



西南林业大学博士研究生招生 “申请-审核制”审核材料

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考生类别：	往届毕业生
申请年度：	2025

4、 外语能力证书

全国大学英语四级考试 成绩报告单



姓 名: 毕珏
学 校: 西南林业大学
院 系: 湿地学院
身份证号: [REDACTED]



笔 试

准考证号: 530060182108622

考试时间: 2018年12月

总分	听力 (35%)	阅读 (35%)	写作和翻译 (30%)
444	158	172	114

口 试

准考证号: --

考试时间: --

等级
--

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高原城市室内灰尘对人角膜上皮细胞损伤研究

毕 珏^{1,2}, 张振宁², 刘雨佳², 杨丹蕾², 郑钦象³, 崔道雷², 向 萍^{2*} (1.西南林业大学湿地学院, 国家高原湿地研究中心, 云南 昆明 650224; 2.西南林业大学生态与环境学院, 环境修复与健康研究院, 云南 昆明 650224; 3.温州医科大学附属眼视光医院, 浙江 温州 325027)

摘要: 收集高海拔城市昆明不同功能区室内灰尘, 利用等离子发射光谱仪分析不同粒径(F1~F4: 100~2000, 75~100, 63~75, 45~63 μ m)灰尘中 Pb, Cu, Cd, Zn, Cr, Ni, Co, As 和 Mn 的含量, 借助人工泪液提取的方法, 测定目标重金属的可溶出率(生物可给性), 并分析室内灰尘人工泪液提取液对人角膜上皮细胞的毒性效应。结果表明, 办公室灰尘中 Ni, Mn, Zn 显著高于家庭及学生宿舍($P<0.01$), 且 Cd, Ni, Zn 的含量高于昆明市土壤背景值的 39.3、9.5、12.3 倍。居民住宅 Co (10.6%)、办公室 As (16.1%) 及学生宿舍 Mn (36.0%) 溶出率最高。重金属元素在粒径分布规律上表现出不同特征, 办公室及宿舍灰尘重金属易在 63~100 μ m 粒径范围内富集。人角膜上皮细胞经室内灰尘人工泪液提取液暴露 24h 后, 低浓度(20 μ g/mL)、高浓度(1280 μ g/mL)分别促进和抑制细胞增殖, 与对照组相比较均具有统计学意义($P<0.05$)。细胞炎症因子 *IL-1 β* 和 *TNF- α* 相对表达量显著增加, 提示昆明室内灰尘暴露有诱发角膜炎症疾病发生的风险。

关键词: 高原城市; 室内灰尘; 重金属; 人角膜上皮细胞; 炎症反应

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Damage to human corneal epithelial cells caused by indoor dust in plateau city. BI Jue^{1,2}, ZHANG Zhen-ning², LIU Yu-jia², YANG Dan-lei², ZHENG Qin-xiang³, CUI Dao-lei², XIANG Ping^{2*} (1.National Plateau Wetland Research Center, College of Wetland, Southwest Forestry University, Kunming 650224, China; 2.Institute of Environment Remediation and Human Health, School of Ecology and Environment, Southwest Forestry University, Kunming 650224, China; 3.Eye Hospital of Wenzhou Medical University, Wenzhou 325027, China). *China Environmental Science*, 2021,41(7): 3360-3370

Abstract: The indoor dust samples were collected from houses, office, and dormitory in a typical high-altitude city Kunming. Each sample was separated into 4 size fractions (F1~F4: 100~2000, 75~100, 63~75, 45~63 μ m), and the concentrations of nine heavy metals (Pb, Cu, Cd, Zn, Cr, Ni, Co, As, and Mn) in indoor dust were detected using ICP-OES. In addition, the solubility rates (bioaccessibility) of the target heavy metals in artificial tears extraction and their cytotoxicity on human corneal epithelial cells (HCECs) were determined. The results showed that Ni, Mn, and Zn in office dust were significantly higher than those in residence and dormitory dust ($P<0.01$), and the contents of Cd, Ni, and Zn were 39.3, 9.5 and 12.3 times higher than the background values of Kunming soils. The solubility rates of Co in residence dust, As in office dust and Mn in dormitory dust were the highest at 10.6%, 16.1%, and 36%, respectively. Heavy metals were highly susceptible to accumulate in office and dormitory dust with particle size ranging from 63 to 100 μ m. Moreover, the typical polygonal and cobblestone appearance of HCECs became spindle shape after artificial tear extracts of office dust exposure. Cell proliferation was enhanced at 20 μ g/mL whereas inhibited at higher concentration ($P<0.05$). The elevated mRNA expression of pro-inflammatory mediators (*IL-1 β* and *TNF- α*) suggested that indoor dust from Kunming may pose a risk to inducing human corneal inflammation.

Key words: plateau city; indoor dust; heavy metals; human corneal epithelial cells; inflammatory reaction

灰尘作为一种复杂、多相的粒子混合物, 异质性强^[1], 来源广泛(土壤、大气沉积颗粒物以及家居材料的磨损脱落等)^[2-4], 化学成分复杂^[5]。室内灰尘被认为是人体摄入和积累污染物的途径之一^[6-8]。据统计, 人们有超过 85% 的时间在室内度过^[9], 且由于室内环境的密闭性, 室内灰尘中的污染物浓度是室外灰尘中污染物浓度的数十倍^[10]。作为室内灰尘中负载的有毒污染物, 重金属因其浓度高、检出率高^[11], 以及暴露后可对人类造成严重危害而被广泛研究。

近年, 国内外已开展室内灰尘中重金属的研究,

结果显示室内灰尘中重金属含量、富集程度高于室外灰尘^[12-13]。不同国家地区、不同功能区室内环境之间的差异, 导致灰尘中重金属含量差异较大, 而污染来源和影响因素也各不相同^[14-15]。粒径作为影响灰尘中重金属含量分布的原因之一。国外学者研究发

