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Contribution of the Alternative Pathway on Spring Rejuvenation of Alfalfa

AN Chang-qi^{1,2,3}, LIU Mei-jun^{1,2,3*}, ZHANG Zheng^{1,2,3}, YAN An^{1,2,3*},

WANG Jie^{1,2,3}, ZHANG Hao-yang^{1,2,3}

(1. College of Grassland Science, Xinjiang Agricultural University, Urumqi, Xinjiang 830052, China;

2. Key Laboratory of Grassland Resources and Ecology of Western Arid Region, Ministry of Education, China;

3. Xinjiang Key Laboratory of Grassland Resources and Ecology, Urumqi, Xinjiang 830052, China)

Abstract: Alfalfa often suffers from low temperature during spring rejuvenation, so it is important to improve the cold tolerance of alfalfa leaves for its smooth rejuvenation, and the alternative pathway (AP) could effectively improve the plant's tolerance. In this study, the contribution of AP on spring rejuvenation of alfalfa was investigated in 'Xinmu No. 4' and 'Gannong No. 5' with different fall dormancy levels. Though the protein and AP capacity were decreased during the rejuvenation, the ratio of AP/TP were increased in two alfalfa varieties, compared to those in alfalfa before overwintering. This indicated that AP had positive response to alfalfa rejuvenation. The limitation of AP significantly affected the leaf length, leaf width and growth rate of greening alfalfa, showing that AP played an important role in alfalfa rejuvenation. Inhibition of AP resulted in a significant decrease in P_n , C_i , G_s and stomatal structure deformity, suggestion that AP affected photosynthesis by influencing stomatal development during rejuvenation. AP reduces oxidative damage to PSII core protein repair in alfalfa leaves and optimizes photosynthesis by up-regulating NADP-MDH activity, decreasing the accumulation of excess reducing power in the chloroplasts, and by increasing SOD and POD activities and decreasing the accumulation of hydrogen peroxide. The higher proportion of AP keeps it more tolerant to low temperature for rejuvenation in 'Xinmu No. 4' with a lower fall dormancy level.

Key words: Alfalfa; Alternative pathway; Photosynthetic activity; Spring rejuvenation

斑块化退化高寒草甸演替进程中植物-土壤-胞外酶变化特征研究

柴 瑜, 李希来*, 李成一, 杜欣儒, 周禧年, 吴西洛

(青海大学农牧学院, 青海 西宁 810016)

摘要:青藏高原高寒草甸退化严重,形成大量的裸露斑块,裸露斑块的恢复演替可能会导致草地生态系统土壤微生物群落稳定性发生变化。目前关于植物-土壤-胞外酶变化特征对裸露斑块恢复演替的响应变化还不清楚。本研究选择4种类型的斑块:裸地斑块(Bare patches, BP)、短期恢复斑块(Initial recovery plaque, IRP)、长期恢复斑块(Long-term recovery plaque, LRP)和健康高寒草甸(Healthy alpine meadows, AM),分析了斑块化退化高寒草甸不同演替阶段的植物、土壤及土壤胞外酶特征的差异。结果表明:斑块化退化高寒草甸的恢复演替增加了植被地下生物量(BGB)、植物群落多样性指数[Simpson 多样性指数(D)、Shannon-Wiener 指数(H)]、土壤水分和土壤电导率以及土壤有机碳、全氮、铵态氮含量,亮氨酸氨基肽酶(LAP)、碱性磷酸酶(AP)活性;而土壤硝态氮含量呈相反趋势。

关键词:高寒草甸;土壤物理性质;裸露斑块恢复;植物特征;土壤胞外酶

纤维素降解菌的筛选以及对水稻秸秆的利用

陈丹丹, 王 垚, 郭田心, 梁秋雨, 张 庆*

(华南农业大学林学与风景园林学院/广东木本饲料工程技术研究中心/广东省森林植物种质创新与利用重点实验室,
广东 广州 510642)

摘要:为提高秸秆的利用,本文从白蚁肠道中通过刚果红初筛、滤纸降解复筛试验筛选到了两株纤维素降解菌,经 NCBI 同源序列比对百分比鉴定分别为沙福芽孢杆菌(*Bacillus safensis*, BS)和伊朗纤维单胞菌(*Cellulomonas iranensis*, CE)。以水稻秸秆为唯一碳源培养沙福芽孢杆菌和伊朗纤维单胞杆菌 14 d 后,秸秆出现不同程度降解,与对照相比,沙福芽孢杆菌和伊朗纤维单胞菌处理下秸秆的酸性洗涤纤维(48.80%, 35.43%DM)和半纤维素含量(19.90%, 17.53%DM)以及可溶性碳水化合物含量(0.11%, 0.18%DM)均显著降低,伊朗纤维单胞菌处理下秸秆的失重率(43.12%DM)显著增加、中性洗涤纤维含量(52.95%DM)显著降低。

关键词:纤维素降解菌;滤纸;水稻秸秆

Screening of Fiber-Degrading Bacteria and Utilization Rice Straw

CHEN Dan-dan, WANG Yao, GUO Tian-xin, LIANG Qiu-yu, ZHANG Qing*

(College of Forestry and Landscape Architecture, South China Agricultural University, Guangdong Province Research Center of Woody Forage Engineering Technology, Guangdong Key Laboratory for Innovative Development and Utilization of Forest Plant Germplasm, Guangzhou, Guangdong Province 510642, China)

Abstract: To increase the utilization rate of straw, the purpose of this study screened two cellulose-degrading bacteria from the intestinal tract of termites by Congo red primary screening and filter paper degradation re-screening test, which were *Cellulomonas iranensis* (CE) and *Bacillus safensis* (BS), respectively. After 14 d fermentation, BS and CE were cultivated with straw as the only carbon source. The straw was degraded to varying degrees. Both of BS and CE significantly ($P < 0.05$) reduced the contents of acid detergent fiber (48.80%, 35.43% DM), hemicellulose (19.90%, 17.53% DM) and water soluble carbohydrate (0.11%, 0.18% DM). In addition, the inoculation of CE also obviously increased ($P < 0.05$) the weight loss rate of straw (43.12% DM) and reduced the content of neutral detergent fiber (52.95% DM).

Key words: Cellulose degrading bacteria; Filter paper; Cellulase

不同添加剂对小麦秸秆微贮品质的影响

陈佳敏¹, 王琳^{1,2*}, 吴慧珍¹, 高子涵¹, 陈炜昊¹, 吕晓阳^{1,2}, 孙伟^{1,2*}

(1. 扬州大学动物科学与技术学院, 江苏 扬州 225009; 2. 扬州大学农业科技发展研究院/国际联合实验室, 江苏 扬州 225009)

摘要:为探讨不同添加剂对小麦秸秆微贮品质的影响,将 4×10^8 cfu $\cdot$ mL⁻¹ 芽孢杆菌(*Bacillus megaterium*)、 1×10^{10} cfu $\cdot$ g⁻¹ 乳酸菌(*Lactic acid bacteria*)、1.5 % 尿素(Urea)和 2 % 糖蜜(Molasses)4 种添加剂添加到小麦秸秆微贮中,发酵 30 d 后开袋测定微贮饲料常规营养成分和发酵品质。结果表明:添加不同添加剂后,小麦秸秆微贮饲料的 pH 值、NDF、ADF、NH₃-N、AA、BA 含量显著降低($P < 0.05$),CP、WSC、LA 含量显著升高($P < 0.05$)。其中,复合添加芽孢杆菌和乳酸菌的组合显著降低小麦秸秆纤维含量、pH 值和乙酸含量以及提高乳酸含量。复合添加巨大芽孢杆菌、乳酸菌、尿素和糖蜜的组合在降低丙酸、丁酸和氨态氮含量方面表现最优。综合营养成分和发酵品质结果,选择复合添加巨大芽孢杆菌和乳酸菌组作为改善小麦秸秆微贮品质的最优处理组合。

关键词:小麦秸秆;微贮;营养品质;发酵品质

Effects of Different Additives on the Quality of Microbial Storage of Wheat Straw

CHEN Jia-min¹, WANG Lin^{1,2*}, WU Hui-zhen¹, GAO Zi-han¹, CHEN Wei-hao¹,
LYU Xiao-yang^{1,2}, SUN Wei^{1,2*}

(1. College of Animal Science and Technology, Yangzhou University, Yangzhou, Jiangsu Province 225009, China; 2. Institute of Agricultural Science and Technology Development(International Joint Laboratory), Yangzhou University, Yangzhou, Jiangsu Province 225009, China)

Abstract:To explore the effects of different additives on the quality of wheat straw micro-storage, four additives— 4×10^8 cfu $\cdot$ mL⁻¹ *Bacillus megaterium*, 1×10^{10} cfu $\cdot$ g⁻¹ lactic acid bacteria, 1.5 % urea and 2 % molasses, were added to the wheat straw micro-storage. After 30 days of fermentation, the nutritional components and fermentation quality were determined. The results showed that the pH value, NDF, ADF, NH₃-N, AA and BA contents of the wheat straw micro-storage significantly decreased ($P < 0.05$), while the CP, WSC and LA contents significantly increased ($P < 0.05$) after adding different additives. Among them, the combination of *Bacillus megaterium* and lactic acid bacteria significantly reduced the fiber content of wheat straw micro-storage, decreased the pH value and acetic acid content, and increased the lactic acid content. The combination of *Bacillus megaterium*, lactic acid bacteria, urea and molasses performed best in reducing the contents of propionic acid, butyric acid and ammonia nitrogen. Based on the results of nutritional components and fermentation quality, the combination of *Bacillus megaterium* and lactic acid bacteria was selected as the optimal treatment for improving the quality of wheat straw micro-storage.

Key words: Wheat straw; Microbial storage; Nutritional quality; Fermentation quality

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作者简介:陈佳敏(2001-),女,江苏盐城人,硕士研究生,主要从事饲草加工与利用研究,E-mail: yolo020529@163.com; * 通信作者 Author for corresponding,孙伟(1972-),男,江苏睢宁人,博士,江苏省二级教授,主要从事肉羊健康高效低碳养殖研究,E-mail: dkxmsunwei@163.com;王琳(1986-),女,安徽合肥人,助理研究员,主要从事饲草调制与加工研究,E-mail: lynn1215@yzu.edu.cn

内生真菌介导继代效应对醉马草解剖结构的影响

崔龙轩, 何文, 夏超*

(草种创新与草地农业生态系统国家全国重点实验室/农业农村部草牧业创新重点实验室/草地农业教育部工程研究中心/
甘肃省西部草业技术创新中心/兰州大学, 甘肃 兰州 730020)

摘要:醉马草(*Achnatherum inebrians*)广泛分布于我国西北地区,在自然界中与香柱菌属(*Epichloë*)禾草内生真菌形成互利互惠的共生体。内生真菌可以调控由水分亏缺引起的植物解剖结构变化,通过有效控制寄主植物泡状细胞失水实现叶片卷缩伸展来应对干旱胁迫。本研究以来自干旱生境和湿润生境的带内生真菌(Endophyte-infected, EI)和不带内生真菌(Endophyte-free, EF)的醉马草幼苗为试验材料,在温室条件下进行盆栽试验,设置不同水分梯度,探究供试植物叶片解剖结构的变化,以期明确内生真菌在干旱胁迫下对宿主植物继代效应(Transgenerational effect, TGE)的影响及作用途径。盆栽试验结果表明,来自干旱生境的 EI 醉马草子代幼苗泡状细胞周长面积比更小,更利于物质和能量的转换,在 15% 土壤相对饱和含水量(Relative saturation moisture content, RSMC)下,来自干旱生境的 EI 醉马草子代幼苗,泡状细胞组高度/叶脉厚度显著高于 EF 醉马草,表明内生真菌通过介导继代效应,极大缓解了干旱胁迫对叶脉厚度、泡状细胞周长面积比和泡状细胞组高度/叶脉厚度等指标的消极影响,提高了子代幼苗的抗旱能力。研究结果有助于更加深入地了解内生真菌的生物学功能,为有效地利用内生真菌培育抗旱牧草新品种提供理论基础。

关键词:香柱菌属内生真菌;醉马草;含水量;叶片解剖结构

Transgenerational Effect Mediated by Endophyte Affects Anatomical Structure of Drunken Horse Grass (*Achnatherum inebrians*)

CUI Long-xuan, HE Wen, XIA Chao*

(State Key Laboratory of Grassland Agro-Ecosystems, Key Laboratory of Grassland Livestock Industry innovation, Ministry of Agriculture and Rural Affairs, College of Pastoral Agriculture Science and Technology, Lanzhou University, Lanzhou, Gansu Province 730020, China)

Abstract: *Achnatherum inebrians* (drunken horse grass, DHG) is widely distributed in the arid and semi-arid regions of northwest China, where it naturally forms a mutualistic symbiosis with *Epichloë* endophytes. These endophytes can modulate plant anatomical adaptations to water deficit by regulating bulliform cell dehydration, thereby enabling dynamic leaf curling and unfolding to cope with drought stress. In this study, endophyte-infected (EI) and endophyte-free (EF) DHG seedlings derived from maternal plants originating in arid and humid habitats were used to conduct a greenhouse pot experiment under controlled water gradients. The aim was to investigate drought-induced changes in leaf anatomical traits and to elucidate the role and pathways through which *Epichloë* endophytes mediate transgenerational effects (TGE) under drought conditions. The results showed that EI offspring from arid habitats exhibited a smaller bulliform cell circumference-to-area ratio, which may enhance material and energy exchange efficiency. Under 15% relative saturation moisture content (RSMC), these EI seedlings also displayed significantly greater bulliform cell group height relative to leaf vein thickness compared to EF seedlings, indicating that endophyte-mediated TGE can alleviate the negative impact of drought on leaf anatomical traits such as vein thickness and bulliform cell structure. These changes contributed to enhanced drought tolerance in the offspring. This study advances our understanding of the biological functions of *Epichloë* endophytes and provides a theoretical foundation for the development of drought-resistant forage cultivars through the utilization of beneficial endophytes.

Key words: *Epichloë* endophyte; *Achnatherum inebrians*; Water content; Leaf anatomical structure

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作者简介:崔龙轩(2001-),男,河南新乡人,硕士研究生,主要从事禾草内生真菌研究, E-mail: cuilx2023@lzu.edu.cn; * 通信作者 Author for correspondence, E-mail: xiac@lzu.edu.cn

转录组分析揭示紫花苜蓿半乳糖代谢通路中耐寒关键基因

代蕊¹, 贾苗苗¹, 穆乙鑫¹, 杨翌³, 邵进翠⁴, 云岚^{1,2*}

(1. 内蒙古农业大学草业学院, 内蒙古 呼和浩特 010010; 2. 内蒙古农业大学草地资源教育部重点实验室, 内蒙古 呼和浩特 010010; 3. 黑龙江省农业科学院畜牧兽医研究所, 黑龙江 哈尔滨 150086; 4. 北京正道种业有限公司, 北京 100081)

摘要:为探究紫花苜蓿(*Medicago sativa* L.)响应低温胁迫的分子机制,本研究整合生理指标分析与转录组测序,解析‘龙牧 806’(LM)与‘赛迪 10’(SD)在 4℃低温胁迫下的响应机制。LM 48 h 低温处理后 Pro,SS 含量及 SOD, POD,CAT 活性显著升高,SD 则 MDA 含量升高,REC 达 53%且膜损伤严重。结合 WGCNA 筛选出抗寒相关“MEblue”模块,核心基因富集于 2 条代谢通路,ALT,GOT1 等关键基因在低温下上调。qRT-PCR 验证基因表达趋势与转录组一致,为紫花苜蓿耐寒分子育种提供关键靶点与理论依据。

关键词:低温胁迫;生理指标;转录组测序;加权共表达网络

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作者简介:代蕊(1999-),女,蒙古族,内蒙古赤峰人,博士研究生,主要从事牧草遗传育种方面研究,E-mail:18747659997@163.com; * 通信作者,云岚(1970-),女,内蒙古呼和浩特人,教授,博士生导师,主要从事牧草种质资源与遗传育种研究,E-mail:yunlan@imau.edu.cn

野大麦不同生态型农艺性状、品质特性及耐盐性的评价筛选及关系研究

翟纤润, 陈振江, 李春杰*

(草种创新与草地农业生态系统全国重点实验室/兰州大学草地农业科技学院, 甘肃 兰州 730000)

摘要:野大麦作为优良的牧草,在内生真菌侵染后其耐盐性进一步增强,但不同野大麦内生真菌-共生体生态型之间的农艺性状、品质和耐盐性是否存在差异,还尚未可知。为明确各个生态型的优劣,并探索农艺性状、品质特性及耐盐性的关系,以 16 种野大麦-内生真菌共生体生态型开展田间试验与温室试验。研究发现,E1 和 D2 农艺性状最优,B2 和 B3 牧草品质最高,D2 的耐盐性最强。千粒重、酸性洗涤纤维(ADF)、细胞膜相对透性(RMP)对相对饲用价值(RFV)的直接作用最大,在提高 RFV 的品种选育中应加强对它们的重视。品质与农艺性状、品质与耐盐性之间均呈显著负相关($P<0.05$),农艺性状与耐盐性呈显著正相关($P<0.01$)。与综合评价结果结合来看,D2 的农艺性状和耐盐性最好,但品质最差;B2 的品质较高,而农艺性状和耐盐性较差;LZ 在各方面表现均处于中等水平,这三种生态型可作为培育耐盐性强、品质高的野大麦-内生真菌共生体新品系的主要材料。未来可解析其共生机制,明确品质和耐盐性提高的关键途径,为靶向育种提供理论依据。

关键词:野大麦;内生真菌;盐胁迫;牧草;品种筛选;综合评价;相关性;通径分析

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作者简介:翟纤润,女,河北邯郸人,博士研究生,主要从事禾草内生真菌共生体研究,E-mail:zhaiyurun@163.com; * 通信作者 Author for correspondence, chunjie@lzu.edu.cn

豆科植物裂荚机制研究进展

杜 雨

(新疆农业大学, 新疆 乌鲁木齐 830052)

摘要: 豆科植物的裂荚现象是荚果在成熟过程中沿特定缝合线开裂释放种子的过程, 这一现象对种子传播、种群扩散和生态适应具有重要意义。然而, 在农业生产中, 裂荚往往导致种子损失和产量降低, 是大豆等豆科作物育种中的重要挑战。本文综述了豆科植物裂荚的形态学特征、生理调控、分子机制及抗裂荚育种的研究进展。研究表明, 裂荚的发生受纤维细胞排列、细胞壁成分降解和机械张力释放的共同作用, 并由赤霉素、生长素、乙烯和脱落酸等激素协同调控。在分子层面, 抗裂荚基因 *pdh1* 及其相关调控网络对裂荚性状有重要影响。此外, 分子标记辅助选择和基因编辑技术的应用, 显著推动了抗裂荚育种进程。本文旨在为未来抗裂荚研究和豆科植物育种提供参考。

关键词: 豆科植物; 裂荚; 机制

Research Progress on the Dehiscence Mechanism of *Leguminous* Plants

DU Yu

(Xinjiang Agricultural University, Urumqi, Xinjiang 830052, China)

Abstract: The dehiscence phenomenon in *legumes* refers to the process by which pods split along specific sutures during maturation to release seeds. This is significant for seed dispersal, population spread, and ecological adaptation. However, in agriculture, dehiscence often leads to seed loss and reduced yield, posing a major challenge in soybean breeding programs. This review summarizes current progress on the morphological characteristics, physiological regulation, molecular mechanisms, and breeding for dehiscence resistance in leguminous plants. Research indicates that dehiscence is influenced by fiber cell arrangement, cell wall component degradation, and mechanical tension release, all synergistically regulated by hormones such as gibberellins, auxins, ethylene, and abscisic acid. At the molecular level, the *pdh1* anti-dehiscence gene and its associated regulatory networks are crucial. Additionally, molecular marker-assisted selection and gene editing technologies have significantly advanced dehiscence resistance breeding. This review aims to provide reference for future research on dehiscence resistance and *legume* plant breeding.

