，the length and surface

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罗永清，赵学勇，王涛，李玉强，左小安，丁杰萍．植物根系分解及其对生物和非生物因素的响应机理研究进展．草业学报，2017，26(2)：197 207．

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植物根系分解及其对生物和非生物因素的响应机理研究进展

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摘要：植物根系在生态系统物质循环和能量流动过程中具有重要意义，其分解是固定于植物体内的物质返回土壤和大气环境的重要过程，受生物和非生物等多重因子影响。其中：生物因素方面，根系化学特征是影响根分解的主要因素，根系寿命、直径、菌根及物种差异等生物因素主要是通过改变根系化学性质产生作用，根系分泌物、土壤微生物等主要通过改变分解者的数量和活性影响根系分解。非生物因素方面，水热因子是影响根分解的关键。另外，在全球变化背景下，大气氮沉降、CO_2浓度增加等因素也对植物根系分解产生影响。本文从植物根系分解过程和影响根分解的因素两方面，综述了植物根系分解过程中物质释放规律，总结和归纳了主要生物和非生物因素对植物根系分解的影响机理，并对根系分解的研究进行展望。

关键词：根系；分解过程；生物因素；环境因素；响应机理

Plant root decomposition and its responses to biotic and abiotic factors

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Abstract: The plant root system plays an important role in ecosystem matter exchange and energy flux, and root decomposition is one of the main contributors to these processes. Matter accumulates in roots and is then released back into the roots' surroundings, including the atmosphere and soil, via the decomposition process. Root decomposition is affected by multiple biotic and abiotic factors. In terms of biotic factors, the chemical characteristics of roots are among the main factors affecting their decomposition. Other factors such as root lifespan, size/diameter, and the abundance and types of fungi and other microbes in soil also affect plant root decomposition, and their effects can be explained by their ability to alter the chemical characteristics of plant roots. Root exudates and changes in the abundance and activities of soil microorganisms that degrade plant roots affect the root decomposition rate. In terms of abiotic factors, water and temperature are the main factors affecting root decomposition. Other factors related to climate change, for example, nitrogen deposition and carbon dioxide concentrations, will affect the root decomposition rate to different degrees, the extent of which is currently unknown. In this study, we reviewed the process of matter release during plant root decomposi-

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科尔沁沙地奈曼地区地下水水质时空变化特征

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摘要: 区域地下水水质是水质评价的重要内容，也是合理制定地下水开发利用及保护治理方案的基本前提。以科尔沁沙地奈曼地区地下水水质为研究对象，选取2005—2014年地下水水质监测数据，分析地下水水质时空变化特征。结果表明：近10年来奈曼地区地下水水质各指标均值均低于地下水Ⅱ类标准，pH值、NO_3^-含量、化学需氧量(COD_{cr})在局部地区出现超标现象，但水质总体较好；该地区地下水矿化度(TDS)与Ca^{2+}、Mg^{2+}、Na^+、HCO_3^-、SO_4^{2-}浓度及COD_{cr}具有明显的正相关关系，即随着Ca^{2+}、Mg^{2+}、Na^+、HCO_3^-、SO_4^{2-}、COD_{cr}浓度的增加，TDS也会增加；各主要指标浓度随时间呈下降趋势，SO_4^{2-}、Na^+、HCO_3^-浓度及TDS较稳定，而Ca^{2+}、Mg^{2+}、Cl^-、PO_4^{3-}浓度及COD_{cr}随时间变化较为明显；Ca^{2+}、Mg^{2+}、HCO_3^-、SO_4^{2-}浓度及TDS农田非灌溉井>农田灌溉井>沙地水位井，Na^+、COD_{cr}浓度沙地水位井>农田非灌溉井>农田灌溉井，NO_3^-浓度沙地水位井>农田灌溉井>农田非灌溉井；该地区地下水水质变化主要与碳酸盐岩溶解、农药化肥的使用、工业及生活污水排放有关。