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昆明市湿地公园地表灰尘重金属污染特征及健康风险评价

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摘 要:城市湿地公园是人们休闲娱乐的重要场所,但其地表灰尘的人群暴露健康风险却鲜有报道。该研究收集昆明市 3 个最受欢迎的湿地公园景区地表灰尘样品,利用等离子发射光谱仪(ICP-OES)测定灰尘中 Pb、Cd、Hg、As、Zn、Cr、Cu、Ni、Co、Mn 含量,使用地累积指数法(I_{geo})、污染负荷指数法(PLI)和潜在生态风险指数法(RI)探讨湿地公园灰尘重金属污染特征,借助美国环保署健康风险评价模型,开展成人和儿童的重金属健康风险评价。结果表明:灰尘中 10 种重金属平均含量均超昆明市土壤背景值,其中 Cd、Hg 和 Zn 平均含量超背景值 6 倍,Cr、Ni、Co 的 $I_{geo} < 1$ 。污染负荷指数法结果显示 Hg、Cd、Zn 中度污染,Pb、Cu 和 As 则具有中等以上生态风险。人体健康风险评价结果显示,经口摄入为重金属主要暴露途径,其次是皮肤直接接触和呼吸吸入。Ni、As、Cd、Co 和 Cr 的致癌风险值均小于 10^{-6} ,但若长期处于此种环境,可能会存在潜在的致癌风险。对于非致癌元素而言,Pb、Zn、Cu、Mn 非致癌健康风险值都远小于 1,即风险可以忽略。

关键词:高原城市;湿地公园;灰尘;重金属;人体健康风险

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Heavy Metals Pollution Characteristics and Health Risk Assessment of Road Dust in Wetland Parks of Kunming, Southwest China

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Abstract: Urban wetland park is an important place for residents' recreation, however, the pollution characteristics and human health risks of road dust from urban wetland park are still not fully understood. In this study, dust samples on the surface of three main wetland park scenic spots in Kunming City were collected. The content of Pb, Cd, Hg, As, Zn, Cr, Cu, Ni, Co, and Mn were determined by inductively Coupled Plasma Optical Emission Spectrometer (ICP-OES). Index of geo-accumulation (I_{geo}), Pollution Load index (PLI), and Potential Ecological Risk index (RI) were employed to assess the pollution characteristics of heavy metal in wetland park dust. Heavy metal health risk assessments for adults and children were carried out by the U S Environmental Protection Agency's health risk assessment models. The results showed that the average contents of 10 heavy metals in dust exceed the soil background value of Kunming, with Cd, Hg, and Zn exceeding the background value by more than 6 times. The geo-accumulation index (I_{geo}) of Cr, Ni, and Co were below 1. The pollution load index (PLI) indicated that Hg, Cd, and Zn were moderate pollution while Pb, Cu, and As had potential ecological risk that above moderate levels. Human health risk index (HQ) implied that human exposed to heavy metals mainly via mouth, then via skin and respiratory. Though the hazard index (HI) of Ni, As, Cd, Co, and Cr were below 10^{-6} , suggesting cancer risk if staying in this environment for long times. For non-carcinogenic elements, the hazard index (HI) of Pb, Zn, Cu, and Mn were far below 1, indicating that their risks were negligible.

Keywords: plateau city; wetlands parks; dust; heavy metals; human health risks

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第一作者简介:毕 珏(1995-),女,傣族,云南西双版纳人,在读硕士研究生。

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考生类别：	往届毕业生
申请年度：	2025

4、 外语能力证书

全国大学英语四级考试 成绩报告单



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笔 试

准考证号: 530030162103518

考试时间: 2016年12月

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446	133	183	130

口 试

准考证号: --

考试时间: --

等级	--
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成绩报告单编号: 162153003004335



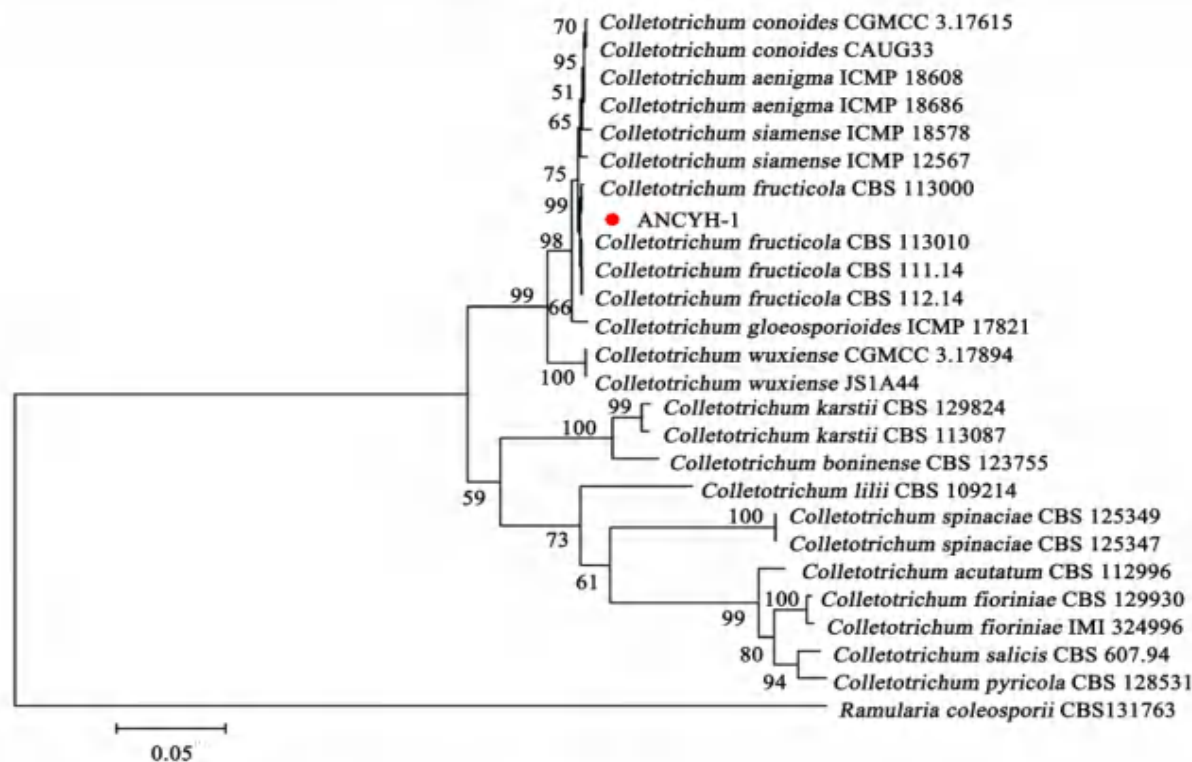


Fig. 3 Phylogenetic tree constructed based on rDNA-ITS, *ACT*, *TUB* and *CHS* sequences with the MEGA 7 software using the maximum-likelihood method