Key words: Leguminous plants; Pod dehiscence; Mechanism

不同管理方式对羊草草甸草原植物和土壤碳氮储量的影响

高肖甜¹, 辛晓平¹, 俞天琦¹, 侍梦圆¹, 李颖¹, 刘方林^{1,2}, 贺森雅¹, 闫瑞瑞^{1*}

(1. 中国农业科学院农业资源与农业区划研究所, 北京 100080; 2. 新疆农业大学, 新疆 乌鲁木齐 830052)

摘要:为探讨不同管理方式对羊草草甸草原植物-土壤碳氮耦合关系的影响,本研究于 2024 年夏季在呼伦贝尔地区选择围封、打草和放牧三种长期管理样地,测定了植被(活体、凋落物和根系)及土壤(0~100 cm)碳氮储量与 C:N 比,并采用线性混合效应模型分析了植物与土壤碳氮比的耦合关系。结果表明:(1)围封显著提高了植物碳氮储量及 C:N 比($P<0.01$),并在浅层(0~50 cm)土壤维持较高的碳氮储量和 C:N;打草处理降低了植物碳氮储量,但提高了深层(50~100 cm)土壤的 C:N,放牧处理则降低了各层植物和土壤的碳氮储量($P<0.05$)。(2)在围封下,根系 C:N 与土壤 C:N 呈正相关($R^2=0.18$),打草处理下根系及总植物 C:N 与土壤 C:N 呈负相关,而凋落物 C:N 与土壤 C:N 呈正相关($P<0.05$);放牧处理下植物-土壤 C:N 相关性不显著。研究表明,不同管理方式通过调控植物和土壤碳氮储量及 C:N,影响草原碳氮循环与耦合强度,适度干扰(打草处理)有助于激活植物-土壤反馈机制,而过度或缺乏干扰可能削弱这一循环,对草原可持续管理具有指导意义。

关键词:草甸草原;碳氮;管理方式;植物-土壤耦合

Effects of Different Management on Plant-Soil Carbon and Nitrogen Stocks and Coupling in *Leymus chinensis* Meadow Steppe

GAO Xiao-tian¹, XIN Xiao-ping¹, YU Tian-qi¹, SHI Meng-yuan¹, LI Ying¹,
LIU Fang-lin^{1,2}, HE Sen-ya¹, YAN Rui-rui^{1*}

(1. Institute of Agricultural Resources and Regional Planning, Chinese Academy of Agricultural Sciences, Beijing 100080, China;

2 Xinjiang Agricultural University, Urumqi, Xinjiang 830052, China)

Abstract: To investigate the effects of different management practices on plant-soil carbon-nitrogen coupling in sheepgrass meadow grasslands, this study selected three long-term management plots—enclosure, mowing, and grazing—in Hulunbuir during summer 2024. Vegetation (aboveground, litter, and roots) and soil (0–100 cm) carbon and nitrogen stocks along with C:N ratios were measured. Linear mixed-effects models analysed the coupling between plant and soil carbon-nitrogen ratios. Results indicated: (1) Enclosure significantly increased plant carbon and nitrogen reserves and C:N ratios ($P<0.01$), maintaining elevated carbon and nitrogen reserves and C:N ratios in shallow soil layers (0–50 cm); mowing reduced plant carbon and nitrogen reserves but increased the C:N ratio in deep soil (50–100 cm), while grazing reduced plant and soil carbon and nitrogen reserves at all depths ($P<0.05$). (2) Under enclosure, root C:N correlated positively with soil C:N ($R^2=0.18$). Under mowing, root and total plant C:N correlated negatively with soil C:N, whereas litter C:N correlated positively with soil C:N ($P<0.05$). Under grazing, plant-soil C:N correlation was not significant. Findings indicate that different management practices influence grassland carbon-nitrogen cycling and coupling intensity by regulating plant and soil carbon-nitrogen reserves and C:N ratios. Moderate disturbance (mowing treatment) helps activate plant-soil feedback mechanisms, whereas excessive or insufficient disturbance may weaken this cycle, providing guidance for sustainable grassland management.

Key words: Meadow steppe; Carbon and nitrogen; Management practices; Plant-soil coupling

乳酸菌对甜菊糖苷的利用及甜叶菊渣青贮发酵品质的研究

郭 香¹, 臧美琪¹, 田 静¹, 王育涵¹, 周天宇¹, 李国栋², 张建国^{1*}

(1. 华南农业大学南方草业中心, 广东 广州 510642; 2. 华微(广州)农业生物科技有限公司, 广东 广州 510700)

摘要:为评估甜叶菊(*Stevia rebaudiana*)渣作为饲料原料的开发潜力与应用价值,本研究探讨了乳酸菌对甜菊糖苷的利用能力、不同添加剂[酶菌复合剂、植物乳杆菌(*Lactiplantibacillus plantarum* YM3)、布氏乳杆菌(*Lactobacillus buchneri*, LB)和高地芽孢杆菌(*Bacillus altitudinis* GT)]和不同青贮时长(20, 30, 40 和 50 d)对甜叶菊渣发酵的影响。结果表明,乳酸菌利用甜菊糖苷的能力不如葡萄糖,其中 YM3 和 LB 对甜菊糖苷的利用优于其他菌株。添加酶菌复合剂显著改善了青贮发酵品质,且随青贮时间延长乳酸含量增加,在 50 d 时,乳酸含量增高至 $37.2 \text{ g} \cdot \text{kg}^{-1} \text{ DM}$, pH 值降至 3.55,而其他处理在青贮 30 d 后发酵品质无显著变化。综上,甜叶菊渣青贮时建议添加酶菌复合剂青贮 50 d。本研究结果为甜叶菊渣的饲料化利用提供了理论依据和技术支持。

关键词:甜叶菊渣;青贮;纤维素酶;乳酸菌

Study on the Utilization of Steviol Glycosides by Lactic Acid Bacteria and the Fermentation Quality of Stevia Residue Silage

GUO Xiang¹, ZANG Mei-qi¹, TIAN Jing¹, WANG Yu-han¹, ZHOU Tian-yu¹, LI Guo-dong², ZHANG Jian-guo^{1*}

(1. South Pratacultural Research Center, South China Agricultural University, Guangzhou, Guangdong Province 510642, China;

2. Huawei (Guangzhou) Agricultural Biotechnology Co., Ltd, Guangzhou, Guangdong Province 510700, China)

Abstract: This study aims to evaluate the potential and application value of stevia (*Stevia rebaudiana*) residue as a feed ingredient. This study investigated the capability of lactic acid bacteria (LAB) to utilize steviol glycosides, the effects of additives (cellulase-LAB complex, *Lactiplantibacillus plantarum* YM3, *Lactobacillus buchneri* LB, *Bacillus altitudinis* GT) and ensiling period (20, 30, 40, and 50 d) on the fermentation quality. The results showed that LAB utilized steviol glycosides less than glucose, and YM3 and LB utilized steviol glycosides more than other strains. Adding cellulase-LAB complex significantly improved the silage fermentation quality, with lactic acid content increasing over the ensiling period, and the lactic acid content increased to $37.2 \text{ g} \cdot \text{kg}^{-1} \text{ DM}$ and the pH decreased to 3.55 on 50 d, while other treatments showed no significant changes in the fermentation quality after 30 days of ensiling. In conclusion, it is recommended that stevia residue should be ensiled with cellulase-LAB complex addition for 50 days fermentation. These findings provide theoretical and technical support for the resource utilization of stevia residue.

Key words: *Stevia* residue; Silage; Cellulase; Lactic acid bacteria

肉牛不同载畜率对羊草草甸草原土壤呼吸的影响

贺森雅¹, 俞天琦¹, 侍梦圆¹, 刘方林², 李颖¹, 邗丽¹, 冀莉¹, 辛晓平¹, 闫瑞瑞^{1*}

(1. 北方干旱半干旱耕地高效利用全国重点实验室/中国农业科学院农业资源与农业区划研究所, 北京 100081;

2. 新疆农业大学草业学院, 新疆 乌鲁木齐 830052)

摘要:土壤呼吸(含总呼吸、自养呼吸、异养呼吸)是草原碳循环核心环节,其组分动态对评估生态系统碳源/汇功能至关重要。本研究以呼伦贝尔羊草草甸草原为对象,探究肉牛不同载畜率(0, 0.23, 0.46, 0.92 只·hm⁻², 分别为对照、轻度放牧、中度放牧、重度放牧)对土壤呼吸组分及驱动因子的影响。试验采用随机区组设计(3次重复),于2024年生长季(6—9月)开展观测;通过静态箱-气相色谱法测定土壤总呼吸速率;采用根去除法区分自养呼吸与异养呼吸,同步测10 cm 土层温度、土壤含水量、有机碳、微生物生物量碳及植物生物量等指标。结果表明:(1)载畜率显著影响土壤呼吸组分($P<0.05$)。生长季平均总呼吸速率为对照>轻度放牧>中度放牧>重度放牧,重度放牧与对照处理相比降低49.6%;重度放牧自养呼吸显著低于对照处理,降幅为64.5%;对照处理异养呼吸较重度放牧降低39.9%,且自养呼吸占总呼吸比例随载畜率升高略降。(2)环境因子关联有差异:总呼吸、异养呼吸与10 cm 土层温度显著正相关($P<0.01$),与土壤含水量呈二次函数关系($P<0.01$);自养呼吸与植物地上、根系生物量相关性更强($P<0.01$)。载畜率通过双重路径影响呼吸:降土壤有机碳和微生物生物量碳抑制异养呼吸;减植物地上、根系生物量削弱自养呼吸。(3)轻度放牧下,各呼吸组分与对照无显著差异,且草地生产力未受明显抑制。综上,呼伦贝尔羊草草甸草原中,肉牛载畜率升高通过改变植物群落与土壤微环境抑制呼吸组分,对自养呼吸影响更显著;轻度放牧是兼顾草地生产力与碳循环功能的适宜模式,可为温带草甸草原精准放牧管理提供依据。

关键词:肉牛载畜率;呼伦贝尔;羊草草甸草原;土壤呼吸;自养呼吸;异养呼吸;碳循环

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作者简介:贺森雅(2000-),女,汉族,山西晋城人,硕士研究生,主要从事草地生态研究,E-mail: 821012430101@caas.cn; * 通信作者 Author for correspondence, E-mail: yanrui@caas.cn

野大麦内生真菌共生体对盐渍化土壤氧化亚氮排放的影响

康莹, 吴欣豪, 陈振江*

(草种创新与草地农业生态系统全国重点实验室/兰州大学草地农业科技学院, 甘肃 兰州 730000)

摘要:土壤盐渍化是制约农业生产和土壤养分高效利用的关键逆境因子之一。*Epichloë* 属内生真菌可与冷季型禾草形成互利共生体,在增强宿主抗逆性的同时,也参与土壤养分和氮循环过程。然而,*Epichloë* 属内生真菌对盐渍化土壤氧化亚氮(N₂O)排放的影响机制尚不明确。本研究以带菌(E+)、不带菌(E-)的耐盐碱野大麦为研究对象开展盆栽试验,设置高盐低氮、中盐中氮、低盐正常氮三种盐氮复合处理,比较不同处理间土壤 N₂O 排放通量的变化差异,以确定野大麦内生真菌共生体对土壤 N₂O 排放的影响。结果显示:在三种盐氮组合中,E+野大麦土壤中的 N₂O 排放通量均显著低于 E-处理($P<0.05$);随时间推移,各组合土壤 N₂O 的排放量呈逐渐上升趋势。从盐氮梯度来看,N₂O 排放整体随盐度升高和氮水平降低而下降。其中,高盐低氮处理下,E-野大麦土壤的 N₂O 通量降低,且低于正常氮和中氮处理。而 E+野大麦在不同盐氮处理间土壤的 N₂O 通量无显著差异。综上,利用野大麦-内生真菌共生体进行盐渍土壤生态修复,并结合合理的氮肥管理策略,可有效抑制 N₂O 排放、降低氮素损失,从而改善土壤肥力与养分可持续性。

关键词:野大麦;禾草内生真菌;盐胁迫;N₂O 排放

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作者简介:康莹,女,甘肃定西人,硕士研究生,主要从事禾草内生真菌共生体研究,E-mail: kangx2024@lzu.edu.cn; * 通信作者 Author for correspondence, E-mail: chenchenjiang@lzu.edu.cn

切根和施肥对退化羊草割草地植物群落与土壤碳氮的影响

李 颖¹, 俞天琦¹, 侍梦圆¹, 刘方林², 贺森雅¹, 邴 丽¹, 高肖甜¹, 辛晓平¹, 闫瑞瑞^{1*}
(1. 中国农业科学院农业资源与农业区划研究所, 北京 100081; 2. 新疆农业大学草业学院, 新疆 乌鲁木齐 830052)

摘要:为了研究施肥和切根对退化天然割草地的影响,结合野外试验与室内实验分析,以内蒙古呼伦贝尔退化羊草割草地为研究对象,通过设置不同处理:对照(CK)、切根+颗粒有机肥 60 kg(QK60)、切根 3 次+颗粒有机肥 60 kg(Q3K60),分析不同处理下土壤 0~15 cm 和 15~30 cm 的土壤的碳(C)、氮(N)和微生物生物量碳(MBC)、微生物生物量氮(MBN)的变化,以及土壤碳、氮和 MBC、MBN 间的关系,探究施肥和切根对退化羊草割草地植物群落特征、土壤碳氮及微生物碳氮的影响及变化规律。结果表明:“切根+施肥”显著改善群落结构,其中 QK60 处理地上生物量、群落高度和密度提升最明显。该措施有效改善表层土壤理化性质和水分状况,促进 SOC 和 TN 积累以及深层 C:N 升高。植被特征与 SOC, TN, MBC, MBN 显著正相关,与 BD 负相关,表层相关性最强。总体而言, QK60 处理综合效益最佳,表层土壤在植被恢复和生产力形成中发挥关键作用。

关键词:羊草割草地; 植被; 土壤碳氮; 微生物量碳氮

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Flexible Regulation of Photosynthesis to Low Temperature in Alfalfa Contributed to Spring Rejuvenation

ZHANG Zheng^{1,2,3}, LIU Mei-jun^{1,2,3*}, YAN An^{1,2,3}, WANG Yu-xiang^{1,2,3},
YU Miao^{1,2,3}, ZHAO Wen-jing^{1,2,3}

(1. College of Grassland Science, Xinjiang Agricultural University Urumqi, Xingjiang 830052; 2. Key Laboratory of Grassland Resources and Ecology of Western Arid Region, Ministry of Education Urumqi, Xingjiang 830052; 3. Xinjiang Key Laboratory of Grassland Resources and Ecology, Urumqi, Xingjiang 830052, China)

Abstract: Alfalfa (*Medicago sativa* L.) often suffers from low temperature during spring rejuvenation. Photosynthetic cold resistance, which is associated with fall dormancy (FD), is crucial for successful rejuvenation. Different dormancy levels of alfalfa (‘Xinmu No. 4’, FD=3 and ‘Ganong No. 5’, FD=8) were investigated to study the contribution of photosynthesis to spring rejuvenation of alfalfa, and elucidate the relationship between FD level and cold resistance. The results showed that photosynthesis was significantly inhibited during rejuvenation compared to the post-rejuvenation period, as evidenced by damaged chloroplast ultrastructure, reduced Calvin cycle enzyme activity, and photoinhibition in both PSI and PSII. These changes negatively affected yield and nutritive value. But cold-induced damage was lighter in low FD alfalfa during rejuvenation. The yield and nutritive value of the first crop were higher in low FD alfalfa. In low FD alfalfa during the rejuvenation, more stable photosynthesis was indicated by the higher stomatal opening, Rubisco activity, Rubisco activating enzyme activity, and net photosynthetic rate, as well as more stable chloroplast ultrastructure. Moreover, ETR(I) and ETR(II) were decreased, while the expression of Lhcb2 and D1 proteins were reduced, NPQ and Y(NO) were up-regulated, which indicated electron transfer from PSII to PSI was decreased. Y(ND) and CEF were up-regulated, and the expression of Lhca1 protein was reduced which would reduce the accumulation of excess electrons in PSI. The reduced electron flow from PSII to PSI and increased energy dissipation on the donor side of PSI, as well as a relatively efficient Calvin cycle alleviated PSI photoinhibition. In a word, stable chloroplast ultrastructure, light PSI photoinhibition and relatively efficient Calvin cycle were contributed to cold resistance of photosynthesis in low FD alfalfa during spring rejuvenation.

Key words: Photosynthesis; Fall dormancy; Cold resistance; Alfalfa; Spring rejuvenation

木聚糖酶与植物乳杆菌对茶树修剪枝青贮饲料发酵品质、细菌群落及抗氧化性的影响

孔令钿¹, 张文锐¹, 张 庆^{2*}

(1. 华南农业大学林学与风景园林学院, 广东 广州 510642; 2. 青岛农业大学草业学院, 山东 青岛 266109)

摘要: 茶树修剪枝作为茶园生产的重要副产物, 富含能显著提高抗氧化活性的多酚类物质, 然而其日常利用率低且常被废弃, 造成资源浪费。值得关注的是, 目前关于通过添加外源酶与益生菌调控茶树修剪枝青贮过程中发酵特性及细菌群落演替的研究尚未系统开展。为此, 本研究创新性引入木霉木聚糖酶($200\text{ U} \cdot \text{g}^{-1}$, A)、乳酸菌($1 \times 10^5\text{ CFU} \cdot \text{g}^{-1}$, B)及其复合制剂($150\text{ U} \cdot \text{g}^{-1}$ 木聚糖酶 + $7.5 \times 10^5\text{ CFU} \cdot \text{g}^{-1}$ 植物乳杆菌, AB), 系统探究上述处理对黄枝香单枞(HZ)与红柄单枞(HB)茶树修剪枝青贮过程的动态发酵品质演变、微生物群落演替规律、营养成分转化效率及抗氧化能力动态变化。将新鲜切碎的 HZ 与 HB 茶树修剪枝分别设对照组及 A、B、AB 处理组, 于青贮 3、7、14、30 d 动态取样分析。结果显示: 相较于对照组, B 与 AB 处理组在 30 d 时 pH 值均显著降至 4.5 以下, A 组亦降至 4.75 以下; 尤为关键的是, B 和 AB 组同步实现乳酸产量显著提升($P < 0.05$), 且乳酸杆菌与芽孢杆菌相对丰度显著占优。进一步发现, 两处理组在青贮 30 d 后抗氧化能力(DPPH/FRAP)及黄酮含量均显著增强, 表明其同步优化了发酵与抗氧化体系。然而, 长期青贮稳定性呈现原料依赖性差异: HZ 凭借持续低 pH 值环境与稳定的微生物群落, 发酵品质整体优于 HB; 尽管 HB 在后期表现出更高乳酸积累量, 但其菌群多样性指数显著上升($P < 0.05$), 反而加剧了腐败菌增殖风险。

关键词: 木聚糖酶; 乳酸菌; 青贮品质; 抗氧化活性

Effects of Xylanase and Lactobacillus Plantarum on Fermentation Quality, Bacterial Community, and Antioxidant Activity of Silage from Pruned Tea Branches

KONG Ling-dian¹, ZHANG Wen-rui¹, ZHANG Qing^{2*}

(1. College of Forestry and Landscape Architecture, South China Agricultural University, Guangzhou, Guangdong Province 510642, China;

2. Qingdao Agricultural University, Qingdao, Shandong Province 266109, China)

Abstract: As an important by-product of tea production, pruned tea branches are rich in polyphenols, which possess significant antioxidant activity. However, they are underutilized and often discarded, leading to resource waste. It is noteworthy that systematic studies on regulating the fermentation characteristics and bacterial community succession during the ensiling of pruned tea branches through the addition of exogenous enzymes and probiotics are still lacking. To address this, our study innovatively introduced *Trichoderma* xylanase ($200\text{ U} \cdot \text{g}^{-1}$, Treatment A), lactic acid bacteria (LAB, $1 \times 10^5\text{ CFU} \cdot \text{g}^{-1}$, Treatment B), and a composite additive ($150\text{ U} \cdot \text{g}^{-1}$ xylanase + $7.5 \times 10^5\text{ CFU} \cdot \text{g}^{-1}$ *Lactiplantibacillus plantarum*, Treatment AB). We systematically investigated the effects of these treatments on the dynamic changes in fermentation quality, microbial community succession, nutrient conversion efficiency, and antioxidant capacity during the ensiling of pruned branches from two tea cultivars: Huangzhi Xiang Dancong (HZ) and Hongbing Dancong (HB). Freshly chopped pruned branches of HZ and HB were separately assigned to a control group and treatment groups (A, B, AB). Dynamic sampling and analyses were performed on days 3, 7, 14, and 30 of ensiling. The results demonstrated that, compared to the control, the pH values in treatments B and AB significantly decreased to below 4.5 by day 30, while treatment A also reduced the pH to below 4.75. Crucially, treatments B and AB achieved a simultaneous significant increase in lactic acid production ($P < 0.05$), with a marked dominance in the relative abundance of *Lactobacillus* and *Bacillus*. Furthermore, after 30 days of ensiling, both treatments B and AB showed significantly enhanced antioxidant capacity (as assessed by DPPH and FRAP assays) and increased flavonoid content, indicating a concurrent optimization of the fermentation and antioxidant systems. However, long-term ensiling stability exhibited dependence on the raw material: HZ displayed overall superior fermentation quality, which was attributed to its consistently low pH and stable microbial community. Although HB accumulated higher lactic acid in the later stage, its bacterial diversity index increased significantly ($P < 0.05$), thereby heightening the risk of spoilage bacteria proliferation.