关键词: 奈曼；地下水水质；时空变化

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0 引言

地下水是中国北方农业、工业、生活及生态用水的重要来源，在维持农业发展、支撑社会经济发展、保障居民生活、维持生态平衡等方面有着十分重要的作用[1]。在地表水资源相对匮乏的干旱、半干旱地区，地下水资源具有不可替代的作用。目前，中国地下水开采总量占总供水量的18%，北方地区65%的生活用水、50%的工业用水和33%的农业灌溉用水来自地下水[2]。全国657个城市中，有400多个以地下水为主要饮用水源[2]。而近年来，随着现代工业的快速发展、城市规模的不断扩大以及农业生产中农药、化肥、除草剂等化学试剂的大量使用，使许多饮用水水源受到污染，特别是浅层地下水污染严重[3-8]，2005年的统计数据表明，农村饮用污染严重的地下水人口达4 681万[9]。其中，在农业生产过程中化肥、农药残余随雨水渗入地下是造成中国城镇地下水污染的主要原因。硝态氮淋溶是旱地农田氮素损失的主要途径，也是引起地下水中硝态氮含量升高的重要原因[10-20]。此外，农药的使用也是地下水遭受污染的一个主要因素，比化肥的污染更具危害性。农药喷施后，一部分被农作物吸收，大部分进入土壤，并通过淋滤作用进入地下从而对地下水造成污染[21-26]。

在奈曼地区，由于气候干旱和水资源的过度利用，很多区域出现了河流断流、湖泊萎缩、甚至干涸的现象[27-28]，这种地表水资源数量的明显减少凸显出地下水资源的重要性，尤其是其作为饮用水源以及农业灌溉水源的作用。以往研究较多关注该地区降水、地表水、地下水或土壤水分的时空变化及其与植被生长的关系[27-34]。至2004年，奈曼旗大部分区域浅层地下水资源都已经超采，深层地下水符合居民生活用水标准，浅层水需作处理后方可饮用[35]。其中，大沁他拉镇周边地区浅层地下水水质较差，总铁、氨氮、总锰超标比较普遍；八仙筒镇供水水源井除铁、锰超出地下水质量标准Ⅲ类标准外，个

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沙质草地生长季生态系统碳净交换量特征及土壤呼吸贡献率

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摘　要　以科尔沁沙质草地为研究对象，利用开路涡度相关系统和LI-8150土壤呼吸自动观测系统，分析了生长季生态系统二氧化碳(CO_2)净交换量(NEE)的变化特征，土壤呼吸(R_s)对生态系统呼吸(R_{eco})的贡献率，以及生态系统总初级生产力(GPP)的大小。结果表明：生长季NEE存在明显的月均日变化特征，总体呈单峰型，其中7月的日变化最为明显，NEE月均日最大吸收速率($-5.62\ \mu mol \cdot m^{-2} \cdot s^{-1}$)和最大释放速率($3.14\ \mu mol \cdot m^{-2} \cdot s^{-1}$)均出现在7月份；生长季内生态系统总体表现为碳汇，固碳量为25.85 $g\ C \cdot m^{-2}$；R_s对R_{eco}的贡献率为78.39%，R_{eco}对GPP的贡献率为90.62%，生长季内GPP总累积量为275.51 $g\ C \cdot m^{-2}$。

关键词　沙质草地；碳通量；土壤呼吸；生态系统呼吸；总初级生产力

The characteristics of net ecosystem carbon exchange and the contribution of soil respiration during the growing season in sandy grassland. NIU Ya-yi[1,2], LI Yu-qiang[1*], GONG Xiang-wen[1,2], WANG Xu-yang[1,2], LUO Yong-qing[1], ZHANG Jian-peng[1,2] ([1]*Northwest Institute of Eco-Environment and Resources, Chinese Academy of Sciences, Lanzhou* 730000, *China*; [2]*University of Chinese Academy of Sciences, Beijing* 100049, *China*).