对供试菌株进行分子生物学鉴定。以 ITS、*ACT*、*TUB* 和 *CHS* 这 4 个基因为靶标进行 PCR 扩增,将扩增产物测序,所得序列提交 GenBank,获得登录号分别为 OK483320 (546bp)、OP932953 (289bp)、OP941411 (734bp)、OP941412 (299bp)。利用这些序列在 NCBI 数据库中进行 BLAST 比对,发现 ANCYH-1 菌株的 ITS、*ACT*、*TUB* 和 *CHS* 序列与 *Colletotrichum fruticola* 的模式菌株 CBS113000 相对应的基因序列 KC566781、KC566927、KC566203 和 KC566348 的同源性高达 99%~100%。利用 MEGA 7 中的最大似然法 (Maximum-likelihood, ML),以 ITS-*ACT*-*TUB*-*CHS* 多基因序列构建系统发育树,结果表明,ANCYH-1 菌株与 *Colletotrichum fruticola* 的 4 个菌株单独聚为一支,支持值达到 98% (图 3)。结合菌落形态学特征及多基因序列分析结果,将 ANCYH-1 菌株鉴定为果生炭疽菌 (*Colletotrichum fruticola*)。

本文对云南红梨产区引起彩云红梨炭疽病的

病原进行分离和鉴定,确定该病由 *C. fruticola* 感染引起,与 CHIO 等^[7]、KUANG 等^[8]、QING^[9] 等报道的 *C. fruticola* 具有一致的形态特征^[10]。本研究首次明确了彩云红梨炭疽病的病原,并详细描述了病害症状,为病害发生和流行规律的调查,以及病害监测和防控研究的开展奠定了基础。研究结果对于保障云南省特色红梨产业的健康发展具有重要意义。

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云南彩云红梨炭疽病的病原鉴定

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(云南省农业科学院园艺作物研究所, 昆明 650205)

Identification of the pathogen causing anthracnose on Caiyunhong pear in Yunnan Province HE Yingyun, WANG Lina, YANG Guangzhu, ZHANG Wen, SHU Qun, SU Jun* (Horticulture Research Institute, Yunnan Academy of Agricultural Science, Kunming 650205, China)

Abstract: Anthracnose is one of the most important fungal diseases that pose significant threat to the production of Yunnan red pear cultivar 'Caiyunhong'. The disease mainly causes fruit rot, resulting in a disease incidence of more than 35% in normal conditions. The causal agent was identified as *Colletotrichum fructicola* based on the morphological characteristics, phylogenetic relationship inferred from ITS, *ACT*, *TUB* and *CHS* sequences, and the result of pathogenicity test. This is the first report of *C. Fructicola* causing anthracnose on 'Caiyunhong' fruit in China, which provides a theoretical basis for effective prevention and control of the disease.

Keywords: 'Caiyunhong' pear; anthracnose; *Colletotrichum fructicola*; pathogen identification

中图分类号: S432.1

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文章编号: 0412-0914(2024)01-0000-00

彩云红梨是‘幸水’×‘火把梨’F1杂交优系‘P125’自交选育的红色砂梨新品种,2015年通过云南省林木委员会认定^[1]。该品种肉细、松脆,自然着色率约90%,可溶性固形物大于14%,品质极优,目前主要在云南省安宁市、开远市、泸西县等地种植,远销浙江、广东、上海等地,市场前景广阔。2020—2023年,本研究团队连续3年对彩云红梨示范园的炭疽病发生情况和发病规律进行调查,发现该病主要为害果实,病果于6月份开始出现,然后以较快的速度扩展;一般情况下发病率为35%~52%,在降水密集的7~8月梨果受害率高达60%以上,大大降低了商品果率。鉴于植物炭疽病病原群体的复杂性,明确引起彩云红梨炭疽病的病原种类,对于制定有效的病害防控措施十分重要。

从云南省安宁市史家庄村、云南省农业科学院园艺作物研究所的科技示范园(海拔1900 m,年均

温度19.3℃,年降水量688.6 mm,无霜期360 d)^[2]彩云红梨园(树龄7年,株行距1 m×3.5 m,树势较好,总种植面积350亩)采集病果。梨果感病后,果面初期出现黑色点状病斑,后病斑逐渐扩大,中心凹陷,上有呈同心轮纹状排列的黑色点状物。切开病斑,可见果实内部腐烂至果心(图1-A, B)。采用常规组织分离法^[3]分离病菌,进一步通过单孢分离获得纯培养菌株。经初步观察,所获菌株具有一致的菌落形态,从中选取代表菌株ANCYH-1进行后续研究。

采用分生孢子悬浮液(1×10^6 个·mL⁻¹)喷雾接种法进行离体果实无伤接种测定致病性,以喷洒无菌水处理的作为对照组。将接种后的梨果置于培养箱(28℃,相对湿度(80±5)%,12 h光照/12 h黑暗)培养,每日观察发病情况^[4]。接种后第1 d,果面开始出现黑色小斑点,之后病斑逐渐扩大;接

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计划类别： 人才引培

项目编号： 2023RCYP-02

云南省农业科学院科研项目合同书

项 目 名 称： 彩云红和美人酥梨对炭疽病抗/感病差异基因的筛选和功能分析

承担管理单位（甲方）： 云南省农业科学院

项目承担单位（乙方）： 云南省农业科学院园艺作物研究所

项 目 负 责 人： 何英云 电话： 15198938007

项 目 起 止 年 限： 2023.01.01-2024.12.31

云南省农业科学院制

五、项目经费预算表

金额单位： 万元

预算科目	总预算数	财政资金	自筹资金	备注
一、资金来源合计	30	30	0	
（一）财政资金	30	30	0	
（二）自筹资金	0	0	0	
1. 承担单位自有货币资金				
2. 从银行获得的贷款				
3. 其他财政拨款				
4. 其他资金				
二、支出预算合计	30	30	0	
（一）直接费用	30	30	0	
1. 设备费	0	0	0	
2. 业务费	28	28	0	
3. 劳务费	2	2	0	
（二）间接费用	0	0	0	
三、分年度用款计划				
年度	第一年	第二年	第三年	合计
用款总额	15	15	0	30
财政资金	15	15	0	30
自筹资金	0	0	0	0

九、合同书各责任方

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申请年度：	2025

4、 外语能力证书

Liang, W.K., Li, M.J., Chen, F.L., Wang, Y.Q., Wang, K., Wu, C.Y., Zhu, J.Y. (2025). A venom serpin from the assassin bug *Sycanus croceovittatus* exhibiting inhibitory effects on melanization, development, and insecticidal activity towards its prey. *Pesticide Biochemistry and Physiology*, 209, 106322. (中科院一区 TOP, IF: 4.2)

论文链接: <https://doi.org/10.1016/j.pestbp.2025.106322>

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A venom serpin from the assassin bug *Sycanus croceovittatus* exhibiting inhibitory effects on melanization, development, and insecticidal activity towards its prey

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Keywords:
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ABSTRACT