Key words: Xylanase; Lactic acid bacteria; Ensiling quality; Antioxidant activity

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作者简介: 李庆玺(1999-), 男, 汉族, 云南曲靖人, 硕士研究生, 主要从事牧草资源及育种研究, E-mail: Overricenoodle@163.com; * 通信作者

Author for correspondence, E-mail: xfmaxiangli@126.com

封育对温性荒漠草地土壤团聚体养分及其化学计量特征的影响

雷雅欣¹, 董乙强^{1,2,3*}, 刘兴义⁴, 姜安静¹, 吴悦¹, 柳泽宇¹, 单兴芸¹, 吴凯¹, 杨春莹¹, 赵久洪¹

(1. 新疆农业大学草业学院, 新疆 乌鲁木齐 830052; 2. 新疆草地资源与生态自治区重点实验室, 新疆 乌鲁木齐 830052; 3. 西部干旱区草地资源与生态教育部重点实验室, 新疆 乌鲁木齐 830052; 4. 新疆博乐市草原工作站, 新疆 博乐 833400)

摘要:为探究封育对温性荒漠草地土壤团聚体养分及其化学计量特征的影响,本研究选取位于天山北坡中段的呼图壁县和玛纳斯县温性荒漠草地作为研究区域,基于湿筛法测定 0~10 cm 土层土壤团聚体,并通过对围栏内外草地植物群落特征,不同粒径团聚体内土壤养分及化学计量特征等指标的测定分析,揭示土壤团聚体及植物 α 多样性对土壤有机碳的影响及其潜在调控路径。结果表明:(1)封育后荒漠草地植物群落高度、盖度和生物量分别显著增加 188.90%~445.90%, 56.19%~137.37% 和 86.92%~351.35% ($P<0.05$);(2)封育后呼图壁县荒漠草地植物物种多样性 Simpson 指数显著增加 43.90%, Patrick 指数、Shannon-Wiener 指数分别显著降低 53.40%, 45.22% ($P<0.05$);(3)封育后玛纳斯县团聚体粒径 >2 mm 土壤有机碳(SOC)和全氮(TN)含量分别显著增加 20.67%, 15.05% ($P<0.05$), 无论封育与否, SOC 含量均在大团聚体(>2 mm)中最高;(4)通过 RDA 冗余分析和最小偏二乘模型分析发现,不同粒径团聚体中 C/P、N/P 与 SOC 和 TN 均表现出较强的正相关性,且 C/P 和 N/P 均正向影响土壤有机碳,并解释有机碳变异的 93%。综上,本研究揭示了封育对温性荒漠草地土壤团聚体养分及其化学计量特征在碳固存中的关键调控作用,这对制定基于土壤团聚体养分调控的生态恢复管理策略具有重要实践价值。

关键词:封育;土壤团聚体;碳氮磷含量;化学计量特征;温性荒漠草地

Effects of Enclosure on Soil Aggregate Nutrients and Stoichiometric Characteristics in Temperate Desert Grassland

LEI Ya-xin¹, DONG Yi-qiang^{1,2,3*}, LIU Xing-yi⁴, JIANG An-jing¹, WU Yue¹, LIU Ze-yu¹, SHAN Xing-yun¹, WU Kai¹, YANG Chun-ying¹, ZHOA Jiu-qi¹

Abstract: To investigate the effects of enclosure on soil aggregate nutrients and their chemical characteristics in temperate desert grasslands, this study selected temperate desert grasslands in Hutuo County and Manas County, located in the middle section of the northern slope of the Tianshan Mountains, as the study area, soil aggregates in the 0-10 cm soil layer were determined using the wet sieve method, by measuring and analyzing indicators such as the characteristics of grassland plant communities inside and outside the fence, soil nutrients and chemical composition characteristics in aggregates of different particle sizes, etc., we reveal the impact of soil aggregates and plant α diversity on soil organic carbon and their potential regulatory pathways. The results showed that: 1) Following enclosure, the height, cover, and biomass of desert grassland plant communities increased significantly by 188.90%-445.90%, 56.19%-137.37%, and 86.92%-351.35%, respectively ($P<0.05$); 2) After enclosure, the Simpson index of plant species diversity in the desert grasslands of Hutuo County increased significantly by 43.90%, while the Patrick index and Shannon-Wiener index decreased significantly by 53.40% and 45.22%, respectively ($P<0.05$); 3) After enclosure, the content of soil organic carbon (SOC) and total nitrogen (TN) in soil aggregates with particle sizes >2 mm in Manas County significantly increased by 20.67% and 15.05%, respectively ($P<0.05$). Regardless of enclosure, SOC content was highest in large aggregates (>2 mm); 4) Through RDA redundancy analysis and least squares model analysis, it was found that C/P, N/P, SOC, and TN all showed strong positive correlations in agglomerates of different particle sizes. C/P and N/P both had a positive effect on soil organic carbon and explained 93% of the variation in soil organic carbon. In summary, this study confirms that enclosure plays a key regulatory role in the nutrient content and chemical characteristics of soil aggregates in warm desert grasslands in terms of carbon sequestration, this has important practical value for the formulation of ecological restoration management strategies based on the regulation of soil aggregate nutrients.

Key words: Grazing exclusion; Soil aggregate; Carbon, nitrogen, and phosphorus conten; Stoichiometric characteristics; Temperate desert meadows

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作者简介: 雷雅欣(1999-), 女, 汉族, 新疆塔城人, 硕士研究生, E-mail: 1311005053@qq.com; * 通信作者 Author for correspondence, E-mail: xjdyq1210@163.com

不同新麦草种质叶片氨基酸组成及营养价值评价

李博华¹, 云 岚^{1,2*}, 穆乙鑫¹, 周成美¹, 艾 芊¹, 李 珍¹, 何雨航¹

(1. 内蒙古农业大学草业学院, 内蒙古 呼和浩特 010010; 2. 草地资源教育部重点实验室, 内蒙古 呼和浩特 010010)

摘要:为系统评价新麦草(*Psathyrostachys juncea*)叶片蛋白质的营养价值,以前期筛选出的高粗蛋白(Crude protein, CP)和低 CP 含量两组新麦草种质为材料,测定其 18 种氨基酸含量,计算必需氨基酸比值(RAA)、比值系数分(SRC)、必需氨基酸指数(EAAI)等参数,并与 FAO/WHO 氨基酸模式谱进行比较。结果表明:高 CP 组氨基酸总量和必需氨基酸含量均显著高于低 CP 组($P<0.05$)。两组材料均含全部 8 种必需氨基酸,药效氨基酸种类达 10 种,总含量超过 65%。与 FAO/WHO 模式相比,除 Lys 和 Met+Cys 外,其余必需氨基酸含量均接近或超过标准。Met+Cys 为第一限制性氨基酸。高 CP 组 SRC 值(47.17~57.37)和 EAAI 均值(约 1.01)优于低 CP 组(SRC: 35.31~43.47;EAAI:约 1.19)。新麦草叶片氨基酸组成合理、营养均衡,是具有开发潜力的优质蛋白饲草资源。

关键词:新麦草;氨基酸组成;FAO/WHO 模式;必需氨基酸指数;营养价值

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作者简介:李博华(2000-),男,汉族,黑龙江哈尔滨人,博士研究生,主要从事牧草种质资源与育种研究, E-mail: libohua@emails.imau.edu.cn; * 通信作者 Author for correspondence, E-mail: yunlan@imau.edu.cn

长穗偃麦草芽期耐盐性全基因组关联分析

许子健^{1#}, 李 薇^{1,2#}, 李轩照^{1#}, 肖 强¹, 贺 飞¹, 郑 琪¹, 李振声¹, 李宏伟^{1*}

(1. 中国科学院遗传与发育生物学研究所, 北京 100020; 2. 长江大学农学院, 湖北 荆州 434020)

摘要:长穗偃麦草(*Thinopyrum ponticum* = *Elytrigia elongata*, $2n=10x=70$, 也称高冰草、长穗冰草或长穗薄冰草)是禾本科小麦族偃麦草属的一种多年生冷季型饲草。长期以来,长穗偃麦草被认为具有突出的耐盐性,但其耐盐性遗传位点尚不明确。本研究旨在通过全基因组关联分析,挖掘调控长穗偃麦草耐盐性的关键遗传位点及候选基因。本研究以一个包含 200 余份长穗偃麦草无性系的 TWG 群体为研究材料,采用二代转录组测序数据,以中间偃麦草(*Th. intermedium*, $2n=6x=42$)基因组序列作为参考检测序列变异。在群体层面以缺失率 $<1\%$,质量值 >30 ,且仅存在 1 个等位变异作为筛选条件,共得到 1,780,705 个 SNP, 217,636 个 INDEL。参考基因组中每 100 kb 平均有 154.6 个 SNP 和 18.9 个 INDEL。基于 SNP 聚类分析, TWG 群体可分为三个亚群。采用 250 mM NaCl 溶液模拟盐胁迫,以去离子水处理作为对照进行芽期耐盐鉴定。结果显示:盐胁迫显著降低了长穗偃麦草种子萌发率。处理 12 天时,萌发抑制率平均为 88.3%、抑制率最大值 100%、最小值 52.8%、中位数值为 89.9%。处理 15 天时,种子萌发抑制率平均为 77.6%、种子萌发抑制率最大值为 100%、种子萌发抑制率最小值为 11.8%、抑制率中位数值为 79.8%。采用全基因组关联分析在第五同源群上检测到 3 个与芽期耐盐性显著关联的 SNP 峰值。其中,在 V05 染色体上的 1 号位点检测到了乌拉尔图小麦 SRSF 蛋白激酶 1 类似物(SRSF protein kinase 1-like)的同源基因,该基因具有 RNA 剪接活性,其中位于蛋白编码区的一个 SNP 导致一个丝氨酸(S)突变为丙氨酸(A)。具有该突变的系在盐胁迫 12-15 天种子萌发抑制率显著降低(5%~10%),该 SNP 可解释表型变异的 15.69%。在 V05 染色体上 2 号位点检测到一个与离子转运相关的 SPIRRIG-Like 蛋白。已有研究表明该蛋白与植物耐盐性相关,SNP 变异可解释表型变异的 20.05%。下一步将继续对这两个耐盐候选基因进行遗传效应验证、分子标记开发和功能研究。

关键词:长穗偃麦草;耐盐性;全基因组关联分析;SNP;候选基因

不同水分条件对冰草生物量及其地上地下权衡的影响

李金梅

(内蒙古农业大学, 内蒙古 呼和浩特 010020)

摘要:通过盆栽试验设置 5 个水分梯度(土壤最大持水量的 60%, 40%, 20%, 10%, 5%)研究蒙古冰草生物量分配特征,结果表明:60%水分处理时地上(株高 37 cm、叶面积 5.2 cm²)和地下生物量(总根长 600 cm)均最优;40%~20%处理时地上生物量下降较地下显著;10%~5%处理时根冠比显著升高(鲜重 1.4, 干重 0.8),显示水分充足时均衡发展,中度干旱优先充足时均衡发展,中度干旱优先维持根系功能,极端干旱时资源向根系显著倾斜,揭示了蒙古冰草通过动态调整生物量分配适应水分胁迫的机制,为干旱区草原管理提供理论依据。

关键词:蒙古冰草;水分处理;地上生物量;地下生物量;生物量权衡

The Effects of Different Moisture Conditions on Agropyron Productivity and Its Trade-offs

LI Jin-mei

(Inner Mongolia Agricultural University, Hohhot, Inner Mongolia 010020, China)

Abstract: A pot experiment with five water gradients (60%, 40%, 20%, 10%, and 5% of soil maximum water holding capacity) was conducted to investigate biomass allocation characteristics in *Leymus chinensis*. The results demonstrated that both aboveground (plant height 37 cm, leaf area 5.2 cm²) and below-ground biomass (total root length 600 cm) reached optimal levels under 60% water treatment. Under moderate drought (40%-20% treatments), aboveground biomass declined more significantly than below-ground biomass. Under severe drought (10%-5% treatments), root-to-shoot ratio increased markedly (fresh weight 1.4, dry weight 0.8), indicating balanced growth under adequate water supply, prioritized maintenance of root function during moderate drought, and significant resource reallocation to roots under extreme drought. These findings reveal the adaptive mechanism of *L. chinensis* through dynamic biomass allocation in response to water stress, providing a theoretical basis for grassland management in arid regions.

Key words: *Agropyron mongolicum*; Moisture treatment; Aboveground biomass; Underground biomass; Biomass Trade-offs

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作者简介:李庆玺(1999-),男,汉族,云南曲靖人,硕士研究生,主要从事牧草资源及育种研究,E-mail:Overricenoodle@163.com; * 通信作者

Author for correspondence, E-mail: xfmaxiangli@126.com

数字素养赋能牧民生计韧性提升的机制研究

——基于新疆牧区的微观实证分析

李先东^{1*}, 张凌菲¹, 秦增洋²

(1. 新疆农业大学经济管理学院, 新疆 乌鲁木齐 830052; 2. 南京农业大学经济管理学院, 江苏 南京 210095)

摘要:揭示数字素养对牧民生计韧性的影响效应,对于更好地推进牧区可持续发展具有重要的理论和现实意义。本研究以新疆4市6县384份牧民微观调研数据为基础,基于可持续发展理论,从自组织能力、缓冲能力和学习能力三个维度构建牧民生计韧性的指标体系,采用熵值法、最小二乘法(OLS)和工具变量法,剖析数字素养对牧民生计韧性的影响及其作用机制。研究表明,数字素养对牧民生计韧性具有显著的正向作用,尤其是数字资源获取素养、数字技术应用素养和数字金融素养维度对生计韧性产生显著正向影响。异质性分析表明,与女性、低收入牧民相比,数字素养对男性、高收入牧民生计韧性具有更大的增强效应。机制分析表明,数字素养可以通过提升生计多样性、推动牧民参与草原确权来提高牧民生计韧性。因此,研究建议加强农村数字素养培训力度,提升牧民数字素养,实现牧民多元化生计发展。与此同时,深化新疆牧区草原确权制度改革,精准划定权属界限并建立数字化管理系统,强化数字素养在草原管理中的作用以提升牧民生计韧性。

关键词:数字素养;生计韧性;牧民;生计多样性;草原确权

Digital Literacy Empowers Improvement of Herdsmen's Livelihood Resilience: Micro Empirical Evidence from Pastoral Areas in Xinjiang

LI Xian-dong^{1*}, ZHANG Ling-fei¹, QIN Zeng-yang²

(1. College of Economics and Management, Xinjiang Agricultural University, Urumqi, Xinjiang 830052, China;

2. College of Economics and Management, Nanjing Agricultural University, Nanjing, Jiangsu Province 210095, China)

Abstract: Revealing the impact effect of digital literacy on herdsmen's livelihood resilience holds important theoretical and practical significance for better promoting the sustainable development of pastoral areas. This study is based on micro survey data of 384 herdsmen from 6 counties in 4 cities of Xinjiang. Guided by sustainable development theory, it constructs an index system for herdsmen's livelihood resilience. The system is built from three dimensions: self-organization capacity, buffering capacity, and learning capacity. The entropy method, ordinary least squares (OLS) and instrumental variable method are used to analyze the impact and mechanism of digital literacy on herdsmen's livelihood resilience. Results demonstrate that digital literacy has a significant positive effect on herdsmen's livelihood resilience. Specifically, the dimensions of digital resource access literacy, digital technology application literacy, and digital financial literacy have significant positive impacts on livelihood resilience. Heterogeneity analysis indicates that compared with female and low-income herdsmen, digital literacy has a greater enhancing effect on the livelihood resilience of male and high-income herdsmen. Mechanism analysis shows that digital literacy can enhance herdsmen's livelihood resilience. It achieves this by improving livelihood diversity. It also does so by promoting herdsmen's participation in rangeland property rights confirmation. Therefore, this study suggests strengthening rural digital literacy training to enhance herders' digital literacy and facilitate diversified livelihood development. Meanwhile, it is recommended to deepen the reform of pastureland tenure system in Xinjiang's pastoral areas, precisely demarcate property boundaries, and establish a digital management system. These measures aim to strengthen the role of digital literacy in pastureland management, thereby enhancing herders' livelihood resilience.

Key words: Digital literacy; Livelihood resilience; Herdsmen; Livelihood diversification; Confirmation of rangeland rights

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作者简介:李先东(1988-),男,安徽阜南人,博士,副教授,主要从事农业经济管理研究

长期氮磷钾添加对温性草甸草原植物群落特征及物种多样性的影响

刘方林¹, 李颖², 俞天琦², 侍梦圆², 贺森雅², 高肖甜², 杨合龙¹, 闫瑞瑞^{2*}

(1. 新疆农业大学草业学院, 新疆 乌鲁木齐 830052; 2. 北方干旱半干旱耕地高效利用全国重点实验室/中国农业科学院农业资源与农业区划研究所, 北京 100081)

摘要:探究长期氮(N)、磷(P)、钾(K)添加对温性草甸草原植物群落结构及物种多样性的影响,为退化草地生态修复与可持续管理提供科学依据。在内蒙古呼伦贝尔中度退化草甸草原设立长期定位试验(2014—2024年),采用“3414”正交设计,3因素、4水平、14处理,测定不同施肥处理下植物群落重要值、生物量、高度、盖度、密度及 α 多样性指数(Shannon-Wiener、Simpson、Pielou、Margalef),结合方差分析与功能群相关性解析群落响应机制。优势种羊草重要值在高氮处理($N_5P_2K_2$)达峰值(0.80),但物种多样性显著降低($P<0.05$);均衡施肥($N_2P_2K_2$)维持羊草重要值(0.61)及多物种共存。氮缺乏使生物量($60\text{ g}\cdot\text{m}^{-2}$)仅为均衡施肥($130\text{ g}\cdot\text{m}^{-2}$)的46%,磷、钾缺乏分别减产23%和54%,过量施肥导致减产。均衡施肥下多样性指数最高,与无肥群落无显著差异,而高氮使Shannon指数降低16.7%($P<0.05$)。功能群分析显示禾本科与菊科呈负相关($r=-0.49$),高氮驱动禾本科单极扩张(相对丰度40%)并压缩菊科生态位。研究结果分析表明,氮磷钾均衡配施($N\ 183\text{ kg}\cdot\text{hm}^{-2}$, $P\ 350\text{ kg}\cdot\text{hm}^{-2}$, $K\ 57\text{ kg}\cdot\text{hm}^{-2}$)可协同提升生产力与多样性,符合退化草地修复的原则。

关键词:温性草甸草原;氮磷钾添加;群落特征;物种多样性

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作者简介:刘方林(1999-),男,汉族,安徽淮北人,硕士研究生,主要从事草地资源生态与管理研究, E-mail: liufanglin-Arden@outlook.com;

* 通信作者 Author for correspondence, E-mail: yanruirui@caas.cn

火烧调控青藏高原高寒草甸叶部病原真菌与群落结构的作用机制

刘佳奇^{1,2}, 薛龙海^{2*}, 李春杰^{1,2*}

(1. 国家林业和草原局/中国林业科学研究院生态保护与修复研究所/草原中心, 北京 100091;

2. 兰州大学草种创新与草地农业生态系统全国重点实验室/草地农业科技学院/草地微生物研究中心, 甘肃 兰州 730020)

摘要:火烧作为一种重要的生态管理手段,近年来在维持草地生态系统健康和调控植物-病原相互作用方面受到越来越多的关注。然而,对于高寒草甸中火烧对病害动态及群落结构的影响,尤其是其在焚烧-未焚烧边界距离梯度上的作用机制,仍缺乏深入研究。为了探究火烧对我国青藏高原高寒草甸病害动态及群落结构和多样性的调节作用,本研究在2023—2024年于青藏高原东南部典型天然高寒草甸开展了野外试验,并进行连续两年的焚烧和田间调查。结果表明:人工控制火烧能够显著降低植物叶部真菌病原载荷,并且在焚烧区中心抑制效应最强,随着接近焚烧-未焚烧边界而逐渐减弱。同时,我们发现植物功能群组成的变化构成了一条间接途径:焚烧后禾本科盖度下降,而杂类草盖度上升,从而间接降低了叶部真菌病原负荷。本研究结果强调了控制火烧在减轻植物病害、维持群落多样性和增强生态系统在全球环境变化背景下的韧性方面的重要意义。

关键词:高寒草甸;火烧;叶斑病;叶部病原真菌;群落结构

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作者简介:刘佳奇,硕士研究生,主要从事生态学及草原植物病害多样性的研究, E-mail: liujiaqi17361645169@126.com; * 通信作者 Author for correspondence, E-mail: xuelonghai@lzu.edu.cn; chunjie@lzu.edu.cn

基于结缕草全基因组开发 SSR 标记及其在品种鉴定和 DNA 分子身份证构建中的应用

刘梦娇, 孙道金, 郝东利, 陈静波, 孔维一*, 郭海林*

(江苏省植物资源保护与利用重点实验室/江苏省中国科学院植物研究所/南京中山植物园, 江苏 南京 210014)

摘要:结缕草属(*Zoysia* Willd.)是禾本科多年生草本植物,作为优良的暖季型草坪草,具有较强的耐盐、耐旱等非生物胁迫能力。然而,由于缺乏特异性分子标记,结缕草属物种的鉴定仍存在困难。本研究基于已公布的 *Zoysia japonica* ‘Nagirizaki’基因组序列,共检测到 18981 个 SSR 位点。根据二核苷酸、三核苷酸、四核苷酸、五核苷酸和六核苷酸等标准重复单元设计 SSR 引物,引物重复次数不低于 5 次,扩增片段大小范围为 150~280 bp。从中筛选出 400 对 SSR 引物,利用 6 份结缕草种质资源检测其多态性,其中 179 对引物扩增出多态性条带,多态率为 44.75%。进一步筛选出 39 对多态性丰富的 SSR 引物用于遗传多样性研究,结果显示,36 份供试材料的扩增条带多态信息含量(PIC)为 0.099~0.866,平均值为 0.656。在此基础上,发现 10 对引物可构建 36 份结缕草品种的 DNA 分子身份证,并能根据扩增条带大小实现品种间的有效区分。本研究开发的 SSR 标记有助于未来结缕草遗传多样性分析、品种鉴定及分子标记辅助育种研究,具有良好的应用前景。