Abstract: Based on the eddy covariance system and LI-8150 automatic soil respiration observation system, this present study investigated the characteristics of net ecosystem CO_2 exchange (NEE), the contribution of soil respiration (R_s) to ecosystem respiration (R_{eco}), and the gross primary productivity (GPP) in Horqin sandy grassland of China. The results showed that the average monthly diurnal variations of NEE changed apparently with a single peak curve; the highest absorption rate ($-5.62\ \mu mol \cdot m^{-2} \cdot s^{-1}$) and the highest release rate ($3.14\ \mu mol \cdot m^{-2} \cdot s^{-1}$) were observed in July. The sandy grassland ecosystem was a carbon sink, with a sequestration amount of 25.85 $g\ C \cdot m^{-2}$ during the growing season. The contribution of R_s to R_{eco} accounted for 78.39%; the GPP was 275.51 $g\ C \cdot m^{-2}$ and the contribution of R_{eco} to GPP accounted for 90.62%.

Key words: sandy grassland; carbon flux; soil respiration; ecosystem respiration; gross primary productivity.

草地生态系统作为全球陆地生态系统最重要、分布最广的生态系统类型之一，在全球碳循环和气候调节中起着非常重要的作用(Scurlock *et al.*, 1998; Scurlock *et al.*, 2002; 朴世龙等，2004)。草地生态系统的碳储量在全球陆地生态系统中仅次于森林生态系统，在全球碳平衡中起着重要作用(Tans *et al.*, 1990)，并且草地是受人类影响最为严重的生态系统之一，脆弱的生态环境与频繁的人类活动使之较其他生态系统对全球气候与环境变化的响应更为敏感，因此研究草地植被与大气间CO_2交换机理对理解全球陆地生态系统碳收支以及碳循环具有非常重要的意义(于贵瑞等，2006)。

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围封对沙漠化草地土壤理化性质和固碳潜力恢复的影响

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摘要： 过度放牧是科尔沁沙地退化的主要原因，禁牧围封可以有效地控制牲畜对植被-土壤系统的破坏，促进退化生态系统的有效恢复。以过度放牧后的沙漠化草地为对象，调查了禁牧围封13年后沙漠化草地土壤理化性质的变化特征，并分析了围封对土壤固碳潜力的影响。结果表明：(1)沙漠化草地围封13年后，土壤砂粒含量减少、粉粒和黏粒含量增加，且粉粒增加最为明显，平均含量增加123%；土壤容重在不同土壤深度均呈下降趋势。(2)围封后土壤有机质、全氮、速效氮和速效钾含量呈增加趋势，分别增加了102%、97%、123%和24%，但土壤有效磷和缓效钾呈减少趋势；土壤pH显著升高，阳离子交换量呈现增加趋势。(3)除土壤有效铁外，其余有效微量元素包括有效铜、有效锰和有效锌平均含量均呈增加趋势，分别增加44%、30%和82%。(4)土壤有机质与pH值、阳离子交换量、全氮、速效氮、速效钾、有效铜、有效锰、有效锌含量呈显著正相关关系。(5)沙漠化草地围封13年后，100 cm深度土壤有机碳储量增加393.45 $g \cdot m^{-2}$，碳截存速率为30.27 $gC \cdot m^{-2} \cdot a^{-1}$。对于因持续过度放牧所导致的严重退化草地，禁牧围封可有效促进土壤有机质、养分和微量元素的增加，影响土壤质地及固碳潜力等的变化，但严重退化沙漠化草地的恢复需要一个长期的过程，土壤有机碳储量要恢复到科尔沁非沙漠化草地水平至少需要百年的时间尺度。

关键词： 科尔沁沙地；禁牧围封；沙质草地；土壤理化性质；固碳潜力

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0 引言

陆地生态系统作为土壤碳储量的库，对全球环境变化有着重要的响应[1]。土壤作为陆地生态系统物质循环、水分平衡、凋落物分解等过程的主要载体，其理化性质是反映土壤生态系统恢复程度的关键指标[2-3]。沙质草地是中国北方干旱半干旱区重要的土地资源，超过1.34×10^8 hm^2的沙质草地分布在北方的广大区域[4]，由于沙质草地极容易受到环境变化和人为干扰的影响，近年来持续过度的放牧导致其严重的退化和沙漠化，这些问题已经成为中国北方主要的生态环境问题。在全球气候变化的大背景下，研究沙质草地土壤理化性质及固碳潜力对放牧管理活动的响应，对评价沙地生态系统的环境质量、调节沙地生态系统过程具有重要的理论和实际意义。