Serine protease inhibitors (SPIs) have been identified as main common components in the venom of the predatory bugs, while their functional roles remain unexplored. In this study, we identified 35 SPI genes belonging to three subfamilies of serpin, canonical SPI, and AZM in genome of the assassin bug, *Sycanus croceovittatus*. The amino acid sequences of these SPI genes reveal conserved functional regions, albeit with mutations or deletions at certain active site residues. Transcriptomic and qPCR analyses of gene expression patterns in various tissues across developmental stages indicate that most SPI genes exhibit high expression levels in venom apparatus, suggesting their role as venom proteins. Notably, the ScSPI5 gene from the serpin class was found to be most abundantly expressed in all three distinct venom glands, indicating its significant role as a venomous protein. Functional characterization demonstrated that this venom serpin effectively inhibits trypsin activity *in vitro* and suppresses phenoloxidase activity, thereby blocking hemolymph melanization in preys, including *Spodoptera frugiperda*, *Achetura yunnanensis*, and *Tenebrio molitor*. When ingested, it reduces the larval and pupal weight of the fall armyworm by impeding trypsin activity in the midgut. Upon injection, ScSPI5 exhibits a dose-dependent insecticidal effect against *T. molitor*, with an LD₅₀ of 5.5 ± 1.1 µg/g. These findings elucidate the specific functions of SPIs in the venom of predatory bugs, enhancing our understanding of their predation efficiency, and highlighting the potential application of venomous SPIs as protease inhibitors in pest management strategies.

5、学术能力证明材料

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ABSTRACT

Serine protease inhibitors (SPIs) have been identified as main common components in the venom of the predatory bugs, while their functional roles remain unexplored. In this study, we identified 35 SPI genes belonging to three subfamilies of serpin, canonical SPI, and A2M in genome of the assassin bug, *Sycanus croceovittatus*. The amino acid sequences of these SPI genes reveal conserved functional regions, albeit with mutations or deletions at certain active site residues. Transcriptomic and qPCR analyses of gene expression patterns in various tissues across developmental stages indicate that most SPI genes exhibit high expression levels in venom apparatus, suggesting their role as venom proteins. Notably, the ScSPI5 gene from the serpin class was found to be most abundantly expressed in all three distinct venom glands, indicating its significant role as a venomous protein. Functional characterization demonstrated that this venom serpin effectively inhibits trypsin activity *in vitro* and suppresses phenoloxidase activity, thereby blocking hemolymph melanization in preys, including *Spodoptera frugiperda*, *Acheta yunnanensis*, and *Tenebrio molitor*. When ingested, it reduces the larval and pupal weight of the fall armyworm by impeding trypsin activity in the midgut. Upon injection, ScSPI5 exhibits a dose-dependent insecticidal effect against *T. molitor*, with an LD₅₀ of 5.6 ± 1.1 µg/g. These findings elucidate the specific functions of SPIs in the venom of predatory bugs, enhancing our understanding of their predation efficiency, and highlighting the potential application of venomous SPIs as protease inhibitors in pest management strategies.

1. Introduction

Serine protease inhibitors (SPIs) constitute the largest family of protease inhibitors, binding to their target proteases through covalent interactions (Knox, 2007). Based on their action modes, SPIs can be classified into serpins, canonical SPIs, non-canonical SPIs, and α2-macroglobulin (A2M) (Knox, 2007; Orlewski et al., 1999). These molecules play a crucial role in regulating the proteolytic activities of serine proteinases, thereby maintaining organismal homeostasis (Krowczynski et al., 2003; Neurath, 1989). Plant-derived SPIs have attracted attention for their capacity to inhibit serine proteinases prevalent in pest guts (Dunse et al., 2010). By inhibiting the digestive proteases in pests' guts, they disrupt growth and development as well as lead to death (Dunse et al., 2010; Jamal et al., 2012; Ye et al., 2023). Several plant SPI genes have been successfully used to develop pest-resistant plants for pest management purposes (Jagdish and Koundal, 2020; Hilder et al., 1987; Srinivasan et al., 2009). This underscores the potential of SPIs as genetic resources for developing pest management strategies, particularly in the context of producing pest-resistant plant varieties.

SPIs have been identified as one of the primary common venom components in a variety of venomous insects, including bees, parasitoids, ants, caterpillars, neuropteran predators, and predatory bugs (Cecilia Mariano et al., 2019; Fischer et al., 2023b; Sanchez et al., 2019; Walker et al., 2017; Walker et al., 2018; Yan et al., 2017; Yang et al., 2024). In bee venoms, SPIs display antifibrinolytic, antimicrobial, and antielastolytic activities (Kim et al., 2022; Lee et al., 2016). In parasitoid

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0048-3575/© 2025 Elsevier Inc. All rights are reserved, including those for text and data mining, AI training, and similar technologies.

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梁文凯, 刘莎, 王玉琴, 陈芬莲, 朱家颖. 蝎蝽丝氨酸蛋白酶抑制剂基因鉴定及其表达特征分析 [J]. 环境昆虫学报, 2024, 46 (3): 641 – 649. LIANG Wen-Kai, LIU Sha, WANG Yu-Qin, CHEN Fen-Lian, ZHU Jia-Ying. Identification and expression profiling of serine protease inhibitor genes in *Arma custos* [J]. Journal of Environmental Entomology, 2024, 46 (3): 641 – 649.

蝎蝽丝氨酸蛋白酶抑制剂基因鉴定及其表达特征分析

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摘要: 丝氨酸蛋白酶抑制剂 (Serine protease inhibitor, SPI) 是调控昆虫生长发育和免疫的关键因子, 本文从蝎蝽 *Arma custos* 基因组中鉴定出 12 个 SPI 基因 (*AcuSPI1-12*), 并对其序列特征进行分析, 采用逆转录-聚合酶链反应 (Reverse transcription-polymerase chain reaction, RT-PCR) 技术分析了 SPI 基因在成虫不同组织中的表达特征。结果表明, 鉴定出的 SPI 基因可根据其作用机制分为 serpin 类和经典类 (canonical SPI)。多序列比对结果表明, serpin 类 *AcuSPI2-3* 与其它昆虫已知抑制性 serpin 铰链区的氨基酸残基是保守的, 经典类 *AcuSPI7* 和 *AcuSPI8* 具有多个抑制结构域, *AcuSPI12* 只具有单个抑制结构域, 但它们都具有保守的半胱氨酸残基。RT-PCR 结果显示, *AcuSPI4*、*AcuSPI7* 和 *AcuSPI9* 基因在蝎蝽毒液器官中高表达, 且在主腺前叶、主腺后叶和副腺中的表达存在差异, *AcuSPI6* 和 *AcuSPI10* 基因在脂肪体中高表达, *AcuSPI3* 在副腺、肠道和脂肪体中具有较高的表达量, *AcuSPI10* 则在主腺后叶和脂肪体中高表达。研究结果, 不仅表明蝎蝽部分 SPI 可作为毒液成分参与调控猎物免疫反应, 而且为后期揭示它们的生理功能奠定了基础。