关键词:结缕草;SSR 标记;遗传多样性分析;DNA 分子身份证

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作者简介:刘梦娇(1999-),女,汉族,山东菏泽人,硕士研究生,主要从事草坪分子标记开发和耐盐基因挖掘研究工作, E-mail: mengjia-oliu0505@163.com; * 通信作者 Author for correspondence, E-mail: weiyi_kong02@126.com; ghlnmg@sina.com

植物乳杆菌与布氏乳杆菌对脆秆水稻秸秆青贮品质、微生物多样性的影响

刘毅童, 程 箫, 任春环, 张子军, 黄桢锋*

(安徽农业大学动物科技学院, 安徽 合肥 230031)

摘要:青贮饲料是反刍动物重要的营养来源,其品质直接影响畜牧业的可持续发展。脆秆水稻秸秆因其高纤维含量,青贮过程中易受腐败微生物侵染,导致发酵品质低下。目前研究多聚焦于乳酸菌添加剂对青贮饲料营养成分和发酵指标的调控,但对微生物群落动态变化及其代谢物的解析仍不够深入。本研究以脆秆水稻秸秆为对象,系统探究植物乳杆菌单菌及植物乳杆菌与布氏乳杆菌混合菌剂对青贮过程中营养成分、发酵特性、体外消化率及微生物多样性的影响,并通过代谢组学揭示其调控机制。通过分析青贮微生物群落的演替规律与关键代谢通路,评估不同乳酸菌制剂的协同效应,旨在阐明其对青贮品质提升的作用机理。本研究将为优化脆秆水稻秸秆青贮工艺提供理论依据,同时为开发高效乳酸菌复合制剂、促进农业副产物资源化利用提供新的技术路径。

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作者简介:刘毅童(1999-),女,山东淄博人, E-mail: 2541473802@qq.com; * 通信作者 Author for correspondence, E-mail: huangyafeng316@163.com

箭筈豌豆对绵羊甲烷排放、瘤胃发酵的影响

刘毅童, 程 箫, 任春环, 张子军, 黄桢锋*

(安徽农业大学动物科技学院, 安徽 合肥 230031)

摘要:箭筈豌豆(*Vicia sativa*)为豆科野豌豆属一年生草料兼用作物,具有产量高、营养品质优良、适口性好等特点,刈割后可晾晒成高品质干草以饲喂家畜。本研究以“牧草-生长性能-甲烷排放-组学分析”为主线,以4月龄黄淮肉羊公羊为供试家畜,饲喂苜蓿干草(40%添加,AR)为对照组,箭筈豌豆苜蓿干草混合组(50%替代AR,CAR)、箭筈豌豆干草(100%替代AR,CR)为试验组,比较绵羊生长性能、血液免疫指标、甲烷(CH₄)排放、瘤胃发酵等指标。

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作者简介:刘毅童(1999-),女,汉族,山东淄博人,E-mail:2541473802@qq.com; * 通信作者 Author for correspondence, E-mail: huan-gyafeng316@163.com

融合机器学习特征选择技术的冬黑麦栽培优化与产量预测

吕林有^{1,2*}, 李佳慧¹, 赵 艳^{1,2}, 张 蕊¹

(1. 辽宁工程技术大学, 辽宁 阜新 123000; 2. 辽宁省沙地治理与利用研究所, 辽宁 阜新 123000)

摘要:冬黑麦作为高寒地区重要的粮饲作物,其产量精准预测与栽培优化对保障粮食安全具有重要意义。针对传统模型难以解析行距-播种密度互作非线性效应的问题。构建了融合递归梯度融合的随机森林(RF-RFE)冬黑麦产量预测模型。田间试验表明,适中行距和600 g 播种密度能够实现了冬黑麦高产稳产的协同调控;产量预测模型筛选行距-播种量、穗重对数变换等8个关键特征,以及较好的模型评估参数,验证表明模型泛化能力强,具有较好的鲁棒性同时表现出优异的预测性能。本研究建立的智能决策体系,为寒区冬黑麦精准栽培提供了兼具理论深度与实践指导价值的技术方案。

关键词:冬黑麦;随机森林;递归梯度融合;产量预测

Optimization of Winter Rye Cultivation and Yield Prediction by Integrating Machine Learning Feature Selection Techniques

LYU Lin-you^{1,2*}, LI Jia-hui¹, ZHAO Yan^{1,2}, ZHANG Rui¹

(1. Liaoning Technical University, Fuxin, Liaoning Province 123000, China;

2. Liaoning Research Institute of Sand Control and Utilization, Fuxin, Liaoning Province 123000, China)

Abstract: As an important grain and forage crop in cold regions, winter rye plays a significant role in ensuring food security, making accurate yield prediction and cultivation optimization crucial. To address the challenge of traditional models in analyzing the nonlinear interaction effect of row spacing and seeding density, a random forest (RF-RFE) winter rye yield prediction model integrating recursive gradient fusion was developed. Field experiments demonstrated that a moderate row spacing combined with a 600 g seeding density effectively achieved synergistic regulation for high and stable winter rye yields. The yield prediction model selected eight key features, including row spacing-seeding rate and logarithmic transformation of spike weight, along with superior model evaluation parameters. Verification results indicated the model's strong generalization ability, good robustness, and excellent predictive performance. The intelligent decision-making system developed in this study offers a technical solution with significant theoretical depth and practical guidance for the precision cultivation of winter rye in cold regions.

Key words: Winter rye; Random forest; Recursive gradient boosting; Yield prediction

黄河源区高寒草甸退化斑块植物群落演替特征及其土壤限制因子分析

马婧娟^{1,2}, 李希来^{1,2*}, 尹通江², 柴瑜^{1,2}, 高佩^{1,2}, 李成一², 吴勇^{1,2}, 周怡志^{1,2}

(1. 青海大学省部共建三江源生态与高原农牧业国家重点实验室, 青海 西宁 810016;

2. 青海大学农牧学院, 青海 西宁 810016)

摘要:本研究以黄河源区斑块化退化高寒草甸为研究对象,选择滩地和坡地 2 种立地条件,按照裸露斑块(BP)、短期恢复斑块(SRP)、长期恢复斑块(LRP)、健康高寒草甸(HAM) 4 种不同斑块类型,通过植物群落样方调查,分析不同类型斑块在自然恢复演替过程中植物群落特征的变化规律,并探讨其与土壤理化性质之间的相关性,揭示不同类型斑块植物群落特征的差异以及关键土壤限制因子。研究结果表明,滩地和坡地植物群落多样性指数显著增加($P<0.05$),禾本科、莎草科、豆科盖度和地上生物量逐渐升高,而杂类草盖度和地上生物量显著降低($P<0.05$);滩地植物群落数量特征、多样性指数以及禾本科、莎草科、杂类草盖度和地上生物量高于坡地,而豆科盖度和地上生物量坡地高于滩地。滩地和坡地植物群落数量特征、物种多样性指数以及功能群盖度和地上生物量与土壤含水量、温度、电导率、有机碳、全氮、全磷、硝态氮、铵态氮呈正相关关系,而与 pH 值呈负相关关系。土壤有机碳、全磷、全氮、铵态氮是滩地植物群落特征的关键限制因子,土壤 pH 值、铵态氮、有机碳是坡地植物群落特征的关键限制因子。总之,斑块化退化高寒草甸的自然恢复演替促进了植物群落的正向演替,此研究结果可为斑块化退化高寒草甸生态修复提供科学依据。

关键词:立地条件;斑块化退化;高寒草甸;恢复演替;植物群落特征;土壤理化性质

Analysis of Plant Community Characteristics and their Soil Limiting Factors during the Succession of Degraded Meadow Patches in the Source Region of the Yellow River

MA Jing-juan^{1,2}, LI Xi-lai^{1,2*}, YIN Tong-jiang², CHAI Yu^{1,2}, GAO Pei^{1,2},
LI Cheng-yi², WU Yong^{1,2}, ZHOU Yi-zhi^{1,2}

(1. State Key Laboratory of Plateau Ecology and Agriculture, Qinghai University, Xining, Qinghai Province 810016, China;

2. College of Agriculture and Animal Husbandry, Qinghai University, Xining, Qinghai Province 810016, China)

Abstract: This study aims to determine succession characteristics of the plant community in the patchily degraded alpine meadow in the source region of the Yellow River, focusing on two kinds of meadows, gently rolling and sloping. All degraded patches were grouped into four types: bare patch (BP), short-term recovering patch (SRP), long-term recovering patch (LRP), and healthy alpine meadow (HAM) (as control), based on field-surveyed plant community characteristics and their changes during natural succession. The surveyed plant community characteristics were correlated with soil physical and chemical properties to determine key soil factors critical to plant community traits in different types of patches. The results showed that the diversity index of plant communities in both gently rolling and sloping meadows increased significantly ($P<0.05$) with succession. The coverage and aboveground biomass of Poaceae, Cyperaceae and Fabaceae increased gradually, while the coverage and aboveground biomass of Forbs decreased significantly ($P<0.05$) with it. The quantitative characteristics, diversity index, coverage of Poaceae, Cyperaceae, Forbs and aboveground biomass of the plant communities in the gently rolling meadow were higher than those in the sloping meadow, while the coverage of Fabaceae and aboveground biomass in the sloping meadow were higher than those in the gently rolling meadow. The quantitative characteristics, species diversity index, functional group coverage and aboveground biomass of the plant communities in both types of meadows were positively correlated with soil water content, temperature, conductivity, organic carbon, total nitrogen, total phosphorus, nitrate nitrogen and ammonium nitrogen, but negatively correlated with pH. Soil organic carbon, total phosphorus, total nitrogen and ammonium nitrogen were identified as the key soil factors critically affecting plant community characteristics in the gently rolling meadow, whereas soil pH, ammonium nitrogen and organic carbon were the key soil factors critical to plant community characteristics in the sloping meadow. In conclusion, the natural recovery of patchily degraded alpine meadow promoted the positive succession of plant communities. The results of this study can serve as the scientific foundation for the ecological restoration of patchily degraded alpine meadows.

Key words: Meadow topography; Patchy degradation; Alpine meadow; Restoration succession; Plant community characteristics; Soil properties

狗牙根 *CdWRKY113* 基因的克隆及亚细胞定位分析

马诗睿

(新疆农业大学草业学院, 新疆 乌鲁木齐 830052)

摘要: WRKY 转录因子家族, 在调控多种胁迫(如盐、干旱、病原菌等)中具有重要作用。狗牙根(*Cynodon dactylon*) 隶属禾本科狗牙根属, 是国内外较温暖地区用于建植运动场、公园绿化以及固土护坡等草坪的常用草种之一。本研究基于狗牙根基因组数据, 采用生物信息学方法对其 WRKY 基因家族成员进行鉴定, 同时基于转录组数据分析其在碱性盐胁迫下的表达模式。为探究候选基因基因功能, 利用 SnapGene 及 NCBI 设计特异性引物并利用 PCR 技术克隆基因, 利用生物信息学软件分析其蛋白质理化性质、二级结构和亚细胞定位情况等, 并使用实时荧光定量 PCR(qRT-PCR) 分析基因在狗牙根对不同非生物胁迫的响应情况, 利用农杆菌介导法将 DNA 酶切及连接构建的亚细胞定位载体导入烟草叶片进行亚细胞定位。结果显示, 狗牙根基因组中共鉴定出 129 个 WRKY 转录因子, 根据其在染色体上的位置进行命名。共线性分析表明, 片段复制主要驱动了狗牙根 *CdWRKYs* 的进化。经 qRT-PCR 分析表明, 推测 *CdWRKY113* 可能在狗牙根碱性盐胁迫耐受中具有重要作用。*CdWRKY113* 基因编码区全长 558 bp, 脂溶指数为 27.78, 理论等电点为 5.16, 平均疏水性为 0.896, 不稳定系数为 51.33, 为不稳定的亲水性蛋白, 不具备跨膜结构。系统进化树和氨基酸序列分析表明 *CdWRKY113* 与弯叶画眉草、穆等禾本科植物亲缘关系较近, 亚细胞定位结果显示其定位于细胞核中。qRT-PCR 结果表明: 干旱、盐及脱落酸(ABA) 处理均能诱导 *CdWRKY113* 基因的表达, 表明 *CdWRKY113* 基因参与狗牙根应对干旱、ABA 胁迫及低温胁迫响应。本研究为狗牙根抗逆分子育种提供了理论依据及候选基因。

关键词: 狗牙根; WRKY 转录因子; 基因克隆; 表达分析; 非生物胁迫

饲喂接种产阿魏酸酯酶乳酸菌苜蓿青贮饲料对奶山羊乳腺炎症细胞因子及基因表达的影响

毛玉青, 张艳威, 王 鹏, 李福厚*

(吉林大学动物科学学院, 吉林 长春 130062)

摘要: 本试验旨在研究饲喂接种产阿魏酸酯酶乳酸菌的苜蓿青贮饲料对奶山羊乳腺炎症细胞因子及其相关基因表达的影响。将 42 只关中奶山羊随机分为 3 组, 分别饲喂不添加菌剂(CON)、接种不产酶罗伊氏乳杆菌 YM13(YM13) 和接种产阿魏酸酯酶罗伊氏乳杆菌 A4-2(A4-2) 的苜蓿青贮饲料, 试验持续 60 天。于第 20、40、60 天采集乳样, 测定抗氧化酶、炎症因子和免疫球蛋白含量; 试验结束时取乳腺组织进行 RT-PCR 分析。结果表明, A4-2 组显著提高了乳清中 GPX 活性和总抗氧化能力(T-AOC), 降低了促炎因子 IFN- γ 和 IL-6 浓度, 提高了抗炎因子 IL-4 和 IL-10 水平。基因表达分析显示, A4-2 组显著上调了 Nrf2-ARE 通路相关抗氧化基因(如 *NFE2L2*、*GPX1*、*HMOX1* 等), 并下调了 NF- κ B 通路相关炎症基因(如 *IFNG*、*TNF*、*NOX4*)。表明饲喂产阿魏酸酯酶乳酸菌苜蓿青贮可通过激活抗氧化通路并抑制炎症反应, 改善奶山羊乳腺健康。

关键词: 阿魏酸酯酶; 苜蓿青贮; 乳腺炎症; 奶山羊; 基因表达

水磷限制条件下燕麦水磷利用效率评价

马翔宇^{1,2}, 刘家佳^{1,2}, 段博文^{1,2}, 张琮滢^{1,2}, 胡晓炜^{1,2}, 周青平^{1,2*}

(1. 西南民族大学草地资源学院, 四川 成都 610041;

2. 西南民族大学/四川若尔盖高寒湿地生态系统国家野外科学观测研究站, 四川 成都 610041)

摘要:为明确水磷胁迫对燕麦(*Avena sativa*)生长的影响,并对不同水磷利用效率的燕麦进行分类,以 14 份燕麦品种为试验材料,采用盆栽试验,设置对照(CK)、低磷胁迫(-P)、干旱胁迫(-W)和水磷复合胁迫(-W-P)处理。结果表明:地上及地上部各器官生物量在复合胁迫下均显著低于其他处理,表明水磷复合胁迫对燕麦的抑制大于单一胁迫;不同品种燕麦在水和磷利用方面存在差异,在此基础上将燕麦分为三类和四类,共同筛选出高效燕麦品种‘艾博’和低效燕麦品种‘青海甜燕麦’。

关键词:燕麦;低磷胁迫;干旱胁迫;复合胁迫

Evaluation of Water Phosphorus Use Efficiency in Oats under Water Phosphorus Limiting Conditions

MA Xiang-yu^{1,2}, LIU Jia-jia^{1,2}, DUAN Bo-wen^{1,2}, ZHANG Cong-yan^{1,2},

HU Xiao-wei^{1,2}, ZHOU Qing-ping^{1,2*}

(1. College of Grassland Resources, Southwest Minzu University, Chengdu, Sichuan Province 610041, China; 2. Sichuan Zoige Alpine Wetland Ecosystem National Observation and Research Station, Southwest Minzu University, Chengdu, Sichuan Province 610041, China)

Abstract: To clarify the effects of water-phosphorus stress on oat (*Avena sativa*) growth and classify oats with different water-phosphorus utilization efficiencies, 14 oat varieties were used as experimental materials in a pot experiment. Treatments included a control (CK), low phosphorus stress (-P), drought stress (-W), and combined water-phosphorus stress (-W-P). Results indicate that both total above-ground biomass and biomass of individual above-ground organs were significantly lower under combined stress compared to other treatments. This demonstrates that combined water-phosphorus stress exerts a greater inhibitory effect on oats than individual stresses. Varieties exhibited differences in water and phosphorus utilization, leading to the classification of oats into three and four categories. This framework facilitated the identification of the highly efficient variety ‘Abbott’ and the low-efficiency variety ‘Qinghai sweet oat’.

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作者简介:马翔宇(1999-),女,汉族,山东东营人,硕士研究生,主要从事牧草抗逆研究, E-mail: jiouyuejingzi@163.com; * 通信作者 Author for correspondence, E-mail: qingzh@aliyun.com

植物乳杆菌复合纤维素酶或芽孢杆菌调节全混合日粮发酵并降低温室气体排放量

牟立宇, 谈重芳*

(郑州大学农学院, 河南 郑州 450000)

摘要:本研究总混合日粮(TMR)精粗比为 4 : 6, 用植物乳杆菌复合枯草芽孢杆菌或纤维素酶进行发酵 60 天。结果显示:所有组在低 pH 值条件下保存效果良好, 其中添加乳酸菌与纤维素酶复合的 TMR 的 pH 值下降更快, 乳酸含量更高, 添加纤维素酶的处理组 NDF 和 ADF 含量下降更多, $\text{NH}_3\text{-N}$ 含量更低。添加添加剂的处理组在第三天的产气量均小于对照组, 其中植物乳杆菌 QZW5 组产气量最低, 所有处理组在 14 天以后产气量基本接近于 0。根据微生物多样性分析, 与温室气体产气量呈显著正相关的菌属有 *Filobasidium*, *Enterobacter* 和 *Leuconostoc*, 而与 *Levilactobacillus* 呈负相关。综上所述, 乳酸菌与纤维素酶或芽孢杆菌复合一定程度上均提高了 TMR 的发酵品质, 并且通过调节微生物和代谢物的种类及比例降低了温室气体的排放量。

关键词:全混合日粮; 植物乳杆菌; 纤维素酶; 温室气体

Lactobacillus plantarum Combined with Cellulase or *Bacillus subtilis* Regulates the Fermentation of Total Mixed Ration and Reduces Greenhouse Gas Emissions

MOU Li-yu¹, TAN Zhong-fang*

(College of Agriculture, Zhengzhou University, Zhengzhou, Henan Province 450000, China)

Abstract: In this study, the concentrate-to-roughage ratio of the TMR was 4 : 6. Fermentation was conducted using a composite of *Lactobacillus plantarum* and *Bacillus subtilis* or cellulase for 60 days. The results show that all groups demonstrated good preservation under low pH conditions. Among them, the TMR supplemented with the lactic acid bacteria-cellulase complex exhibited a faster pH decline and higher lactic acid content. The cellulase-supplemented treatment group showed greater reductions in NDF and ADF content, along with lower $\text{NH}_3\text{-N}$ levels. Gas production in all additive-treated groups was lower than the control group by day 3, with *Lactobacillus plantarum* QZW5 showing the lowest production. Gas production in all groups approached zero after 14 days. Microbial diversity analysis revealed significant positive correlations between greenhouse gas production and the genera *Filobasidium*, *Enterobacter*, and *Leuconostoc*, while a negative correlation was observed with *Levilactobacillus*. In conclusion, both lactic acid bacteria combined with cellulase or *Bacillus* improved TMR fermentation quality to varying degrees. They also reduced greenhouse gas emissions by regulating the types and proportions of microorganisms and metabolites.