科尔沁沙地是中国北方农牧交错带的典型生态脆弱区，近代以来，随着人口的增长带来的农牧压力导致植被不同程度退化，土地沙漠化严重。但从20世纪70年代开始，在科尔沁沙地开始实施一系列草地恢复与沙漠化防治等工程措施。其中，对沙质草地进行禁牧围封是科尔沁沙地生态重建的一项重要举措。近年来，有关持续放牧和禁牧围封对草地土壤性质影响的研究开展较多。苏永中等[5]以围封时间为梯度，选择3个类型样地，研究了科尔沁退化沙地草地持续放牧和围封恢复下土壤和植物系统的碳储存，结果表明，退化沙地草地在采取有效的保护措施后，可以由碳源变为碳汇。文海燕等[6]研究了开垦和封育年限对退化沙质草地土壤性状的影响，结果表明，围封是引起土壤性状逐渐好转的过程，土

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沙埋对科尔沁沙地两种主要作物存活的影响及其光合生理响应

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摘要：为了解沙埋对农作物存活、产量的影响及其光合生理响应特征，在内蒙古科尔沁沙地研究了玉米（*Zea mays*）和绿豆（*Vigna radiata*）在不同沙埋深度下第5、10、15天的净光合速率、气孔导度、蒸腾速率、水分利用效率的变化，并于作物生长末期对其存活率及产量进行了测定。结果表明：(1)玉米较绿豆具有较强的耐沙埋能力，埋深等于株高时绿豆全部死亡，玉米仍有12.5%的存活率；(2)埋深超过株高的25%后，玉米和绿豆的产量均显著下降，但玉米的下降幅度明显小于绿豆；(3)随着沙埋胁迫的加剧，两种植物的净光合速率下降，表明沙埋胁迫对植物的光合作用破坏很大。但相比于绿豆，玉米对于沙埋胁迫有着更好的光合适应机理，随着胁迫的时间增加，其净光合速率有所恢复。且可以通过降低蒸腾速率和提高水分利用效率来适应沙埋胁迫。

关键词：科尔沁沙地；沙埋；农作物；产量；光合生理

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0 引言

由于气候干旱、风沙流活动强烈，沙埋现象普遍存在于中国北方干旱、半干旱地区。在这些区域，大面积天然草场、人工植被和农田经常遭受沙埋危害[1-2]。科尔沁沙地是中国北方农牧交错带最为典型的一段，也是中国主要的生态脆弱带之一[3]。地貌类型以缓起伏沙地为主，相间分布平坦的沙质草甸和农田。玉米（*Zea mays*）的种植面积占农作物总种植面积的70%，随着当地居民对膳食结构改善需求的增加，近年来绿豆（*Vigna radiata* 被广泛种植，成为当地主要作物[4-5]。

科尔沁沙地风沙活动强烈，起沙风频繁、强劲，生长在此区域的农作物难以避免沙埋的胁迫，大约有30%的农田每年受到风沙危害而减产[6-8]。已有研究揭示，影响风沙环境下植物存活与生长的最主要因素是由沙埋引起的叶片光合面积下降，从而造成生产力降低，直至死亡[9-10]。目前，有关沙埋对植物造成的影响及植物对其适应方面的研究，大多集中于沙埋对种子萌发与幼苗出土的影响[11-14]。对于沙埋后植物在形态、能量分配、抗逆生理及无性繁殖等方面的改变也有一些报道[15-18]。而关于植物的光合特性在沙埋后的改变及其适应机制的研究却不多见[8,19-23]，这其中对于农作物的报道更是少见。