关键词: 捕食性蝎; 蝎蝽; 毒液; 丝氨酸蛋白酶抑制剂; 表达特征
中图分类号: Q963; S433 文献标识码: A 文章编号: 1674-0858 (2024) 03-0641-09

Identification and expression profiling of serine protease inhibitor genes in *Arma custos*

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Abstract: Serine protease inhibitors (SPIs) play a crucial role in regulating insect growth, development and immunity. In this study, 12 SPI genes (*AcuSPI1-12*) were identified in *Arma custos* genome and their sequence characteristics were analyzed. The expression pattern of these SPI genes in different adult tissues were examined using reverse transcription-polymerase chain reaction (RT-PCR). According to the action mechanism, the identified SPI genes could be classified into two types, serpin and canonical SPI. Multiple sequence alignment results indicated that the hinge region amino acid residues in *AcuSPI2-3* of the serpin type were conserved with those of known inhibitory serpins from other insects. *AcuSPI7* and *AcuSPI8* belonging to the classical type had multiple inhibitory domains, while *AcuSPI12* only had a single

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申请年度：	2025

4、 外语能力证书

全国大学英语四级考试

成绩报告单





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准考证号: 530060212102903

考试时间: 2021年12月

总分	听力 (35%)	阅读 (35%)	写作和翻译 (30%)
462	167	159	136

口 试

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Article

Elevation and Human Disturbance Interactively Influence the Patterns of Insect Diversity on the Southeastern Periphery of the Tibetan Plateau

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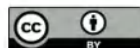
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Simple Summary: In the face of global climate change and escalating human disturbances, insect diversity is facing significant threats. This study aims to investigate the impacts of altitude and human disturbances, as well as their interactions, on insect diversity to establish a strong scientific foundation for effective management measures. The study site selected is located on the southeastern margin of the Tibetan Plateau, one of the world's prominent biodiversity hotspots. We believe that insect diversity plays an important role in the maintenance of biodiversity in this region. A sufficient survey of insect diversity in the area, analyzed in relation to elevation and human disturbances, revealed that insect diversity declined with increasing elevation, moderate disturbance promoted insect diversity to a certain extent, and heavy disturbances significantly reduced it, with an interaction between elevation and human disturbance. Further analyses revealed that the effects of human disturbance on insect diversity varied across elevation. The insect diversity below ~2200 m elevation was higher under low disturbance compared to moderate and heavy disturbance, while above ~2200 m elevation, it was higher under moderate disturbance than low and heavy disturbance. Additionally, different insect taxa showed varying responses to the combination of elevation and disturbance. In this study, the majority of insect taxa exhibited a higher diversity at lower elevations and under low to moderate disturbance conditions, while Hymenoptera demonstrated their ability to maintain high diversity even in areas with high elevation and human disturbances. The findings suggest that when implementing integrated insect management, it is crucial to consider the impacts of elevation and human disturbances on specific insect taxa. Our results not only enhance our comprehension of the factors influencing the diversity and distribution of insects, but also establish a scientific foundation for formulating effective biodiversity conservation and management programs.

Abstract: The maintenance of biodiversity and ecological balance heavily relies on the diversity of insects. In order to investigate the impacts of elevation and human disturbance, as well as their interactions on insect diversity, we conducted an intensive survey of insects in the Hengduan Mountain Range, which is situated on the southeastern periphery of the Tibetan Plateau in China. A total of 50 line transects were established in this study to investigate the impact of elevation and human disturbance on insect diversity and distribution patterns. Designed insect surveys were conducted at various elevations and levels of human disturbance, and statistical methods such as generalized linear modeling and redundancy analysis were employed for data analysis. The results of this study indicated a negative correlation between insect diversity and elevation. Additionally, moderate disturbance was found to have a positive impact on insect diversity to some extent. The explanatory power of the model for the distribution of insect diversity could be improved if elevation and human disturbance were included as an interaction effect into the model, and there

青藏高原东南缘昆虫多样性的海拔梯度格局研究

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摘要:为阐明青藏高原地区昆虫多样性与海拔梯度间的相关性,在青藏高原东南缘的迪庆藏族自治州开展了昆虫多样性的海拔梯度格局研究,调查海拔范围为1 600–3 800 m。基于alpha多样性指数和Jaccard相似性系数,使用回归分析、主成分分析和beta多样性分解等方法探讨了海拔梯度对昆虫多样性分布格局的影响。结果表明:①青藏高原东南缘具有较高的昆虫多样性,4次野外调查共采集到昆虫5 141头,隶属于13目80科;不同海拔梯度上的昆虫群落组成具有差异,相比于高海拔区域,低海拔区域拥有更多的昆虫类群,这可能是由于低海拔地区具有较好的水热条件和生境异质性,可为不同昆虫类群提供适宜生境。②昆虫alpha多样性指数随海拔的升高而降低,可能是由海拔升高引起的温度降低以及植被类型的转变导致。③不同海拔梯度间昆虫群落Jaccard相似性系数在0.36–0.56之间,均表现为中等不相似或中等相似;除低海拔区域外,相邻海拔梯度间昆虫群落的相似性随海拔升高而逐渐降低,这一趋势可能是由海拔梯度升高带来的环境压力改变以及物种对特定海拔的适应性分化引起的。研究显示,青藏高原东南缘的昆虫多样性分布格局受海拔梯度显著影响,低海拔地区具有更高的昆虫多样性,不同海拔梯度具有各自的优势昆虫类群,不同海拔梯度间的多样性差异主要是由于周转而非嵌套导致。该研究结果可为青藏高原昆虫多样性保护提供重要科学依据。

关键词:昆虫多样性;青藏高原;海拔梯度;分布格局;物种周转

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Distribution Patterns of Insect Diversity Along Elevation Gradients in Southeastern Margin of Qinghai-Tibetan Plateau