Key words: Total mixed rations; *Lactobacillus plantarum*; Cellulase; Greenhouse gas

紫花苜蓿低温响应机制的转录组学分析

穆乙鑫¹, 云 岚^{1,2}, 贾苗苗¹, 李博华¹, 代 蕊¹, 杨 翌³, 石凤翎¹

(1. 内蒙古农业大学草业学院, 内蒙古 呼和浩特 010010; 2. 草地资源教育部重点实验室, 内蒙古 呼和浩特 010010; 3 黑龙江农科院畜牧兽医分院, 黑龙江 齐齐哈尔 161005)

摘要:为探究紫花苜蓿(*Medicago sativa* L.)响应低温胁迫的分子机制,本研究以耐寒品种‘龙牧 806’为材料,于 4℃处理 0,6,12,24,48 h 后测定生理指标并进行转录组测序,共筛选出 8101 个共同差异表达基因,富集分析显示谷胱甘肽代谢、糖酵解/糖异生等 6 条通路显著响应低温胁迫。加权基因共表达网络分析鉴定出与生理指标高度相关的 MEblue 模块,其中 MYB-related 家族基因数量最多。进一步从三羧酸循环和糖酵解/糖异生通路中筛选出 12 个关键基因,qRT-PCR 验证其表达趋势与转录组一致。本研究为紫花苜蓿耐寒机制解析和分子育种提供了理论依据。

关键词:紫花苜蓿;抗寒性;生理响应;转录组测序;WGCNA

混播多年生牧草改善盐碱地土壤细菌群落多样性

娜仁图雅¹, 武杰瑞¹, 陈逸凡³, 郭宏宇⁴, 云 岚^{1,2*}

(1. 内蒙古农业大学草业学院, 内蒙古 呼和浩特 010010; 2. 草地资源教育部重点实验室, 内蒙古 呼和浩特 010010; 3. 内蒙古自治区林业和草原检测规划院, 内蒙古 呼和浩特 010020; 4. 赤峰市农牧科学院, 内蒙古 赤峰 024000)

摘要:为探究不同多年生牧草种植模式对土壤微生物群落的长期影响,以内蒙古海流图地区的盐碱地为对象,通过设置 7 种牧草种植处理:单播苜蓿、新麦草、缘毛雀麦和长穗偃麦草,以及苜蓿与 3 种禾草(新麦草、缘毛雀麦、长穗偃麦草)混播,生长 3 年后,以裸盐碱地为对照,采用 16S 测序分析土壤微生物细菌组成结构。结果表明:牧草种植显著改变了土壤细菌多样性和群落结构,其中,苜蓿单播显著提高了土壤中细菌多样性;放线菌门(Actinomycetota)、变形菌门(Proteobacteria)、酸杆菌门(Acidobacteriota)、绿弯菌门(Chloroflexi)是细菌优势菌门,长期种植多年生牧草使土壤优势菌群中的变形菌门(Proteobacteria)相对丰度增加。因此,豆科牧草苜蓿单播、苜蓿与禾草混播模式均显著改善土壤微生物结构,研究结果为相似盐碱地生态修复和利用提供了科学依据。

关键词:盐碱地改良;多年生牧草;土壤微生物;高通量测序

种植混播多年生牧草对盐碱地土壤细菌群落的影响

娜仁图雅¹, 武杰瑞¹, 云 岚^{1,2*}

(1. 内蒙古农业大学草业学院, 内蒙古 呼和浩特 010010; 2. 草地资源教育部重点实验室, 内蒙古 呼和浩特 010010)

摘要:为探究不同多年生牧草种植模式对土壤微生物群落的长期影响,本研究以内蒙古海流图地区的盐碱地为试验对象,通过设置 7 种牧草种植处理:单播苜蓿、新麦草、缘毛雀麦和长穗偃麦草,以及苜蓿与 3 种禾草(新麦草、缘毛雀麦、长穗偃麦草)混播,生长三年后,以裸盐碱地为对照,采用 16S 测序分析土壤微生物细菌组成结构,结合土壤化学性质进行相关性分析。结果表明:牧草种植显著改变了土壤细菌多样性和群落结构($P < 0.05$),其中,苜蓿单播显著提高了土壤中细菌多样性;放线菌门(Actinomycetota)、变形菌门(Proteobacteria)、酸杆菌门(Acidobacteriota)、绿弯菌门(Chloroflexi)是细菌优势菌门,长期种植多年生牧草使土壤优势菌群中的变形菌门(Proteobacteria)相对丰度增加。冗余分析发现,细菌群落结构与 AK 呈正相关;与 AP、OM、TN、pH 和含水率呈负相关。综上,豆科牧草苜蓿单播、苜蓿与新麦草及苜蓿与长穗偃麦草混播模式对土壤微生物结构的改良效果最显著,研究结果为相似盐碱地生态修复和利用提供了科学依据。

关键词:盐碱地改良;多年生牧草;土壤微生物;高通量测序

新疆 60 份披碱草属种质种子萌发期耐低氮性综合评价

潘桂芳¹, 孙宗玖^{1,2,3}, 费瑞华¹, 郭锦华¹, 李培英^{1,2,3}, 阿斯太肯·居力海提¹,
张文龙¹, 胡 蝶¹, 任梦龙¹, 马 鹏¹

(1. 新疆农业大学草业学院, 新疆 乌鲁木齐 830052; 2. 新疆草地资源与生态自治区重点实验室, 新疆 乌鲁木齐 830052;
3. 西部干旱荒漠区草地资源与生态教育部重点实验室, 新疆 乌鲁木齐 830052)

摘要:披碱草作为生态修复植物具有重要价值,研究其种子萌发期低氮胁迫响应,对揭示其耐低氮机制、培育耐低氮种质及提升生态修复能力意义重大。本研究采用培养皿发芽法通过对低氮胁迫($0.01 \text{ mmol} \cdot \text{L}^{-1}$)及对照($1.00 \text{ mmol} \cdot \text{L}^{-1}$)下 60 份披碱草种质种子萌发特征及幼苗生长指标的测定,明确其耐氮差异,并运用耐低氮系数、隶属函数综合评价及系统聚类分析进行了耐低氮性强弱评价。结果表明:低氮胁迫后各披碱草种质种子萌发及幼苗生长指标均呈下降趋势,发芽率、发芽势、发芽指数、苗长、根长、苗鲜重、根鲜重、整体鲜重、苗干重、根干重、整体干重以及根冠比依次下降为 6.74%, 11.20%, 8.24%, 6.40%, 14.77%, 29.08%, 36.46%, 25.49%, 30.24%, 38.58%, 28.74% 和 8.76%。根据耐低氮性隶属函数综合评价值及系统聚类分析,60 份种质的耐低氮性可分为 6 大类,分别为超强、中强、低强、低弱、中弱和超弱。其中超强耐低氮性种质为‘E47’‘E22’‘E58’‘E07’‘E38’‘E60’‘E55’‘E48’‘E01’和‘E08’,而超弱耐低氮性种质为‘E49’‘E32’和‘E11’。本研究为披碱草耐低氮性候选基因挖掘与功能研究、遗传改良及新品种的选育提供优异亲本材料。

关键词:披碱草;种子萌发期;耐低氮性;综合评价;聚类分析;耐低氮系数

草地放牧管理措施对土壤有机碳分布的影响

蒲俊宇¹, 苏颖佳¹, 王新生¹, 杜金山¹, 洪逸楠¹, 刘克思^{1,2*}

(1. 中国农业大学草业科学与技术学院, 北京 100193; 2. 河北沽源草地生态系统国家野外站, 河北 张家口 076550)

摘要:土壤有机碳(Soil organic carbon, SOC)是衡量土壤质量和生态系统功能的关键指标,放牧作为草地主要利用方式,显著影响草地 SOC 动态。本研究以中国北方温带草地为研究对象,通过设置不同放牧强度(轻度、中度、重度)和围封年限(5 年、10 年),分析放牧管理措施对 SOC 含量及储量的影响。结果表明,放牧管理措施主要影响 0~10 cm 土层的土壤容重和 10~20cm 土层的 SOC 含量及储量。重度放牧显著增加 0~10cm 土层容重、显著降低 10~20 cm 土层的 SOC 含量和储量,围封可有效提升 10~20cm 土层 SOC 含量。但长期围封可能导致植被多样性下降,不利于碳积累。综上,适度放牧和围封是维持温带草原土壤碳库平衡的有效管理措施。

关键词:土壤有机碳;放牧管理措施;土层;土壤团聚体

Grassland Grazing Regimes Modulate Organic Carbon Distribution in Soil Aggregates over Varying Soil Depths

PU Jun-yu¹, SU Ying-jia¹, WANG Xin-sheng¹, DU Jin-shan¹, HONG Yi-nan¹, LIU Ke-si^{1,2*}

(1. College of Grassland Science and Technology, China Agricultural University, Beijing 100193, China;

2. National field station of grassland ecosystem in Guyuan, Zhangjiakou, Hebei Province 076550, China)

Abstract: Soil organic carbon (SOC) is a key indicator of soil quality and ecosystem functioning. Grazing significantly influences the dynamics of SOC in grassland ecosystems. This study focuses on temperate grasslands in northern China, analyzing the effects of grazing regimes on SOC concentration and stock by setting different grazing intensities (light, moderate, heavy) and exclosure durations (5 years, 10 years). The results indicate that grazing regimes practices primarily affect the soil bulk density in the 0-10 cm layer and the SOC concentration and stock in the 10-20 cm layer. Heavy grazing significantly increases the bulk density in the 0-10 cm layer while significantly reducing the SOC concentration and stock in the 10-20 cm layer. Exclosure effectively enhances the SOC concentration in the 10-20 cm layer. However, long-term exclosure may lead to a decline in vegetation diversity, which is unfavorable for carbon accumulation. In conclusion, moderate grazing and temporary exclosure are effective measures for maintaining the balance of the soil carbon in temperate grasslands.

Key words: Soil organic carbon; Grazing regime; Soil layer; Soil aggregate

中华羊茅内生真菌菌丝浓度对其生长与营养指标的影响

沈锦慧, 夏 超*

(兰州大学草地农业科技学院, 草种创新与草地农业生态系统全国重点实验室, 甘肃 兰州 730020)

摘要:中华羊茅(*Festuca sinensis*)是禾本科羊茅属多年生疏丛型草本植物,作为我国西北高寒草地的重要牧草,其与 *Epichloë* 属内生真菌的共生关系对其生长与抗逆至关重要。但以往的研究仅注重内生真菌的有无,鲜有探究内生真菌菌丝浓度与宿主生长及抗逆能力间关系的相关研究。本研究以带内生真菌(Endophyte-infected, EI)的中华羊茅为供试材料,测定植株株高、冠幅、分蘖数、生物量等生长指标,以及粗蛋白和粗脂肪含量等营养指标,结合荧光定量 PCR 技术,通过产碱基因丰度计算内生真菌菌丝浓度,探究中华羊茅菌丝浓度与植株生长和营养指标的关系。本研究发现菌丝浓度与宿主干重和分蘖数均呈显著正相关关系($P < 0.05$),而与株高($P = 0.593$)、冠幅($P = 0.338$)、粗蛋白($P = 0.660$)及粗脂肪含量($P = 0.197$)间不存在显著相关性。研究结果进一步揭示了中华羊茅与禾草内生真菌的互作关系,发现内生真菌对中华羊茅的生长增益作用与其菌丝浓度直接相关,这一发现为利用内生真菌培育牧草新品种提供了新的思路——即通过定向提升菌丝密度强化分蘖能力,以增加宿主干物质积累。然而,本研究所用样本数量有限,未来仍需持续扩大样本数量,开展多年、多代、多点的系统研究,以进一步增强研究结果的普适性和可靠性。

呼伦贝尔温性草甸草原植物群落多样性与土壤养分计量驱动机制研究

侍梦圆, 俞天琦, 李 颖, 邴 丽, 辛晓平*, 闫瑞瑞*

(中国农业科学院农业资源与农业区划研究所, 北方干旱半干旱耕地高效利用全国重点实验室, 北京 100081)

摘要:呼伦贝尔草原是我国北方典型的温性草甸草原类型,在维持区域生态功能、调节养分循环及支撑生物多样性方面具有重要生态价值。随着保护与恢复政策的持续推进,封育围封等管理措施在退化草原恢复中被广泛应用,不同植物群落在自然演替过程中逐步形成,并对土壤环境产生反馈。生态化学计量学(Ecological stoichiometry)是研究生态系统物质循环过程中碳(C)、氮(N)、磷(P)、钾(K)等关键元素平衡关系的科学方法,为理解生物地球化学循环机制和植被养分限制特征提供了重要研究手段。为探究封育恢复背景下草甸草原植物-土壤系统的耦合机制,本研究以呼伦贝尔温性草甸草原为对象,选取羊草(*Leymus chinensis*)、贝加尔针茅(*Stipa baicalensis*)和线叶菊(*Filifolium sibiricum*)三类典型植物群落长期围封样地,旨在揭示不同植物群落类型中植物多样性与土壤 C, N, P, K 化学计量特征的生态差异及其调控路径。结果表明:三类群落的植物多样性和土壤养分计量特征差异显著。线叶菊群落的 C : N(11.2), C : K(2.7)和 N : K(0.23)比值均显著高于羊草(C : N=10.5, C : K=1.8, N : K=0.16)和贝加尔针茅群落(C : N=10.9, C : K=1.7, N : K=0.15)($P < 0.05$),表明其具备更强的有机质积累能力和较高的钾供应水平。植物多样性在该群落中与土壤 C : P($R^2 = 0.78$)和 N : P($R^2 = 0.56$)呈正相关,而与 C : K($R^2 = 0.60$)、N : K($R^2 = 0.62$)、P : K($R^2 = 0.76$)呈负相关,说明多样性提升可能伴随更高的磷利用效率和钾资源权衡。结构方程模型($\chi^2(4) = 10.53$, $P = 0.032$)进一步表明,植物多样性通过影响土壤 P, K 含量及多元素比例调控群落构建。因此,线叶菊群落在维持较高植物多样性的同时优化了土壤养分结构,其独特的植物与土壤耦合特征有助于提升草原群落的稳定性与资源利用效率。本文从多元素计量视角深化了对植被与土壤协同机制的理解,为退化草原恢复过程中的群落构建优化与养分管理提供了重要的生态学依据。未来研究可关注不同功能群植物在驱动养分循环过程中的具体贡献,以制定更具针对性的生态管理策略。

关键词: 温性草甸草原; 植物多样性; 土壤养分计量; 植被-土壤调控; 生态化学计量

补播对不同土壤基质退化蒿类荒漠植被特征的影响

宋勇康¹, 董乙强^{1,2,3*}, 颜 安^{1,2,3}, 刘兴义⁴, 符天昊¹, 杨春莹¹, 单兴芸¹, 雷雅欣¹, 吴 凯¹

(1. 新疆农业大学草业学院, 新疆 乌鲁木齐 830052; 2. 新疆草地资源与生态自治区重点实验室, 新疆 乌鲁木齐 830052; 3. 西部干旱区草地资源与生态教育部重点实验室, 新疆 乌鲁木齐 830052; 4. 新疆博乐市草原工作站, 新疆 博乐 833400)

摘要:补播是修复改良退化草地的主要措施之一,其改良效果与土壤基质有重要关系,但目前关于土壤基质对补播改良效果的研究鲜有报道。本研究以不同土壤基质(土质、砾石质、砂砾质)的退化蒿类荒漠为研究对象,采用精量穴播和飞播技术对其进行改良。补播 2a 后,分别对植物种群特征、构件特征及群落多样性进行测定分析,结果表明:(1)补播 2a 后,博乐绢蒿的生长状况显著改善,砾石质(GD)和砂砾质荒漠(GSD)的博乐绢蒿株高、茎长、茎生物量、叶生物量和单株生物量均显著高于土质荒漠($P<0.05$),而根长在砾石质荒漠区最短。(2)砂砾质荒漠(GSD)的植株高度(22.94 cm)和地上生物量($35.27\text{ g}\cdot\text{m}^{-2}$)显著高于土质和砾石质荒漠($P<0.05$),而砾石质荒漠(GD)的植物密度($79\text{ 株}\cdot\text{m}^{-2}$)最高。(3)土质荒漠(SD)补播区的群落盖度和密度均显著高于砾石质(GD)和砂砾质荒漠(GSD)补播区($P<0.05$),砂砾质荒漠(GSD)补播区群落高度最高。补播显著提高了土质(SD)和砾石质荒漠(GD)0~10 cm 土层的地下生物量($P<0.05$)。(4)砾石质(GD)和砂砾质荒漠(GSD)补播区植物群落多样性和均匀度指数显著高于土质荒漠(SD)补播区($P<0.05$),土质荒漠(SD)补播区丰富度指数显著降低($P<0.05$)。综上,土壤基质通过调节水分和根系发育影响补播效果,在补播改良退化草地时,应充分考虑土壤基质对补播效果的影响。

关键词:补播;博乐绢蒿;不同土壤基质;蒿类荒漠

Effects of Reseeding on Vegetation Characteristics of Degraded Artemisia Desert with Different Soil Substrates

SONG Yong-kang¹, DONG Yi-qiang^{1,2,3*}, YAN An^{1,2,3}, LIU Xing-yi⁴, FU Tian-hao¹,
YANG Chun-ying¹, SHAN Xing-yun¹, LEI Ya-xin¹, WU Kai¹

(1. College of Grassland Industry, Xinjiang Agricultural University, Urumqi Xinjiang 830052, China; 2. Xinjiang Key Laboratory of Grassland Resources and Ecology, Urumqi, Xinjiang 830052, China; 3. Key Laboratory of Grassland Resources and Ecology of Western Arid Region, Ministry of Education, Urumqi, Xinjiang 830052, China; 4. Bole Prairie Workstation of Bole City, Bole, Xinjiang 833400, China)

Abstract:Reseeding is one of the primary measures for restoring and improving degraded grasslands, and its effectiveness is closely related to soil substrate. However, there has been limited research on the influence of soil substrate on reseeded outcomes. This study focuses on degraded Artemisia desert ecosystems with different soil substrates (soil desert, gravelly desert, and gravelly-sandy desert) and employs precision hole sowing and aerial seeding techniques for restoration. After two years of reseeded, plant population characteristics, modular traits, and community diversity were measured and analyzed. The results indicate that:(1)After two years of reseeded, the growth of *Seriphidium borotalense* significantly improved. In GD and GSD, plant height, stem length, stem biomass, leaf biomass, and individual plant biomass were significantly higher than in SD ($P<0.05$), while root length was shortest in GD. (2)Plant height (22.94 cm) and aboveground biomass ($35.27\text{ g}\cdot\text{m}^{-2}$) were significantly higher in GSD than in SD and GD ($P<0.05$), whereas plant density ($79\text{ individuals}\cdot\text{m}^{-2}$) was highest in GD. (3)Community coverage and density in reseeded SD were significantly higher than in reseeded GD and GSD ($P<0.05$). The highest community height was observed in reseeded GSD. Reseeding significantly increased belowground biomass in the 0-10 cm soil layer in SD and GD ($P<0.05$). (4)The diversity and evenness indices of plant communities were significantly higher in reseeded GD and GSD than in reseeded SD ($P<0.05$), while the richness index decreased significantly in reseeded SD ($P<0.05$). In summary, soil substrates modulate reseeded outcomes by influencing water availability and root development. Restoration strategies for degraded Artemisia deserts should account for substrate-specific effects to optimize rehabilitation.

Key words:Reseeding; *Seriphidium borotalense*; Different soil substrates; Artemisia deserts

不同饲养模式对肉羊血液抗氧化指标的影响

孙羽翔, 程 箫, 任春环, 张子军, 王冠军, 黄钰锋*

(1. 安徽农业大学动物科技学院, 安徽 合肥 230031; 2. 颍上县农业绿色发展推进中心, 安徽 颍上 236200)

摘要:随着人民生活质量提高和消费观念的改变,高蛋白、低脂肪的羊肉备受消费者的青睐,食物消费结构的升级为肉羊产业快速发展提供了巨大的推动力,市场上羊肉消费量逐年增加。本研究以全舍饲养模式(CON)为对照组、舍饲加短时放牧饲养($2\text{ h} \cdot \text{d}^{-1}$, G2)和舍饲加限时放牧饲养($4\text{ h} \cdot \text{d}^{-1}$, G4)模式为试验组,5月龄黄淮肉羊母羔羊为供试家畜,探究不同饲养模式对肉羊血液抗氧化指标的影响。试验选用黄淮肉羊母羔羊45只(5月龄,体重 $27.31 \pm 0.73\text{ kg}$)。将45只羔羊随机分为三组($n=15$):CON组,全舍饲养模式,每天饲喂两次(08:00和18:00);G2组,舍饲加短时放牧2小时饲养模式,上午8:00饲喂,下午16:00放牧2小时,下午18:00补充喂养($n=15$);G4组,舍饲加限时放牧4小时饲养模式,日粮上午8:00饲喂,8:30放牧2小时+下午16:00放牧2小时,18:00补饲。在生长试验期结束时,早上喂食前采集每只羊颈静脉的10 mL血样。采集的血样在室温下静置30 min,以 $3000\text{ r} \cdot \text{min}^{-1}$ 离心10 min,分离血清并在 -20°C 下冷冻保存。每份血清样品通过 $3000\text{ r} \cdot \text{min}^{-1}$ (4°C)离心15 min进行分离,并在 -80°C 下冷冻以进行后续分析。血清总抗氧化能力(T-AOC)、超氧化物歧化酶(SOD)活性和谷胱甘肽过氧化物酶(GSH-Px)活性根据试剂盒制造商的说明书使用商用比色测定试剂盒(Camaishu Biotechnology Co., 中国上海卡迈舒生物科技有限公司)测定。本研究中G2和G4组黄淮肉羊血浆T-AOC显著高于CON组。这可能是CON组绵羊在全舍饲养体内脂肪沉积过多,导致脂质过氧化反应增加,进而引发炎症反应,产生过量的自由基,使血浆T-AOC显著降低。而三组血浆中SOD和GSH-Px活性均无显著变化,但G2组羔羊的SOD活性有升高的趋势。说明舍饲基础上进行限时放牧,提高绵羊运动量可促进机体抗氧化物质的产生和抗氧化系统稳态,提高机体健康水平。因此,与传统的全舍饲养模式相比,舍饲加短时放牧,能更有效的提高动物的免疫力,避免出现亚健康状况,间接促进了生长性能的提高。

Epichloë gansuensis Enhances *Achnatherum inebrians* Seedlings Growth and Antioxidant Capacity Under UV-B Stress

WAN Cui-ling¹, LI Xiu-zhang^{1,2}, SHI Qian^{1*}

(1. State Key Laboratory of Plateau Ecology and Agriculture, Qinghai University, Xining, Qinghai Province 810016, China;

2. Qinghai Academy of Animal and Veterinary Science, Qinghai University, Xining, Qinghai Province 810016, China)

Abstract: Strong ultraviolet-B (UV-B) radiation is a major characteristic of the climate on the Qinghai-Tibet Plateau. To adapt to the intense UV-B radiation characteristic of this region, local plants have evolved efficient adaptive mechanisms to mitigate such environmental stress. However, the response mechanisms of grass-endophytic fungal symbioses to UV-B radiation in this region still lack systematic and in-depth investigation, while the intrinsic mechanisms underlying their adaptive interactions remain poorly understood. In this study, we examined how *Epichloë gansuensis* influences the growth and antioxidant activity of *Achnatherum inebrians* seedlings under varying levels of UV-B radiation, with the objective of assessing the growth and antioxidant capacity of *A. inebrians* seedlings under UV-B stress. Under different intensities of UV-B radiation treatments, the morphological, physiological and biochemical indicators of *A. inebrians* seedlings were measured, including plant height, tiller number, biomass, electrical conductivity, soluble sugar content, malondialdehyde (MDA) content, proline content, hydrogen peroxide (H_2O_2) content, as well as the activities of superoxide dismutase (SOD), polyphenol oxidase (POD), and catalase (CAT). The results showed that with the increase in UV-B radiation intensity, the plant height, tiller number and biomass of *A. inebrians* seedlings showed a decreasing trend. Concurrently, electrical conductivity, MDA content, and H_2O_2 levels increased, while soluble sugars, proline, and the activities of SOD, POD, and CAT decreased. These results indicate that UV-B radiation inhibits morphogenesis and exacerbates membrane lipid peroxidation in *A. inebrians* seedlings, while endophytic fungi enhance the plant's growth and antioxidant capacity. The tolerance of the *A. inebrians*-*E. gansuensis* symbiont to UV-B radiation likely contributes to its high infection rate in the Qinghai-Tibet Plateau region.