光合作用对于植物的存活、繁殖及抗逆性等方面具有决定性的作用，因此，光合作用的强弱可作为判断植物在逆境下能否正常生长的指标[19-23]。本文以种植在典型的风沙生态环境脆弱区科尔沁沙地的主要农作物玉米和绿豆为研究材料，明确沙埋对它们的生长造成的影响，揭示其光合响应特征，对比两种作物对于沙埋胁迫的忍受能力及机制，以期为当地农业合理生产提供一定建议，进而增加农民收入。

1 研究方法

1.1 研究区概况

研究依托位于科尔沁沙地东南部奈曼旗境内的中国科学院奈曼沙漠化研究站（奈曼站）。研究区年

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科尔沁城镇化过程对沙地景观的影响①

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摘 要： 城镇空间扩展所表征的城镇化过程及其对区域景观的影响，是景观生态学研究中的重要方向之一，也是景观生态学中格局－过程研究的重要组成部分。以1985—2013年遥感数据为基础，GIS技术与景观格局分析方法为手段，采用主要指标构建的城镇化指数定量分析了城镇化过程对科尔沁沙地景观的影响。结果表明：近28 a来，区域城镇化发展较快，年均提高0.64%，并呈现阶段性特征，研究区景观变化明显。在斑块水平上，农田、固定沙丘、林地、居工地的面积增加，其余景观类型的面积减少；农田、居工地与林地的破碎化程度增加；农田、固定沙丘最大斑块面积增加最显著，在区域中的优势作用增强。在景观水平上，区域景观破碎化程度减轻，空间集聚程度增加，景观类型组成趋于简单。区域内城镇化过程对不同类型景观的影响存在差异性，其特征表现为城镇化对农田、居工地的影响最大，对其他类型景观的影响较小。城镇化指数与斑块数量、散布与并列指数、香农多样性指数之间存在显著的负相关关系，城镇化指数与蔓延度指数为显著的正相关关系，表现为研究区景观破碎化程度、空间散布程度、异质性均随城镇化水平提高而减小，反映出城镇化与景观变化存在一定的内在联系，选取的景观指数能够反映城镇化过程对区域景观的影响。

关键词： 城镇化；景观变化；时空变化；科尔沁沙地

景观变化是景观生态学研究的主要内容之一，是自然与人文驱动力相互作用而呈现景观结构与功能在时空尺度上的转变[1-2]。由于景观变化研究是探求区域景观在时空尺度上变化原因与机制的一种有效方法，从而得到了国内外学者的广泛关注，研究范围几乎涵盖了除海洋之外的所有生态系统，在解释景观变化机制、认知景观功能特征等方面取得了丰硕的研究成果[3-7]。

从国内外的研究特点来看，主要表现在如下几个方面：利用RS与GIS技术分析景观变化特征[3-4]；借助景观格局分析软件，选取相应的景观指数开展景观格局变化研究，并对景观变化的驱动力进行分析[5-6]；采用缓冲分析等方法，结合景观指数研究景观变化过程中的机制和尺度效应等[7]。这些研究的共同特点表明，景观格局指数能够很好地描述景观的空间结构和时空尺度上的量变，“3S”技术结合合适的景观指数分析能够为区域生态环境恢复与重建决策提供理论支持。

传统的城镇化过程是以城镇人口数量的比重来表达，但是从景观生态学空间组分特点认知的角度来看，城镇化也是不同因素相互作用下，农村或自然景观转变为城镇景观的空间变化过程[8]。近年来，由于全球气候变化与人类活动的共同作用[9]，特别是城镇化的加速发展，所处区域景观结构与功能在时空尺度上发生了一系列的变化，城镇化对区域自然景观产生负面的影响，如林地、草地、湿地景观萎缩与破碎化[10-11]。因此，从完善区域规划和管理角度来看，必须重视城镇化背景下的区域景观动态变化研究。遥感数据的易获取性和连续性，使利用“3S”技术定量化研究城镇扩展成为近年来的热点[12-14]，这些研究主要集中在城市化水平高度发展的大中城市或城市群[12,15]，而很少涉及等级较低的中小城镇，尤其是生态脆弱地区城镇化方面的研究。所以，从保护生态脆弱区自然环境与景观的角度，更

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