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Abstract: In order to elucidate the correlation between insect diversity and elevation gradient on the Qinghai-Tibetan Plateau, a study was conducted on the elevation gradient pattern of insect diversity in the Diqing Tibetan Autonomous Prefecture on the southeastern edge of the Tibetan Plateau, with an elevation range of 1600–3800 m above the sea level. Based on the alpha diversity index and Jaccard similarity index, the effect of elevation gradient on the distribution pattern of insect diversity was explored using regression analysis, principal component analysis and beta diversity decomposition. The results showed that the southeastern edge of the Tibetan Plateau had high insect diversity. 5141 insects belonging to 13 orders and 80 families were collected in four field surveys. The composition of insect communities varies along the elevation gradient, with a greater number of insect groups observed at lower elevations than at higher elevations. This may

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申请年度：	2025

4、 外语能力证书

全国大学英语四级考试 成绩报告单



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准考证号：530060192120403

考试时间：2019年12月

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521	190	180	151

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准考证号：--

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5、 学术能力证明材料

1. 已发表的学术论文

[1] 覃悦,杨妍,张磊,卢丽丽,李先平,蒋伟.二倍体和四倍体马铃薯 StGAox 基因鉴定与比较分析 [J]. 生物技术通报, 2025, 41(03): 146-160. (卓越期刊领军期刊)

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DOI:10.13300/j.cnki.hnlkxb.2020.06.005

黄单胞菌分泌蛋白的理化性质及特征分析

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摘要 基于全基因组序列已经公布的黄单胞菌 *Xanthomonas campestris* B100、*Xanthomonas campestris* pv. *campestris* 8004、*Xanthomonas campestris* CN14 中分泌蛋白序列为基础数据,采用 ProtScale、SMART、TargetP 2.0 Server 等生物信息学分析软件对上述分泌蛋白展开理化性质、保守结构域以及转运肽等分析,结果显示:黄单胞菌中分泌蛋白理论等电点与氨基酸长度之间无相关关系,44.73%的蛋白为不稳定蛋白,83.21%的蛋白亲水性小于0,属于亲水性蛋白。同时,在每种黄单胞菌的分泌蛋白中,具有明显保守结构域的蛋白数量平均为12个,并且所有分泌蛋白均具有信号肽,转运肽预测可能性分布也较为平均。

关键词 黄单胞菌;分泌蛋白;理化性质;生物信息学分析;植物病原菌;亚细胞定位;转运肽

中图分类号 S 435.1 **文献标识码** A **文章编号** 1000-2421(2020)06-0030-07

黄单胞菌(*Xanthomonas campestris*)在分类上归属于薄壁菌门(Gracilicutes)暗细菌纲(Scotobacteria)假单胞菌科(Pseudomonadaceae)黄单胞菌属(*Xanthomonas*)^[1]。前人研究发现,该菌是专性好氧、化能有机营养型革兰氏阴性植物病原细菌,能引起十字花科蔬菜及芒果、核桃等多种重要农林经济植物病害,给生产上造成巨大的经济损失,严重影响着上述农林产业的健康发展。近年对该菌的研究主要集中在致病基因功能^[2]、HarpinX 耐热机制^[3]、转录调节因子^[4]、效应蛋白^[6]、该菌与黄原胶的作用关系^[7]以及分类研究^[8]等方面。

植物作为生物界的重要生产者之一,在其生长发育的全过程中始终受到来自于真菌、细菌和卵菌等微生物的侵染^[9]。特别是近年随着对上述微生物分泌蛋白、CAZymes 蛋白研究的不断深入^[10],证实病原细菌与植物相互作用过程中,病原细菌通过分泌系统将分泌蛋白输入到寄主组织中,以更好地侵染植物,这些分泌蛋白还可作为效应分子与植物中的防卫反应相关分子发生作用,从而在植物中实现定殖、扩展等^[11]。前人已对稻瘟菌^[12]、致病疫霉菌^[13]和大丽轮枝菌^[14]等植物病原真菌分泌蛋白开

展了大量研究,笔者所在研究室前期已完成对黄单胞菌 *X. campestris* B100、*X. campestris* CN14、*X. campestris* pv. *campestris* 8004(上述菌株登录号分别为 GCA_000070605.1、GCA_000401735.2、GCA_000012105.1,以下分别简称为 XCB100、XC8004、XCCN14)等黄单胞菌中分泌蛋白的预测工作,然而,尚不清楚其理化性质、保守结构域以及亚细胞定位情况,制约着对该病菌分泌蛋白功能的进一步研究。本研究基于前期研究结果,利用 ProtScale、SMART、TargetP 2.0 Server 等生物信息学分析软件对上述分泌蛋白展开理化性质、保守结构域以及转运肽等分析,以期为进一步开展对分泌蛋白在黄单胞菌侵入寄主植物过程中功能解析奠定基础,也为后续开展生物学实验提供重要的理论支撑。

1 材料与方法

1.1 分泌蛋白序列来源

前期笔者所在研究室根据分泌蛋白所具有的典型特征,从信号肽、亚细胞定位以及跨膜结构等方面入手,利用诸多生物信息学分析软件,确定黄单胞菌 XCB100、XCCN14 和 XC8004 中具有典型特征的分

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农业工程领域高质量科技期刊分级目录

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4	T1	Journal of the ASABE	2769-3295		农业工程综合
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基于全基因组序列的黄单胞菌分泌蛋白质预测及其特征分析

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摘要: 黄单胞菌(*Xanthomonas campestris*)作为诸多革兰氏阴性细菌之一,主要危害十字花科农作物和核桃、芒果等经济林植物。前人对植物病原细菌、真菌等的分泌蛋白和相关蛋白质开展了预测及分析研究,明确其分泌蛋白在致病过程中具有非常重要的作用。本研究以已经公布全基因组序列的黄单胞菌 *X. campestris* B100、*X. campestris* pv. *campestris* str.8004、*X. campestris* CN14 中的蛋白质序列为基础,结合细菌中分泌蛋白的基本特征,采用在线分析程序(包括 SignalP v5.0、ProtComp v9.0 等)对上述 3 个黄单胞菌的分泌蛋白序列进行预测和分析,明确上述细菌中分别含有 135 个、128 个、135 个分泌蛋白,并对分泌蛋白所具有的基本特征开展分析,为深入研究黄单胞菌分泌蛋白的功能打下理论基础。

关键词: 黄单胞菌; 全基因组; 信号肽; 生物信息学

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Prediction and characteristic analysis of *Xanthomonas campestris* secretory protein based on whole genome sequence

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Abstract: As a kind of many Gram-negative bacteria, *Xanthomonas campestris* mainly harms cruciferous crops and economic forest plants such as walnut and mango. Some academic predecessors discovered that secretory proteins played an important role in the pathogenic process by predicting and analyzing the secreted proteins and related proteins of plant pathogenic bacteria and fungi. This study was based on the protein sequences of *X. campestris* B100, *X. campestris* pv. *campestris* str.8004 and *X. campestris* CN14 whose whole genome sequences had been published, combined with the basic characteristics of secretory proteins, using online analysis programs (such as SignalP v5.0, ProtComp v9.0, etc.) to predict and analyze the above three protein sequences, it was found that the bacteria contained 135, 128 and 135 secretory proteins, respectively, and analysis on the basic characteristics of secretory proteins was carried out, thus made theoretical foundation for the in-depth study of the function of *X. campestris* secretory proteins.