Key words: Seedlings; Symbiont; Tolerance; Qinghai-Tibet Plateau; Environment

添加艾草对玉米秸秆青贮饲料发酵品质及温室气体的影响

汪晓辉, 闫 阳, 魏海龙, 王纪栋, 谈重芳, 王雁萍, 蔡义民*, 庞会利*

(郑州大学农学院, 河南 郑州 450000)

摘要: 农业是国民经济基础,也是温室气体重要来源。大量玉米秸秆因适口性、消化率差被焚烧或废弃,造成资源浪费与污染。青贮虽能高效利用饲草、减少饲料生产碳排放及反刍动物肠道甲烷排放,但自身发酵会产生温室气体,导致养分损失和环境污染。本研究以玉米秸秆为原料、艾草为添加剂混合青贮,用传统培养法、高通量测序、代谢组学等技术,分析青贮中微生物群落、发酵品质、化学成分及温室气体排放变化。结果显示,艾草可富集乳植杆菌属等有益菌、抑制肠杆菌属等有害菌,降低饲料 pH 值,使乳酸含量提升 57%,还能减少 65% 以上 CO_2 , CH_4 , N_2O 排放。该研究为新型低碳饲料添加剂开发、秸秆青贮优化及畜牧业“双碳”目标实现提供数据与技术支持。

关键词: 玉米秸秆;青贮;温室气体;艾草;乳酸菌

The Effect of Adding *Artemisia argyi* on the Fermentation Quality and Greenhouse Gas Emissions of Corn stover Silage

WANG Xiao-hui, YAN Yang, WEI Hai-long, WANG Ji-dong, TAN Zhong-fang,

WANG Yan-ping, CAI Yi-min*, PANG Hui-li*

(School of Agricultural Sciences, Zhengzhou University, Zhengzhou, Henan Province 450000, China)

Abstract: Agriculture is the foundation of the national economy and also a significant source of greenhouse gas emissions. A large amount of corn stover is incinerated or discarded due to poor palatability and digestibility, resulting in resource waste and pollution. Although silage can realize the efficient utilization of forage grass, reduce carbon emissions in feed production and methane emissions from ruminant intestinal fermentation, the fermentation process of silage itself will produce greenhouse gases, leading to nutrient loss and environmental pollution. In this study, corn stover was used as the raw material and *Artemisia argyi* (AA) as the additive for mixed silage. Technologies such as traditional culture method, high-throughput sequencing and metabolomics were employed to analyze the changes in microbial community, fermentation quality, chemical composition and greenhouse gas emissions during silage. The results showed that AA could enrich beneficial bacteria such as *Lactiplantibacillus* and inhibit harmful bacteria such as *Enterobacter*, reduce the pH value of feed, increase lactic acid content by 57%, and reduce the emissions of CO_2 , CH_4 and N_2O by more than 65%. This study provides data and technical support for the development of new low-carbon feed additives, the optimization of straw silage and the achievement of the “dual carbon” goals in animal husbandry.

Key words: Corn stover; Silage; Greenhouse gases; *Artemisia argyi*; Lactic acid bacteria

数字技术何以破解草原生态产品价值实现困境

——基于要素错配矫正的实证分析

王海春*, 王 升, 肖 潇, 孟超凡

(内蒙古财经大学财政税务学院, 内蒙古 呼和浩特 010070)

摘要:生态产品价值实现包括生态经济价值与生态福利价值两个维度。数字技术作为关键驱动力,可有效破解价值实现过程中的障碍。本研究基于内蒙古 12 盟市 2011—2021 年面板数据,实证分析数字技术对草原生态产品价值实现效率的影响。结果表明:(1)数字技术对价值实现效率具有显著驱动作用,主要体现在生态经济价值阶段,对生态福利价值的驱动作用不显著;(2)数字技术通过缓解资本、土地和劳动力要素错配间接提升效率,其中资本与土地错配缓解具有“即时效应”,劳动力错配缓解具有“滞后效应”;(3)数字技术的驱动效果在经济发达但资源禀赋不足地区尤为显著。建议持续推进牧区数字化建设,强化数字技术在价值分配中的应用,实施差异化区域策略。

关键词:数字技术;草原生态产品;价值实现效率;要素错配

How Digital Technology Overcomes the Challenges of Grassland Ecological Product Value Realization: Evidence from Factor Misallocation Correction

WANG Hai-chun*, WANG Sheng, XIAO Xiao, MENG Chao-fan

(School of Public Finance and Taxation, Inner Mongolia University of Finance and Economics, Hohhot, Inner Mongolia 010070, China)

Abstract: The realization of ecological product value encompasses two dimensions: ecological economic value and ecological welfare value. As a key driving force, digital technology can effectively overcome obstacles in the value realization process. Based on panel data from 12 leagues and cities in Inner Mongolia from 2011 to 2021, this study empirically analyzes the impact of digital technology on the efficiency of grassland ecological product value realization. The results show that: (1) Digital technology has a significant driving effect on value realization efficiency, mainly reflected in the stage of ecological economic value, while its effect on ecological welfare value is not yet significant; (2) Digital technology indirectly improves efficiency by alleviating the misallocation of capital, land, and labor factors. Specifically, the mitigation of capital and land misallocation exhibits an “immediate effect”, whereas the mitigation of labor misallocation shows a “lagged effect”; (3) The driving effect of digital technology is particularly prominent in economically developed regions with insufficient resource endowments. It is recommended to continue promoting digital construction in pastoral areas, strengthen the application of digital technology in value distribution, and implement differentiated regional strategies.

Key words: Digital technology; Grassland ecological products; Value realization efficiency; Factor misallocation

非常规饲料发酵条件优化及发酵和有氧暴露过程中微生物、发酵品质的变化

王纪栋, 魏海龙, 闫 阳, 汪晓辉, 谈重芳, 王雁萍, 蔡义民*, 庞会利*
(郑州大学农学院, 河南 郑州 450000)

摘要:近年来,我国养殖业面临快速发展与“玉米—豆粕”型常规饲料供需失衡的困局。针对这一现状,本研究以典型非常规饲料—油菜秸秆、酒糟、马铃薯渣为原料,利用植物乳杆菌 ZA3 和枯草芽孢杆菌 QB8,通过单因素试验和响应面分析法优化发酵条件,探究发酵及有氧暴露过程中饲料品质与微生物群落的动态变化。研究发现最佳发酵条件为:发酵时间 88 h、接种量 10%、菌种添加比例(ZA3 : QB8)1 : 1。与豆粕加菌组相比,非常规饲料加菌组在 30 d 发酵及有氧暴露期间,pH 值显著降低,乳酸、乙酸含量增加,大肠杆菌、梭菌等有害菌数量减少,乳酸菌成为优势菌群。发酵 88 h 时,非常规饲料组的 pH 值、粗纤维含量与豆粕组无显著差异,大肠杆菌数量均显著低于豆粕相关组($P<0.05$)。本研究为非常规饲料安全高效替代豆粕应用于畜禽养殖提供了新的技术路径与理论支撑。

关键词:非常规饲料;发酵品质;微生物群落;有氧暴露

Optimization of Unconventional Feed Fermentation Conditions and the Microbial Dynamics and Fermentation Quality Changes during Fermentation and Aerobic Exposure Processes

WANG Ji-dong, WEI Hai-long, YAN Yang, WANG Xiao-hui, TAN Zhong-fang,
WANG Yan-ping, CAI Yi-min*, PANG Hui-li*
(School of Agricultural Sciences, Zhengzhou University, Zhengzhou, Henan Province 450000, China)

Abstract: In recent years, China’s livestock industry has faced the dilemma of rapid development coupled with supply-demand imbalances in conventional “corn-soybean meal” feeds. Addressing this challenge, this study utilized typical unconventional feeds: rapeseed straw, distillers’ grains, and potato residue as raw materials, employing *Lactobacillus plantarum* ZA3 and *Bacillus subtilis* QB8. Through single-factor experiments and response surface methodology, fermentation conditions were optimized to investigate dynamic changes in feed quality and microbial communities during fermentation and aerobic exposure. The optimal fermentation conditions were determined as: fermentation time 88 h, inoculation rate 10%, and bacterial strain ratio (ZA3 : QB8) 1 : 1. Compared to the soybean meal with bacterial inoculation group, the unconventional feed with bacterial inoculation group showed significantly reduced pH values, increased lactic acid and acetic acid content, decreased populations of pathogenic bacteria such as *E. coli* and *Clostridium*, with lactic acid bacteria becoming the dominant microbial community during 30 days of fermentation and aerobic exposure. At 88 h of fermentation, the unconventional feed group showed no significant difference in pH and crude fiber content compared to the soybean meal group. In contrast, *E. coli* counts were significantly lower than the corresponding soybean meal groups ($P<0.05$). This research provides novel technical pathways and theoretical support for the safe and efficient substitution of soybean meal with unconventional feeds in livestock and poultry production.

Key words: Unconventional feedstuffs; Fermentation quality; Microbial communities; Aerobic exposure

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作者简介:王纪栋(2002-),男,汉族,山东聊城人,硕士,主要从事农业废弃物资源饲料化研究,E-mail: wangjd_zzu@163.com; * 通信作者
Author for correspondence, E-mail: pang@zzu.edu.cn

Epichloë 内生真菌对醉马草可培养内生微生物组成与多样性的影响

王美君, 夏 超*

(草种创新与草地农业生态系统国家全国重点实验室/农业农村部草牧业创新重点实验室/
草地农业教育部工程研究中心/甘肃省西部草业技术创新中心/兰州大学, 甘肃 兰州 730020)

摘要:醉马草(*Achnatherum inebrians*)是广泛分布于我国西北干旱和半干旱草原的重要多年生禾草,其与香柱菌属内生真菌(*Epichloë* endophyte)能够形成稳定的互惠共生关系,从而赋予宿主一定的抗旱优势。然而,这种互作关系易受环境条件及宿主的影响,表现出一定的不稳定性。近年来,植物微生物组被视为植物的“第二基因组”,在调控植物的生长发育和环境适应过程中发挥着至关重要的作用。然而,*Epichloë* 内生真菌是否通过塑造其他内生微生物群落,以实现调控植株生长及抗旱能力的目的,仍需进一步研究。本研究以相同遗传背景下的带菌(Endophyte-infected, EI)和不带菌(Endophyte-free, EF)醉马草为研究对象,在干旱胁迫条件下,系统采集其不同发育阶段的叶、根、茎和穗组织,并结合传统分离培养方法,进一步分析 *Epichloë* 内生真菌与干旱互作对宿主内生微生物群落的影响。

结果表明,在干旱条件下共分离得到 730 株细菌(隶属 7 门 67 属)和 727 株真菌(隶属 2 门 65 属)。细菌群落以鞘氨醇单胞菌属(*Sphingomonas*)和假单胞菌属(*Pseudomonas*)为优势类群,真菌群落则以枝孢菌属(*Cladosporium*)和曲霉属(*Aspergillus*)为优势类群。与 EF 植株相比,EI 植株在地上部显著提高了内生细菌多样性($P<0.05$),并显著增加鞘氨醇单胞菌属和假单胞菌属的丰度(最高分别提升 2.85% 和 6.02%);同时,EI 植株的内生真菌多样性亦显著增强($P<0.05$),其中枝孢菌属的丰度较 EF 植株显著提升,最高增幅达 2.06%。值得注意的是,鞘氨醇单胞菌属、假单胞菌属可以促进植株的茎和根的生长,进而增强宿主的水分利用效率,还可以降低超氧化物歧化酶(SOD)活性、黄酮类物质含量和自由基清除活性来调节抗氧化剂,从而保护植物免受干旱胁迫。而枝孢菌属能显著提升幼苗生物量以及促进根系发育,曲霉属能够通过分泌小分子信号物质抑制立枯丝核菌(*Rhizoctonia solani*)的侵染过程,同时对稻曲病菌(*Fusarium fujikuroi*)等病原菌表现出显著的拮抗活性。

综上,在干旱胁迫条件下,*Epichloë* 内生真菌不仅显著提升宿主地上部微生物多样性,还富集和重组对植物有益的鞘氨醇单胞菌属、假单胞菌属、枝孢菌属及曲霉属,使这些有益菌在干旱条件下协同发挥促进生长和抗旱的功能。更重要的是,*Epichloë* 内生真菌可能作为微生物群落的枢纽,调控和优化其他内生微生物的分布、丰度及功能,形成高度协同的微生物网络,从而整体增强宿主植株的抗旱能力和生态适应性。这表明,宿主抗旱性并非是单一内生真菌作用的结果,而是内生真菌与整个微生物群落协同调控下的综合效应。

关键词: *Epichloë* 内生真菌;内生微生物;干旱胁迫;醉马草

不同苜蓿品种在呼市生产性能综合评价

王思仪^{1,2,3}, 高凤芹^{1*}, 景媛媛¹, 杨国淋¹, 何镇南^{1,2,3}

(1. 中国农业科学院草原研究所, 内蒙古 呼和浩特 010010; 2. 青岛农业大学草业学院, 山东 青岛 266109;
3. 黄河三角洲草地资源与生态国家林业和草原局重点实验室, 山东 青岛 266109)

摘要:为探索‘WL343HQ’‘WL358HQ’‘WL298HQ’‘Adina’4个苜蓿品种在中国的生长情况及适应性,本研究对不同品种的生产性能、营养价值等进行综合分析,以期为内蒙地区苜蓿产业化种植提供借鉴。结果表明,‘WL358HQ’在鲜草产量、株高、叶茎比、叶绿素等方面均较突出。‘Adina’品种的DM含量显著高于其他品种($P<0.05$),‘WL358HQ’的WSC含量、RFV显著高于其他品种($P<0.05$),‘WL358HQ’品种CP含量显著高于‘WL298HQ’和‘WL343HQ’($P<0.05$)。经综合评价分析,‘WL358HQ’综合表现最优异,在内蒙地区具有较高的推广利用价值。

关键词:苜蓿;适应性;生产性能;综合评价;营养价值

Comprehensive Evaluation of Production Performance of Different Alfalfa Varieties in Hohhot

WANG Si-yi^{1,2,3}, GAO Feng-qin^{1*}, JING Yuan-yuan¹, YANG Guo-lin², HE Zhen-nan^{1,2,3}

(1. Grassland Research Institute, Chinese Academy of Agricultural Sciences, Hohhot, Inner Mongolia 010010, China;
2. College of Grassland Science, Qingdao Agricultural University, Qingdao, Shandong Province 266109, China; 3. Key Laboratory of Grassland Resources and Ecology in the Yellow River Delta, National Forestry and Grassland Administration, Qingdao, Shandong Province 266109, China)

Abstract: To explore the growth conditions and adaptability of four alfalfa varieties, namely ‘WL343HQ’, ‘WL358HQ’, ‘WL298HQ’ and ‘Adina’, in China, a comprehensive analysis was conducted on the production performance and nutritional value of different varieties, with the aim of providing reference for the industrialized planting of alfalfa in Inner Mongolia. The results show that ‘WL358HQ’ stands out in terms of fresh grass yield, plant height, leaf-to-stem ratio and chlorophyll. The DM content of ‘Adina’ variety was significantly higher than that of other varieties ($P<0.05$), the WSC content and RFV of ‘WL358HQ’ variety were significantly higher than those of other varieties ($P<0.05$), and the CP content of ‘WL358HQ’ variety was significantly higher than that of ‘WL298HQ’ and ‘WL343HQ’ ($P<0.05$). After comprehensive evaluation and analysis, ‘WL358HQ’ has the most outstanding overall performance and has high promotion and utilization value in the Inner Mongolia region.

Key words: Alfalfa; Adaptability; Production performance; Comprehensive evaluation; Nutritional value

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作者简介:王思仪(2001-),女,汉族,硕士,研究方向为青贮微生物,E-mail:17860788357@163.com; *通信作者:高凤芹(1978-),女,研究员,博士生导师,研究方向为草产品生产加工与利用,E-mail:gaofq1211@126.com

不同肥料配施对苜蓿产量、品质的影响

王晓龙, 杨 翌, 柴 华, 李莎莎, 吴 玥

(黑龙江省农业科学院畜牧兽医分院, 黑龙江 齐齐哈尔 161005)

摘要:为探究氮、磷、钾肥对紫花苜蓿产量和品质的影响,以‘龙牧 801’苜蓿为试验材料,通过对不同施肥处理下苜蓿的生长特性、产量及营养成分等指标进行综合评价,以确定适宜紫花苜蓿生长的最佳肥料配比。结果表明: $N_1P_1K_0$ 处理的供试材料株高、生长速度和鲜干比最高,茎叶比最小; $N_1P_1K_0$ 处理下的产量最高,为 $11\,396.04\text{ kg}\cdot\text{hm}^{-2}$,显著高于其他处理($P<0.05$); $N_1P_1K_0$ 处理的粗蛋白(20.25%)和相对饲用价值(129.61%)最高,而中性洗涤纤维(45.15%)和酸性洗涤纤维(33.36%)最低。依据供试材料生长特性、产量及营养成分的综合表现,利用隶属函数法对不同施肥处理的生产性能进行评价,得出苜蓿生产性能强弱为: $N_1P_1K_0>N_1P_0K_1>N_0P_1K_1>N_0P_0K_0$ 。

关键词:紫花苜蓿;氮磷钾肥;配施;产量;品质

添加艾草活性物质对青贮全株玉米有氧稳定性影响

魏海龙, 闫 阳, 王纪栋, 汪晓辉, 谈重芳, 王雁萍, 蔡义民*, 庞会利*

(郑州大学农学院, 河南 郑州 450001)

摘要:本研究通过向全株玉米中添加桉叶油醇(A)、艾草精油(J)、艾草黄酮(H)及其混合物(M)进行发酵,以空白组和布氏乳杆菌组作为对照。在青贮 90 d 后,对其进行 0, 1, 3, 5, 7 d 的有氧暴露,分析其发酵品质、化学成分及微生物群落的变化。结果显示:在青贮 90 d 时, M 组的 pH 值最低(4.63), 乳酸含量最高($82.61\text{ g}\cdot\text{kg}^{-1}\text{ DM}$), 可溶性糖含量也最高($26.44\text{ g}\cdot\text{kg}^{-1}\text{ DM}$)。在有氧暴露期间, A 组的 pH 值显著低于 CK 组, 而 J, H 和 M 组的可溶性糖含量均高于 CK 组。其中, M 组的干物质、粗蛋白和可溶性糖含量最高, 氨态氮含量最低, 且其群落多样性较高, 有害微生物的相对丰度较低。综上所述, 添加艾草活性物质能有效抑制好氧微生物的代谢, 提升青贮的发酵品质, 这为开发新型饲料添加剂及提高传统中草药资源的利用率提供了理论依据。

关键词:全株玉米;艾草;活性物质;青贮;有氧暴露

Effects of *Artemisia argyi* Active Matter on the Aerobic Stability of Whole Plant Corn Silage

WEI Hai-long, YAN Yang, WANG Ji-dong, WANG Xiao-hui, TAN Zhong-fang,

WANG Yan-ping, CAI Yi-min*, PANG Hui-li*

(School of Agricultural Sciences, Zhengzhou University, Zhengzhou, Henan Province 450001, China)

Abstract: In this study, whole plant corn was fermented by adding eudesmol, essential oil, flavanone, and their mixtures extracted from *Artemisia argyi* (AA), with a blank group and a group treated with *Lentilactobacillus buchneri* (LB) serving as controls. After 90 days (d) of ensiling, samples were exposed to oxygen for 0, 1, 3, 5, and 7 d to analyze changes in fermentation quality, chemical composition, and microbial populations. The results indicated that after 90 d of ensiling, group M exhibited the lowest pH value (4.63), the highest content of acetic acid ($82.61\text{ g}\cdot\text{kg}^{-1}\text{ DM}$), and the highest content of dissolved sugar ($26.44\text{ g}\cdot\text{kg}^{-1}\text{ DM}$). During the oxygen exposure period, group A had a significantly lower pH value than the control group (CK), while groups J, H, and M had a higher content of dissolved sugar than the control group. Group M, in particular, had the highest dry matter, crude protein, and dissolved sugar content, the lowest nitrogen content, and a higher microbial community richness with a lower relative abundance of harmful microorganisms. In summary, the addition of wormwood active substances effectively suppressed microbial metabolism and improved the fermentation quality of silage, providing a theoretical basis for the development of new feed supplements and the enhanced utilization of traditional Chinese herbal medicine resources.