Key words: *Xanthomonas campestris*; genome; signal peptide; bioinformatics

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植物作为生物界的重要生产者,其在生长过程中始终面临着诸如真菌、细菌等微生物的侵害^[1]。在危害茄科、十字花科以及胡桃科等多种重要经济作物的诸多病原细菌中,尤以黄单胞菌(*Xanthomonas campestris*)造成的危害较重,该细菌在分类



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4、 外语能力证书



Article

Characterization of PEBP-like Genes and Function of *Capebp1* and *Capebp5* in Fruiting Body Regeneration in *Cyclocybe aegerita*

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Abstract: Phosphatidylethanolamine-binding proteins (PEBPs) play a crucial role in the growth and development of various organisms. Due to the low sequence similarity compared to plants, humans, and animals, the study of *pebp* genes in fungi has not received significant attention. The redifferentiation of fruiting bodies is exceedingly rare in fungal development. Hitherto, only a few studies have identified the *Capebp2* gene as being associated with this phenomenon in *Cyclocybe aegerita*. Thus, exploring the role of *pebp* genes in fruiting body development is imperative. In the present study, four *Capebp* genes (*Capebp1*, *Capebp3*, *Capebp4*, and *Capebp5*) were cloned from the ACD007 strain of *C. aegerita* based on genome sequencing and gene prediction. The findings indicate that the *pebp* family, in *C. aegerita*, comprises a total of five genes. Moreover, the sequence similarity was low across the five CAPEBP protein sequences in *C. aegerita*, and only a few conserved sequences, such as HRY and RHE, were identical. Expression analyses revealed that, similarly to *Capebp2*, the four *Capebp* genes exhibit significantly higher expression levels in the fruiting bodies than in the mycelium. Furthermore, overexpressed and RNA interference *Capebp1* or *Capebp5* transformants were analyzed. The results demonstrate that overexpression of *Capebp1* or *Capebp5* could induce the regeneration of the lamella or fruiting body, whereas the knockdown of *Capebp1* or *Capebp5* could lead to the accelerated aging of fruiting bodies. These findings highlight a significant role of *Capebp* genes in the generation of *C. aegerita* fruiting bodies and provide a foundation for further exploration into their involvement in basidiomycete growth and development.

Keywords: *Cyclocybe aegerita*; fruiting body development; lamella redifferentiation; overexpression; PEBP; RNA interference

1. Introduction

Phosphatidylethanolamine-binding protein (PEBP) was initially identified as a cytoplasmic soluble protein in the bovine brain and is known to have a strong affinity to phosphatidyl ethanolamine [1]. The structural domains conserved across the PEBP family in plants and animals consist of a large beta-sheet flanked by small beta-sheets on either side and two alpha-helices at the C-terminal. Also, the structure contains a highly conserved phosphate-binding pocket, which plays a crucial role in the functionality of the PEBP family [2,3]. The PEBP superfamily comprises over 400 members, markedly conserved across the evolutionary spectrum from bacteria to humans [4].

Mammals have four types of PEBP proteins: PEBP1, PEBP2, PEBP3, and PEBP4 [5]. The PEBP1 protein binds to RAF-1 and acts as an inhibitor of MEK phosphorylation and activation, thereby playing a critical role in cell signaling [6]. On the other hand,



A Putative Guanosine Triphosphate Cyclohydrolase I Named CaGCH1 Is Involved in Hyphal Branching and Fruiting Development in *Cyclocybe aegerita*

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Guanosine triphosphate (GTP) cyclohydrolase I (GCH1) is the limiting enzyme of the tetrahydrobiopterin (BH4) synthesis pathway. The disruption of *gch1* gene may cause conditional lethality due to folic acid auxotrophy in microorganisms, although the function of *gch1* in basidiomycetes has not been deciphered so far. In the present study, *gch1* expression in *Cyclocybe aegerita* (*cagch1*) was downregulated using the RNAi method, which resulted in growth retardation in both solid and liquid medium, with the hyphal tips exhibiting increased branching compared to that in the wild strain. The development of fruiting bodies in the mutant strains was significantly blocked, and there were short and bottle-shaped stipes. The transcriptional profile revealed that the genes of the MAPK pathway may be involved in the regulation of these effects caused by *cagch1* knockdown, which provided an opportunity to study the role of *gch1* in the development process of basidiomycetes.

Keywords: GCH1, fruiting body development, *Cyclocybe aegerita*, RNAi, hyphal branch

INTRODUCTION

Guanosine triphosphate (GTP) cyclohydrolase I (GCH1; EC 3.5.4.16) is the first enzyme to act in the biosynthesis of tetrahydrobiopterin (BH4). GCH1 catalyzes the conversion of GTP into dihydroneopterin triphosphate and formic acid (Nardese et al., 1996), and this reaction is the rate-limiting step in the *de novo* synthesis of BH4 in plants and microorganisms (Burg and Brown, 1968). Although bacteria, fungi, and plants can synthesize tetrahydrofolic acid; mammals consume folates in the form of vitamins in food. BH4 is crucial to invertebrates as it serves as a coenzyme of aromatic amino acid hydroxylase (Werner et al., 2011) and a cofactor of nitric oxide synthase (NOS) (Gorren and Mayer, 2002), in addition to being an essential regulatory factor of melanin biosynthesis (Chen et al., 2015) and a component of the synthesis process of various hormones and neurotransmitters (Werner et al., 2011). BH4 also serves as a cofactor for a variety of inflammatory factors and neurotransmitters (Latremoliere et al., 2015). In addition to being crucial for BH4 synthesis, GCH1 is reported to play an important role in the pathogenesis of neuropathological pain (Kim et al., 2009), Parkinson's disease (Xu et al., 2017), diabetes (Wang et al., 2020), and cardiovascular diseases (Chuaiphichai et al., 2014).