Key words: Whole corn; Wormwood; Active substances; Silage; Oxygen exposure

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作者简介:魏海龙(2000-), 男, 汉族, 河南南阳人, 硕士, 主要从事农业有机废弃物向饲料资源转化的应用研究, E-mail: 2898457683@qq.com; * 通信作者 Author for correspondence, E-mail: pang@zzu.edu.cn

短期封育对温性草甸草原和山地草甸草地植物群落特征及稳定性的影响

吴 凯¹, 董乙强^{1*}, 刘兴义², 杨合龙¹, 孙宗玖¹, 管廷贤²

(1. 新疆农业大学草业学院, 新疆 乌鲁木齐 830052; 2. 新疆博乐市草原工作站, 新疆 博乐 833400)

摘要:短期封育作为一种经济有效的修复措施,在退化草地治理中被广泛实施。为探究短期封育对温性草甸草原和山地草甸草地植物群落特征及稳定性的影响,本研究以新疆昭苏县温性草甸草原和山地草甸草地植物为研究对象,综合使用野外植被调查观测和室内分析的方法,对禁牧区和放牧区的草地植物群落数量特征和多样性等指标进行测定,并结合稳定性和草场质量指数定量评价短期封育效果。结果表明,短期封育后,温性草甸草原草地植物群落高度、盖度和地上生物量分别显著增加了 32.46%, 23.11% 和 199.57%, 而山地草甸草地植物群落的分别显著增加了 226.81%, 26.96% 和 139.67%; 且短期封育能显著增加多年生禾草的重要值,降低多年生莎草科类植物的重要值 ($P < 0.05$)。温性草甸草原群落稳定性降低,山地草甸群落稳定性增加。群落稳定性与 Shannon-Wiener 多样性指数呈负相关关系。短期封育使温性草甸草原草地的草场质量指数增加 568.49%, 山地草甸草地的草场质量指数增加 892.50%。综上所述,短期封育对温性草甸草原和山地草甸的草地恢复有显著改善效果,但不同类型草地群落稳定性的响应不同。本研究首次将草场质量指数与 Godron 稳定性结合,构建“结构-功能”双维度评估体系,揭示了短期封育对不同草地植物群落特征及稳定性的差异化影响,为同类型草地的治理与恢复提供科学依据和技术支撑。

关键词:短期封育; 群落稳定性; 草场质量指数; Godron 指数

Effects of Short-term Grazing Exclusion on Vegetation Community Characteristics and Stability in Temperate Meadow Steppe and Mountain Meadow

WU Kai¹, DONG Yi-qiang^{1*}, LIU Xing-yi², YANG He-long¹, SUN Zong-jiu¹, GUAN Ting-xian²

(1. College of Pratacultural and Environmental Science, Xinjiang Agricultural University 830052, Urumqi, Xinjiang 830052, China;

2. Bole Grassland Workstation, Bole, Xinjiang 833400, China)

Abstract: Short-term grazing exclusion is widely implemented as a cost-effective restoration measure in the management of degraded grasslands. This study focused on temperate meadow steppe and mountain meadow grasslands in Zhaosu County, Xinjiang. Field surveys and laboratory analyses were conducted to measure quantitative vegetation characteristics and diversity indices in enclosed and grazed areas. The short-term grazing exclusion effects were quantitatively evaluated using stability index and index of grassland quality. The results were as follows: The height, coverage, and aboveground biomass of plant community in the temperate meadow steppe significantly increased by 32.46%, 23.11%, and 199.57%, respectively, while those in the mountain meadow increased by 226.81%, 26.96%, and 139.67% after short-term grazing exclusion ($P < 0.05$). The importance value of Perennial grasses significantly increased but Sedges decreased. Community stability in temperate meadow steppe decreased significantly but in mountain meadow ecosystems increased notably, stability exhibited a significant negative correlation ($P < 0.05$) with the Shannon-Wiener diversity index. The index of temperate meadow steppe grassland quality increased by 568.49% and 892.50% in the mountain meadow after grazing exclusion. In conclusion, this study pioneers the integration of the index of grassland quality (IGQ) with Godron stability analysis, establishing a “structure-function” dual-dimensional assessment framework, revealing the differential impact of short-term grazing exclusion on the vegetation characteristics and stability of various grasslands, offering a scientific foundation and technical guidance for the conservation and recovery of similar grassland types.

Key words: Short-term grazing exclusion; Community stability; Index of grassland quality; Godron index

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作者简介: 吴凯(1998-), 女, 江西赣州人, 硕士研究生, 主要从事草地资源与生态研究, E-mail: 1102511707@qq.com; * 通信作者: 董乙强(1989-), 男, 江苏邳州人, 副教授, 硕士, 博士, 主要从事草地资源与生态研究, E-mail: xjdyq1210@163.com

苜蓿种子萌发期抗旱性评价

吴 玥，王晓龙*，杨 翌*，柴 华，李莎莎
(黑龙江省农业科学院畜牧兽医分院，黑龙江 齐齐哈尔 161005)

摘要:为筛选适宜干旱地区种植的苜蓿品种,本研究以不同苜蓿品种为试验材料,采用聚乙二醇(PEG)模拟干旱胁迫处理,测定苜蓿种子发芽率、发芽指数、简化活力指数和抗旱指数,并利用隶属函数对供试苜蓿材料的抗旱性进行评价。结果表明:随着 PEG 胁迫加剧,供试苜蓿种子的发芽率、发芽指数、简化活力指数及抗旱指数均呈现下降趋势,重度胁迫下,‘龙牧 801’的发芽率、发芽指数及抗旱指数显著高于其他品种($P<0.05$);而‘赛特’和‘赛迪’发芽率、发芽指数、简化活力指数及抗旱指数显著低于其他品种($P<0.05$)。运用隶属函数法评价得出供试苜蓿材料抗旱性强弱顺序为:‘龙牧 801’>‘草原 3 号’>‘WL168HQ’>‘赛特’>‘赛迪’。此研究最终得出‘龙牧 801’苜蓿的抗旱性较强,适宜干旱、半干旱地区种植。

关键词:苜蓿;萌发期;抗旱性;评价

香豆素类衍生物的合成及生物活性研究与香豆素类物质在除草方面的应用研究

陈智超
(扬州大学, 江苏 扬州 450000)

摘要:化学农药在农业病虫害防治中发挥着重要作用,但其残留和抗药性问题日益严峻,开发绿色、高效、高选择性、低毒、低残留的新型农药迫在眉睫。香豆素(学名苯并- α -吡喃酮),作为一种天然产物,广泛存在植物于植物体内,具有低毒、高生物活性、良好环境相容性,是创制绿色新型农药的重要途径。研究结果表明,香豆素类物质的活性因母体苯环或吡喃环上取代基的不同而异,也与取代基的位置密切相关。香豆素类物质在 8 位与 6 位有取代基时活性较更强,在 7 位时则较弱,而当取代基中有羟基等极性较大的基团时活性则会有所降低。另外,4-羟基香豆素类易于合成且具有一定的除草活性,可以作为先导结构进行化学修饰提高其活性。香豆素类化合物普遍具有分子量小的特点,合成相对简单,生物利用度高,对香豆素类物质进行一些简单的化学修饰,如改变取代基的位置、增加官能团等,可以得到比天然产物更高的活性,展现出开发香豆素类除草剂或成为农药中间体的良好潜力,通过抑制杂草种子萌发和幼苗生长,有望开发为环保高效的新型生物源农药。

鸭茅锈病相关病原真菌生理特性研究及毒性分析

吴长凤¹, 易治鑫¹, 江 淮¹, 李林祥¹, 陈玉慧¹, 熊雪梅², 闵星星², 韩玉竹^{1*}

(1. 巴中市农林科学研究院, 四川 巴中 636000; 2. 西南大学动物科学技术学院, 重庆 402460)

摘要:鸭茅是世界著名的优良冷季型牧草,具有耐牧性强、耐荫性强且适应性广的特点,在世界各地广泛种植。锈病是危害鸭茅最重要的病害之一,破坏性强、传播速度快,严重影响其生长、产量和饲草品质。为明确四川(雅安)和重庆(丰都、黔江和荣昌)地区鸭茅锈病病原菌种类及其生物学特性,以荣昌区为试点,从已采集的样品中选取具有各地区代表性的样本进行分子鉴定。样本包括荣昌地区 3 株(编号 PD,PD1,PD2),雅安 2 株(编号 PD3,PD4),丰都 1 株(编号 PD5)和黔江 1 株(编号 PD6),共 7 株病原菌。经形态学和分子生物学进行鉴定,7 株病原菌均为禾柄锈菌(*Puccinia graminis*)。本试验从温度、pH、光照、营养物质等 4 个方面研究锈菌的生物学特性,结果表明:夏孢子萌发的最适宜温度为 20℃,pH 值为 7,12 h 时萌发率分别为 91.86%,93.04%,且 4 h 内孢子萌发速度最快;0.1%的蔗糖对 8 h 内孢子的萌发有促进作用,20%的榨汁能抑制孢子的萌发;光照条件对夏孢子的萌发影响不显著;夏孢子致死温度为 40℃、10 min。回接试验表明,鸭茅接种锈菌后第 4 d 出现褪绿斑点,第 7 d 可观察到裸露孢子堆。同时发现,该地区共存在 4 个生理小种,其中,I 型出现频率为 40.91%,是该地区鸭茅锈病的优势生理小种。本研究报道了由禾柄锈菌引起鸭茅锈病,并从生理学特征方面揭示鸭茅锈病发病特点及毒性,为鸭茅锈病的研究和防治提供参考。

关键词:鸭茅;生物学特性;禾柄锈菌;分离鉴定

Physiological Identification and Toxicity Analysis of Pathogenic Fungi Related to *Dactylis glomerata* L. Rust

WU Chang-feng¹, YI Zhi-xin¹, JIANG Huai¹, CHEN Yu-hui¹,
XIONG Xue-mei², MIN Xing-xing², HAN Yu-zhu^{1*}

(1. Bazhong Academy of Agriculture and Forestry Sciences, Bazhong, Sichuan Province 636000, China;
2. College of Animal Science and Technology, Southwest University, Chongqing 402460, China)

Abstract: Orchardgrass (*Dactylis glomerata* L.) is a well-known cold-season perennial forage species. It has the characteristics of high grazing resistance, shade tolerance and wide adaptability. It is widely cultivated all over the world. Rust is one of the most important diseases that harms Orchardgrass. It is destructive and fast, which seriously affects its growth, yield and forage quality. Through morphological and molecular biological identification, 7 strains of pathogenic bacteria were identified as *Puccinia graminis*. In this experiment, the biological characteristics of rust fungi were studied from four aspects : temperature, pH, light and nutrients. The results showed that the optimum temperature and pH for urediospore germination were 20℃, 7 and 12 h, respectively. The germination rates were 91.86% and 93.04%, respectively, and the spore germination rate was the fastest within 4 h, 0.1% sucrose could promote the germination of spores within 8 h, and 20% juice could inhibit the germination of spores. Light conditions had no significant effect on the germination of urediospores. The lethal temperature of urediospores was 40℃ for 10min. The re-inoculation test showed that chlorotic spots appeared on the 4th day after inoculation with rust, and bare spore piles were observed on the 7th day. At the same time, it was found that there were four physiological races in this area. Among them, the frequency of type I was 40.91%, which was the dominant physiological race of orchardgrass rust in this area. This study reported that *Dactylis glomerata* rust was caused by *Puccinia graminis*, and revealed the characteristics and toxicity of *Dactylis glomerata* rust from the physiological characteristics, which provided a reference for the research and prevention of *Dactylis glomerata* rust.

Key words: Orchardgrass; Biological Characteristics; *Puccinia graminis*; Isolation and identification

作者简介:吴长凤(1993-),女,汉族,助理畜牧师,硕士,主要从事草业科学研究方向,E-mail:15002391137@163.com; * 通信作者:韩玉竹,联系方式:18375854782,E-mail:hanyuzhu@swu.edu.cn

等离子体水处理对秸秆饲料青贮发酵的影响

闫 阳, 魏海龙, 汪晓辉, 王纪栋, 谈重芳, 王雁萍, 蔡义民*, 庞会利*

(郑州大学农学院, 河南 郑州 450000)

摘要:为探究等离子体水处理对秸秆饲料青贮发酵的影响,本研究以用等离子体水 PAW 浇灌的小麦秸秆和普通小麦秸秆为原料,开展不同时间厌氧发酵及有氧暴露处理,综合评价其青贮效果。结果显示,PAW 处理组在发酵 30 d 时乳酸含量达 $151.40 \text{ g} \cdot \text{kg}^{-1}$,显著高于 CK 组,pH 值显著降低,氨态氮含量显著下降,粗蛋白保存率提高,同时中性与酸性洗涤纤维含量显著降低。因此可得出,等离子体水处理可促进青贮过程中的乳酸菌代谢、减少蛋白质分解及强化纤维降解,从而提升小麦秸秆青贮品质,为秸秆饲料化利用提供技术支撑。

关键词:等离子水;小麦秸秆;青贮发酵

Effect of Plasma Water Treatment on Straw Feed Silage Fermentation

YAN Yang, WEI Hai-long, WANG Ji-dong, WANG Xiao-hui, TAN Zhong-fang,
WANG Yan-ping, CAI Yi-min*, PANG Hui-li*

(Zhengzhou University College of Agriculture, Zhengzhou, Henan Province 450000, China)

Abstract: In order to explore the effect of plasma water treatment on straw feed silage fermentation, anaerobic fermentation and aerobic exposure treatment at different times were carried out using wheat straw and ordinary wheat straw watered with plasma water PAW as raw materials, and the fermentation effect was comprehensively evaluated. The results showed that the lactic acid content of the PAW treatment group reached 151.40 g/kg at 30 days of fermentation, which was significantly higher than that of the CK group, the pH was significantly reduced, the ammonia nitrogen content was significantly reduced, the crude protein preservation rate was improved, and the neutral and acidic detergent fiber content was significantly reduced.

Key words: Plasma water; Wheat straw; Silage fermentation

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作者简介:闫阳(2002-),女,陕西延安人,汉族,硕士,主要从事农业废弃物资源饲料化研究,E-mail: 1206100237@qq.com; * 通信作者
Author for correspondence, E-mail: pang@zzu.edu.cn

不同年龄短花针茅根相关微生物组组成的差异

邢佳庆

(内蒙古农业大学草业学院, 内蒙古 呼和浩特 010010)

摘要:短花针茅是干旱半干旱草原的优势建群种,其根相关微生物(根际、非根际、根内生)具有关键作用。本研究以不同放牧强度(无牧、轻度放牧、中度放牧、重度放牧)下的短花针茅幼苗和成株为对象,通过主坐标分析(PCoA)发现,成熟植株与幼苗的根际及内生菌区微生物组构成存在显著分离,这表明两者在根际和内生菌区微生物组成上存在显著差异,且放牧影响程度小于植株年龄的影响。

关键词:荒漠草原;根相关微生物;短花针茅;放牧强度

紫花苜蓿萌发期耐盐性评价及盐胁迫对苗期的影响

于秀明，王玉祥*，张 博*，曾 怡

(新疆农业大学草业学院，新疆 乌鲁木齐 830052)

摘要:紫花苜蓿是一种多年生牧草，在世界各地被广泛种植。土壤盐渍化是世界性难题，也是我国农业生产亟待解决的问题。为探究紫花苜蓿萌发期的耐盐性及苗期对盐胁迫的响应，本研究设置电导率为 10 mS · cm⁻¹，15 mS · cm⁻¹ 的中性复合盐(NaCl : Na₂SO₄ : NaHCO₃ = 1 : 2 : 1)处理组与对照组(CK)进行试验，通过隶属函数分析和综合比较 D 值等方法，评价出两份耐盐材料 Z08，Z14，中等耐盐材料 Z04，Z06，Z07，Z10，Z11，Z17，P19，P20，P21，P22，P23；通过对苗期形态指标、光合指标、生理指标的测定发现，紫花苜蓿在受到复合盐胁迫时，形态指标相应变小，说明生长速度变慢；光合指标与干物质积累同样受到负面影响。同时，紫花苜蓿通过积累可溶性糖和脯氨酸、提高抗氧化酶活性来应对复合盐胁迫。本研究为后续盐碱地苜蓿种植和育种工作提供理论支持。

关键词:紫花苜蓿；耐盐性评价；生理指标

Evaluation of Salt Tolerance during the Germination Stage of *Medicago sativa* L. and the Impact of Salt Stress on the Seedling Stage

YU Xiu-ming, WANG Yu-xiang* , ZHANG Bo* , ZENG Yi

(College of Grassland Science, Xinjiang Agriculture University, Urumqi, Xinjiang 830052, China)

Abstract: *Medicago sativa* L. , as a perennial forage crop, is widely cultivated around the world. Soil salinization has always been a global challenge, and it is also an urgent issue for agricultural production in China. This study aims to explore the salt tolerance evaluation of *Medicago sativa* L. during germination and the effects of salt stress during the seedling stage. Experiments were conducted using neutral compound salts (NaCl : Na₂SO₄ : NaHCO₃ = 1 : 2 : 1) with conductivity levels of 10 mS · cm⁻¹ and 15 mS · cm⁻¹, compared to a control group (CK). Through subordinate function analysis and comprehensive comparison of D values, two salt-tolerant materials, Z08 and Z14, and moderately salt-tolerant materials Z04, Z06, Z07, Z10, Z11, Z17, P19, P20, P21, P22, and P23 were identified. By measuring morphological, photosynthetic, and physiological indicators during the seedling stage, it was found that under compound salt stress, the morphological indicators of *Medicago sativa* L. decreased accordingly, indicating a slower growth rate. Photosynthetic indicators were closely related to dry matter accumulation and were also negatively affected. *Medicago sativa* L. responded to salt stress by accumulating soluble sugars and proline, and by enhancing antioxidant enzyme activity. This study provides theoretical support for subsequent planting and breeding work of *Medicago sativa* L. in saline-alkali soil.

Key words: *Medicago sativa* L. ; Salt tolerance evaluation; Physiological indicators

新疆羊茅种质苗期形态及生理对高温胁迫的响应

于正发¹, 朱莉莉¹, 马诗睿¹, 喻启坤¹, 潘桂芳¹, 李培英^{1,2,3*}, 孙宗玖^{1,2,3}

(1. 新疆农业大学草业学院, 新疆 乌鲁木齐 830052; 2. 新疆草地资源与生态自治区重点实验室, 新疆 乌鲁木齐 830052; 3. 西部干旱区草地资源与生态教育部重点实验室, 新疆 乌鲁木齐 830052)

摘要:全球气候变化导致极端天气频发,极端高温对冷季性草种极为不利,会导致交播草坪建植过程中冷季型草坪草成坪不理想或者返青受阻。羊茅(*Fescue ovain*)在新疆地区广泛分布,且往往作为温性草原、温性荒漠化草原等草地类型建群种或优势伴生种存在,是被广泛应用的冷季型草坪草之一,也是生态修复用“先锋草种”。针对新疆地区羊茅种质夏季越夏困难等问题,本研究以新疆地区分布的 19 份野生材料为研究对象,人工模拟高温环境(35~30℃),测定株高、叶长、叶宽、叶面积等形态指标;光和参数、叶绿素含量、相对电导率、丙二醛、脯氨酸等渗透调节物质,对供试材料进行抗热等级评定。结果表明:高温胁迫下株高、叶长、叶宽、叶面积显著低于 CK,以株高表现最为直观,叶面积变异系数最大为 36%;叶绿素 a 含量在高温胁迫下显著降低,相对电导率上升;F13 在高温环境下净光合速、气孔导度、胞间 CO₂ 浓度显著高于 CK,其余材料均显著下降;丙二醛及脯氨酸含量均呈增加趋势;对 19 份材料进行指标筛选、系统聚类等方法划分为 3 类,分别是耐热型(F3, F13, F24);敏热型(F2, F4);其余材料为中间型。F3, F13, F24 可作为选育耐高温品种优良材料;株高、叶面积、叶绿素含量、光合参数等指标可作为新疆羊茅耐热种质筛选与评价关键指标。

关键词:羊茅种质;高温胁迫;耐热评价;种质资源

短期围栏封育下退化草地补播恢复区植被群落和土壤特征的响应

袁颖^{1,2}, 李希来^{1,2*}, 张静^{2*}, 高佩^{1,2}, 柴瑜^{1,2}, 马婧娟^{1,2}

(1. 青海大学省部共建三江源生态与高原农牧业国家重点实验室, 青海 西宁 810016; 2. 青海大学农牧学院, 青海 西宁 810016)

摘要:为明确短期围栏封育对不同退化斑块高寒草甸的补播恢复效应,本研究针对斑块化退化草甸人工牧草补播恢复区,选取健康草甸(AM)、长期恢复斑块(LP)、短期恢复斑块(SP)三类典型斑块,在河南县设置围栏封育(BQ)与自由放牧(FK)单因素对照试验。结合植被调查、土壤理化性质分析,系统探究了短期围栏封育下植被特征及土壤养分的响应。结果表明:植被与土壤方面 BQ 处理显著提升地上生物量和株高,其中 SP, LP, AM 斑块地上生物量分别较 FK 处理增加 60.99%, 79.65%, 78.19%;AM 斑块株高增加 214.23%;SP 斑块速效磷(AP)在 BQ 处理下分别显著高于 FK 处理 192.67%和 81.10%($P<0.05$)。综上,短期围栏封育通过提升植被生产力、改善土壤养分有效性(尤其是 AP),促进土壤有机碳积累与水分保持,表明其可促进斑块化退化高寒草甸的生态恢复,但不同退化斑块的响应存在异质性。

关键词:斑块化退化;围栏封育;植被特征;土壤特征;二次退化

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作者简介:袁颖(2001-),女,汉,硕士研究生,主要从事退化草地生态修复的研究, E-mail: yying04111208@163.com; * 通信作者 Author for correspondence, E-mail: xilai-li@163.com; qhlxl2001@163.com

盐胁迫下苜蓿中活性氧清除基因的鉴定 及相关抗氧化酶活性研究

余如刚¹, 杜雪玲¹, 韦英铭¹, 李昕霞¹, 王国良^{2*}, 王一凡¹

(1. 淮北师范大学生命科学学院, 安徽 淮北 235000; 2. 山东省农业科学院休闲农业研究所, 山东 济南 250010)

摘要:为鉴定苜蓿耐盐相关的活性氧清除基因,本研究以耐盐品种 HSD-1(G)和盐敏感品种 HSD-2(L)为材料,进行了根和叶比较转录组学分析。共鉴定出 635 个 ROS 清除相关的基因,其中 240 个在各组比较中差异表达。盐胁迫下 *MsAAO1*、*POD72* 和 *GSTU26* 基因在 G 品种中上调表达,在 L 中无差异表达或下调表达。此外,两品种之间比较发现叶中的 POD 活性在 G 品种中高于 L 品种。由此推测这些基因可能是影响两个品种耐盐性差异的调控因子。我们基于同源基因克隆法,成功克隆 *AAO1*、*POD72* 和 *GSTU26* 基因,并利用 RT-qPCR 分析相关基因在不同盐耐性苜蓿品种中的表达模式。实验结果为进一步揭示紫花苜蓿耐盐分子机理奠定基础,为苜蓿耐盐品种改良提供基因资源。

关键词:紫花苜蓿;盐胁迫;活性氧清除;抗氧化酶

Identification of Active Oxygen Scavenging Genes and Study on Related Antioxidant Enzyme Activities in Alfalfa Under Salt Stress

YU Ru-gang¹, DU Xue-ling¹, WEI Ying-ming¹, Li Xin-xia¹, WANG Guo-liang^{2*}, WANG Yi-fan¹

(1. College of Life Sciences, Huaibei Normal University, Huaibei, Anhui Province 235000, China;

2. Institute of Leisure Agriculture, Shandong Academy of Agricultural Sciences, Jinan, Shandong Province 250010, China)

Abstract: To identify the active oxygen scavenging genes related to salt tolerance in alfalfa, the comparative transcriptome analysis of roots and leaves was carried out with salt-tolerant variety HSD-1(G) and salt-sensitive variety HSD-2(L). A total of 635 genes related to ROS scavenging were identified, of which 240 were differentially expressed in each group. Of them, *MsAAO1*, *POD72* and *GSTU26* genes were up-regulated by salinity treatment in HSD-1, but there was no difference or down-regulation in HSD-2. In addition, the comparison between the two varieties showed that the POD activity in leaves of HSD-1 was higher than that of HSD-2. It is speculated that these genes might be the regulatory factors affecting the difference of salt tolerance between the two varieties. Based on homologous gene cloning method, we successfully cloned *AAO1*, *POD72* and *GSTU26* genes, and analyzed the expression patterns of related genes in alfalfa varieties with different salt tolerance by RT-qPCR. The experimental results laid a foundation for further revealing the molecular mechanism of alfalfa salt tolerance and provided genetic resources for the improvement of alfalfa salt-tolerant varieties.

Key words: *Medicago sativa* L.; Salinity stress; Active oxygen scavenging; Antioxidase

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作者简介:余如刚(1976-),男,宁夏盐池人,副教授,博士,主要从事植物逆境生理与分子生物学研究,E-mail: yurugang@126.com; * 通信作者 Corresponding author, E-mail: wangguoliang@126.com

施肥对甘南高寒退化草地的植被恢复效应

张 睿¹, 李春杰^{1,2*}

- (1. 草种创新与草地农业生态系统全国重点实验室/农业农村部草牧业创新重点实验室/草地农业教育部工程研究中心/甘肃省西部草业技术创新中心/兰州大学草地微生物研究中心/兰州大学草地农业科技学院, 甘肃 兰州 730020;
2. 中国林业科学研究院国家林业和草原局草原研究中心, 北京 100091)

摘要:该论文以青藏高原东部甘南玛曲县不同程度退化的高寒草地为研究对象,通过微生物菌剂和有机肥的施用,研究其对草地植被覆盖度、生产力、养分组成的影响,以及土壤理化性质、土壤细菌与真菌丰度与多样性等方面的变化。获得以下主要结果:重度退化草地植被群落结构更易受施肥措施的影响。微生物菌剂和有机肥处理使重度退化草地多样性指数和均匀度指数显著增加 55.55%~78.57%,77.27%和 59.09%~73.33%,76.19% ($P<0.05$)。微生物菌剂+有机肥使重度退化草地的总盖度、多样性指数和均匀度指数显著增加 9.68%,58.54%和 45.24% ($P<0.05$),而对轻度退化草地的影响不明显。微生物菌剂显著提高土壤硝态氮含量,微生物菌剂+有机肥处理显著提高了土壤有机碳含量 ($P<0.05$)。

关键词:高寒退化草地;有机肥;微生物菌剂;植被群落

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作者简介:张睿(1999-),男,安徽合肥人,硕士研究生,主要从事草学方向研究,E-mail:zhr2024@lzu.edu.cn; * 通信作者 Author for correspondence,E-mail: chunjie@lzu.edu.cn

饲喂接种产阿魏酸酯酶罗伊氏乳杆菌苜蓿青贮饲料对奶山羊机体抗氧化和免疫的影响

张艳威, 王 鹏, 毛玉青, 李福厚*

(吉林大学动物科学学院, 吉林 长春 130062)

摘要:为探究接种产阿魏酸酯酶乳酸菌苜蓿青贮饲料对家畜的生产和健康的影响,本研究以紫花苜蓿青贮饲料为材料,通过接种产阿魏酸酯酶乳酸菌(罗伊氏乳杆菌 A4-2)与不产酶菌株(YM13)及空白对照组进行对比,探究其对青贮品质、抗氧化特性及奶山羊健康的影响。结果显示,A4-2 处理显著提高了青贮饲料中乳酸和游离阿魏酸含量,降低了 pH 值,并增强了超氧化物歧化酶(SOD)、过氧化氢酶(CAT)、谷胱甘肽过氧化物酶(GPX)活性及总抗氧化能力(T-AOC)。饲喂试验显示,A4-2 组在 60 d 时显著提升了奶山羊血清抗氧化酶活性,降低了促炎因子 IFN- γ ,TNF- α ,IL-1 β ,IL-2,IL-6 浓度,增加了抗炎因子 IL-4,IL-10 浓度,免疫球蛋白 IgM 浓度。结果表明,饲喂接种产阿魏酸酯酶乳酸菌苜蓿青贮饲料能明显改善奶山羊机体的抗氧化和免疫性能,对预防因氧化应激引发的炎症性疾病具有积极作用

关键词:阿魏酸酯酶;苜蓿青贮;抗氧化;奶山羊;免疫

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作者简介:张艳威(2002-),男,山东聊城人,硕士研究生,主要从事饲草生产加工与高效转化利用研究,E-mail:19861208291@163.com; *通信作者 Author for correspondence,E-mail: lifh@jlu.edu.cn

小黑麦遗传转化体系的条件筛选

张银霞, 田 甜, 马 军, 陈 钰, 杜文华*, 赵方媛, 李 雪, 王玉鹏

(甘肃农业大学草业学院/草业生态系统教育部重点实验室/中-美草地畜牧业可持续发展研究中心, 甘肃 兰州 730070)

摘要:建立小黑麦(*×Triticosecale* Wittmack)遗传转化体系可便于验证和深入探索小黑麦各类功能基因的调控机制, 为引入更多功能基因, 优化小黑麦表型性状和营养品质奠定基础。本研究借助农杆菌介导法以‘甘农2号’小黑麦的1/2成熟胚为外植体, 通过比较侵染浓度($OD_{600\text{ nm}}=0.4$ 和 1.0)、侵染时间(5, 10, 15, 20, 25 min)和共培养时间(1, 2, 3, 4, 5 d)对愈伤组织分化率的影响, 抗生素种类和浓度(头孢霉素(Cefotaxime, Cef)/特美汀(Timentin, Tim): 50, 100, 200, 300, 400 $\text{mg} \cdot \text{L}^{-1}$)对农杆菌的抑制效果及添加卡那霉素(kanamycin, Kan)(25, 50, 75, 100, 125 $\text{mg} \cdot \text{L}^{-1}$)对抗性愈伤分化率的影响, 确定小黑麦遗传转化体系的构建条件。结果表明: 农杆菌浓度为 $OD_{600\text{ nm}}=0.4$, 侵染时间为5 min时愈伤组织分化率为13.33%且显著高于其他染菌处理($P<0.05$), 共培养2 d后愈伤组织出现污染, 抗生素选择50 $\text{mg} \cdot \text{L}^{-1}$ 的Tim可完全抑制农杆菌生长, 125 $\text{mg} \cdot \text{L}^{-1}$ 的Kan作筛选剂时愈伤组织抗性分化率为3.94%, 可达到筛选目的。综上所述, 以1/2成熟胚为外植体建立小黑麦遗传转化体系时可采用 $OD_{600\text{ nm}}=0.4$ 的农杆菌侵染愈伤组织5 min, 经2 d共培养后利用50 $\text{mg} \cdot \text{L}^{-1}$ 的Tim进行脱菌处理, 并利用Kan(125 $\text{mg} \cdot \text{L}^{-1}$)筛选阳性苗。

关键词: 小黑麦; 农杆菌浓度; 侵染时间; 共培养时间; 抗生素选择; 筛选剂浓度

Screening of Conditions for Genetic Transformation System of Triticale

ZHANG Yin-xia, TIAN Tian, MA Jun, CHEN Yu, DU Wen-hua*, ZHAO Fang-yuan, LI Xue, WANG Yu-peng
(College of Grassland Science, Gansu Agricultural University/ Key Laboratory of Grassland Ecosystem, Gansu Agricultural University, Ministry of Education/ Sino-U. S. Centers for Grazingland Ecosystem Sustainability, Lanzhou, Gansu Province 730070, China)

Abstract: The establishment of triticale (*×Triticosecale* Wittmack) genetic transformation system can facilitate the verification and in-depth exploration of the regulatory mechanisms of various functional genes within the triticale, thus laying a foundation for introducing more functional genes, ultimately optimizing the phenotypic traits and nutritional quality of triticale. This study compared the effects of infection concentration ($OD_{600\text{ nm}}=0.4$ and 1.0), infection time (5, 10, 15, 20, 25 minutes), and co-culture time (1, 2, 3, 4, 5 days) on the callus differentiation rate, assessed the inhibitory effects of different antibiotic types and concentrations (cefotaxime (Cef) and timentin (Tim) at 50, 100, 200, 300, 400 $\text{mg} \cdot \text{L}^{-1}$) on *Agrobacterium tumefaciens* and the impact of kanamycin (Kan) at concentrations of 25, 50, 75, 100, 125 $\text{mg} \cdot \text{L}^{-1}$ on the differentiation rate of resistant callus to establish the optimal conditions for the genetic transformation system of triticale by *Agrobacterium*-mediated method using 1/2 mature embryos of triticale ‘Gannong No. 2’ as explants. The results showed that the callus differentiation rate was 13.33% when the *Agrobacterium* concentration was $OD_{600\text{ nm}}=0.4$ and the infection time was 5 min, which was significantly higher than that of other infection treatments ($P<0.05$). After 2 days of co-culture, the callus became contaminated. The use of 50 $\text{mg} \cdot \text{L}^{-1}$ Tim completely inhibited the growth of *Agrobacterium*, while 125 $\text{mg} \cdot \text{L}^{-1}$ Kan could achieve the purpose of screening and the differentiation rate of resistant callus at 3.94%. In summary, when 1/2 mature embryos were used as explants to establish the genetic transformation system for triticale, *Agrobacterium tumefaciens* with $OD_{600\text{ nm}}=0.4$ could be used to infect the callus for 5 min. After 2 days of co-culture, a sterilization treatment with 50 $\text{mg} \cdot \text{L}^{-1}$ Tim was applied, and Kan (125 $\text{mg} \cdot \text{L}^{-1}$) was utilized to screen for positive seedlings.

Key words: Triticale; *Agrobacterium* concentration; Infection time; Co-culture time; Antibiotic selection; Screening agent concentration

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作者简介: 张银霞(1999-), 女, 汉族, 甘肃泾川人, 博士研究生, 主要从事草种质资源及育种栽培研究, E-mail: 18419832231@163.com; * 通信作者 Author for correspondence, E-mail: duwh@gsau.edu.cn

日本南九州地区籽粒苋与传统小谷类作物的产量及牧草品质评价

钟梓轩¹, 新美光宏², 飞佐学², 井户田幸子², 石井康之^{2*}

(1. 郑州大学农学院, 河南 郑州 450000; 2. 日本宫崎大学农学部, 宫崎 日本 889-2152)

摘要:为明确籽粒苋(*Amaranthus hypochondriacus*)在日本南九州夏季牧草生产中改善饲料供给的潜力,于2020和2022年通过栽培试验,对籽粒苋与4种传统的小谷类作物,即粟(*Setaria italica*)、日本稗(*Echinochloa esculenta*)、黍(*Panicum miliaceum*)、高粱(*Sorghum bicolor*)的干物质产量及牧草品质进行了比较。结果表明:开花晚期籽粒苋单茬干物质产量最高(2020年为 $2206.8\text{ g}\cdot\text{m}^{-2}$,2022年粘土团处理为 $1855.0\text{ g}\cdot\text{m}^{-2}$),显著高于多数传统作物;2020年籽粒苋全株体外干物质消化率(IVDMD)和粗蛋白(CP)含量最高,中性洗涤纤维(NDF)含量最低,IVDMD达66.01%、CP达13.32%;但籽粒苋易受台风倒伏(2020年倒伏率31.7%),2022年因虫害和成熟导致IVDMD与CP均降低,但NDF含量仍是最低。本研究表明,籽粒苋在南九州夏季具有高产优质潜力,但仍需优化栽培措施以应对台风和虫害影响。

关键词:籽粒苋;小谷类作物;干物质产量;牧草品质

Yield and Forage Quality of Amaranth and Conventional Small-grain Crops as Forage in Southern Kyushu

ZHONG Zi-xuan¹, Niimi Mitsuhiro², Tobisa Manabu², Itoda Sachiko², Ishii Yasuyuki²

(1. Faculty of Agriculture, Zhengzhou University, Zhengzhou, Henan Province 450000, China;

2. Faculty of Agriculture, University of Miyazaki, Miyazaki 889-2192, Japan)

Abstract: Grain-type amaranth (*Amaranthus hypochondriacus*) production is expected to improve the inferior properties of forage quality and quantity in summer gramineous species. As an introductory experiment, amaranth was compared with four conventional small-grain forage species, i. e. foxtail millet (*Setaria italica*), Japanese barnyard millet (*Echinochloa esculenta*), proso millet (*Panicum miliaceum*) and forage sorghum (*Sorghum bicolor*) by sown in early May 2020 and 2022 to test adaptability, dry matter (DM) yield and quality of forages. In both years, the highest DM yield was observed in the first harvested amaranth. In addition, amaranth also ranked the highest for *in vitro* DM digestibility (IVDMD) and CP content with the lowest neutral detergent fiber (NDF) content in 2020. Both IVDMD and CP content were lower in 2022, since the crops were more mature at harvest, although NDF content was the lowest. Among small-grain grass forages, forage sorghum had the second highest DM yield after amaranth and the highest IVDMD in the first harvest crops. The amaranth crop was extensively damaged in 2020, when 31.7% of the crop was lodged by a strong wind caused by typhoon No. 5. Compared to conventional small grain grass forages, amaranth had the potential for high forage DM yields and quality. However, protecting amaranth plants from typhoon damage requires further study.

Key words: Amaranth; Small-grain cereals; Dry matter yield; Forage quality

叶面肥配施对退化草地生产力及其品质的影响

朱 震

(新疆农业大学, 新疆 乌鲁木齐 830052)

摘要:施肥是一种有效的退化草地修复措施,但目前相关研究多集中于无机肥或有机肥的单施效应,关于不同种类肥料配施及其施用量对草地生态系统的影响尚缺乏系统研究。本试验基于正交试验设计方法,设置4种叶面肥种类[12元素、氨基酸、磷酸二氢钾:液体氮(1:1)、磷酸二氢钾:液体氮(1:2)],4个叶面肥施肥梯度(0,50,100,150 L·hm⁻²);有机肥设置4个施肥梯度(0,2,4,6 t·hm⁻²);4个复合肥施肥梯度(0,50,100,150 kg·hm⁻²)。开展不同种类肥料的配施试验,系统探讨不同施肥处理对退化草地生产力及牧草品质的影响,旨在筛选适用于当地退化草地生态恢复的最优施肥组合。结果表明,在叶面肥种类为磷酸二氢钾:液体氮(1:2)、叶面肥施量100 L·hm⁻²、有机肥施量2 t·hm⁻²、复合肥施量150 kg·hm⁻²的处理下,退化草地的牧草株高、盖度、密度、地上生物量、粗蛋白含量、粗脂肪含量及相对饲喂价值均达到最高,较对照组(CK)分别提高了15.17%,0.40%,33.30%,136.38%,3.10%,13.47%和10.23%。该施肥组合可作为退化草地恢复与生产力提升的推荐施肥方案。

关键词:退化草地改良;草地生产力;牧草品质;叶面肥;有机肥

The Effect of Foliar Fertilisation on the Productivity and Quality of Degraded Grasslands

ZHU Zhen

(Xinjiang Agricultural University, Urumqi, Xinjiang 830052, China)

Abstract: Fertilisation is an effective measure for the restoration of degraded grassland; however, current research predominantly focuses on the effects of applying either inorganic or organic fertilisers alone. There is a lack of systematic studies on the effects of different types of fertiliser combinations and application rates on grassland ecosystems. This experiment, based on orthogonal experimental design methods, sets up four types of foliar fertilisers [12 elements, amino acids, mono-potassium phosphate: liquid nitrogen (1:1), mono-potassium phosphate: liquid nitrogen (1:2)], four gradients of foliar fertiliser application (0, 50, 100, 150 L·hm⁻²); organic fertiliser is set with four application gradients (0, 2, 4, 6 t·hm⁻²); and four gradients of compound fertiliser (0, 50, 100, 150 kg·hm⁻²). Different fertiliser combination experiments were conducted to systematically explore the impact of various fertilisation treatments on the productivity and quality of degraded grassland, aiming to identify the optimal fertilisation combination for ecological restoration of local degraded grassland. The results indicate that the treatment with mono-potassium phosphate: liquid nitrogen (1:2), a foliar fertiliser application of 100 L·hm⁻², organic fertiliser application of 2 t·hm⁻², and compound fertiliser application of 150 kg·hm⁻² produced the highest grass height, coverage, density, above-ground biomass, crude protein content, crude fat content, and relative feeding value, which increased by 15.17%, 0.40%, 33.30%, 136.38%, 3.10%, 13.47%, and 10.23% respectively compared to the control group (CK). This fertilisation combination can be recommended as a fertilisation scheme for the restoration and productivity enhancement of degraded grassland.

Key words: Degraded grassland restoration; Grassland productivity; Forage quality; Foliar fertilizer; Organic fertilizer