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4、 外语能力证书

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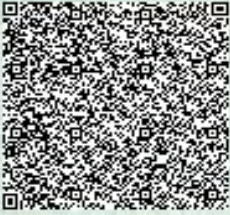
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- 10 -



Article

Monitoring Pine Shoot Beetle Damage Using UAV Imagery and Deep Learning Semantic Segmentation Under Different Forest Backgrounds

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Abstract: The outbreak of Pine Shoot Beetle (PSB, *Tomicus* spp.) posed a significant threat to the health of Yunnan pine forests, necessitating the development of an efficient and accurate remote sensing monitoring method. The integration of unmanned aerial vehicle (UAV) imagery and deep learning algorithms shows great potential for monitoring forest-damaged trees. Previous studies have utilized various deep learning semantic segmentation models for identifying damaged trees in forested areas; however, these approaches were constrained by limited accuracy and misclassification issues, particularly in complex forest backgrounds. This study evaluated the performance of five semantic segmentation models in identifying PSB-damaged trees (UNet, UNet++, PAN, DeepLabV3+ and FPN). Experimental results showed that the FPN model outperformed the others in terms of segmentation precision (0.8341), F1 score (0.8352), IoU (0.7239), mIoU (0.7185) and validation accuracy (0.9687). Under the pure Yunnan pine background, the FPN model demonstrated the best segmentation performance, followed by mixed grassland-Yunnan pine backgrounds. Its performance was the poorest in mixed bare soil-Yunnan pine background. Notably, even under this challenging background, FPN still effectively identified diseased trees, with only a 1.7% reduction in precision compared to the pure Yunnan pine background (0.9892). The proposed method in this study contributed to the rapid and accurate monitoring of PSB-damaged trees, providing valuable technical support for the prevention and management of PSB.

Keywords: pine shoot beetle; forest pest monitoring; UAV imagery; deep learning; semantic segmentation model



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1. Introduction

Forest ecosystems play a pivotal role in maintaining global biodiversity, regulating the climate, and providing essential ecosystem services such as water and air purification, as well as the production of wood, fiber, fuel, and food [1]. As some of the most species-rich ecosystems on Earth, forests are crucial for carbon sequestration and soil protection [2]. However, they are increasingly threatened by a range of disturbances, including wildfires, storms, insect outbreaks, and human activities [3]. Among these, insect infestations represent a natural yet significant driver of forest ecosystem dynamics. In the context of



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(54) 发明名称

一种网隙裂粉韧革菌培养基及其培养方法

(57) 摘要

本发明提供一种网隙裂粉韧革菌培养基及其培养方法。所述培养基包括健康松树木粉、麦芽浸膏和酵母膏。本发明提供的网隙裂粉韧革菌培养基的成分和配比科学合理,培养网隙裂粉韧革菌的生长速度更快,部分能长出子实体,且不容易被污染,为松树蜂共生菌的进一步研究甚至是松树蜂的防治奠定了基础。



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4、 外语能力证书

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YANG Taijiao, ZHANG Wei, LUO Jianmei, et al. Antifungal activity of *Mikania micrantha* extract against *Magnaporthe oryzae* [J]. Journal of South China Agricultural University, 2025, 46(1): 81-88.

薇甘菊提取物对稻瘟病菌的抑菌活性

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(云南省高校森林灾害预警控制重点实验室/西南林业大学林学院, 云南昆明 650224)

摘要: 【目的】以入侵物种薇甘菊 *Mikania micrantha* 为材料, 探究其不同提取物及组分对稻瘟病菌 *Magnaporthe oryzae* 的抑菌活性。【方法】以稻瘟病菌为供试病原菌, 采用生长速率法对采自云南德宏的薇甘菊提取物进行室内抑菌活性测定, 并通过柱层析对提取物的抑菌活性组分进行追踪。【结果】在初筛质量浓度为 1 mg/mL 时, 薇甘菊乙酸乙酯萃取物对稻瘟病菌有较好的抑菌活性, 抑菌率为 49.84%。对薇甘菊乙酸乙酯萃取物的 14 个柱层析组分进行抑菌活性追踪, 组分 Fr₅、Fr₆、Fr₁₂、Fr₁₃ 抑菌效果显著, 在接种后第 9 天的 EC₅₀ 分别为 1.691、2.134、0.865、0.818 mg/mL; 4 个组分均使菌丝质量减轻, MDA 含量升高, 菌丝形态畸变。【结论】本研究发现薇甘菊提取物对稻瘟病菌有较好的抑菌效果, 为综合开发利用薇甘菊提供了新思路, 也为稻瘟病菌的绿色防控提供了科学依据。

关键词: 植物提取物; 稻瘟病菌; 薇甘菊; 生长速率法; 抑菌活性
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Antifungal activity of *Mikania micrantha* extract against *Magnaporthe oryzae*

YANG Taijiao, ZHANG Wei, LUO Jianmei, LI Qing, NIE Shanshan, LIAO Shimei, FU Tao, YAN Xiaohui
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Abstract: 【Objective】*Mikania micrantha*, an invasive species, was used as a material to investigate the antifungal activity of different extracts and components against *Magnaporthe oryzae*. 【Method】The antifungal activity of *M. micrantha* extract from Dehong of Yunnan Province was determined by growth rate method with *M. oryzae* as the test pathogen, and the antifungal active components of the extract were traced by column chromatography. 【Result】At the initial screening mass concentration of 1 mg/mL, *M. micrantha* ethyl acetate extract showed potent antifungal activity against *M. oryzae*, with the inhibition ratio of 49.84%. The antifungal activity tracking of 14 column chromatography components of the ethyl acetate extract showed that the antifungal activities of Fr₅, Fr₆, Fr₁₂ and Fr₁₃ were significant, EC₅₀ values on day 9 after inoculation were 1.691, 2.134, 0.865 and 0.818 mg/mL, respectively. All the four active components resulted in the reduction of

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Morphological and molecular identification for four new wood-inhabiting species of *Lyomyces* (Basidiomycota) from China

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Abstract

Fungi are one of the most diverse groups of organisms on Earth, in which the wood-inhabiting fungi play an important role in forest ecosystem processes and functions. Four new wood-inhabiting fungi, *Lyomyces hengduanensis*, *L. niveomarginatus*, *L. wumengshanensis* and *L. zhaotongensis*, are proposed, based on morphological features and molecular evidence. *Lyomyces hengduanensis* differs in the brittle basidiomata with pruinose hymenial surface, a monomitic hyphal system and ellipsoid basidiospores (3.5–6 × 3–4.5 µm). *Lyomyces niveomarginatus* is distinguished by the subceraceous basidiomata with crackled hymenial surface, a monomitic hyphal system and ellipsoid basidiospores (4.5–7 × 3–4 µm). *Lyomyces wumengshanensis* is distinguished by the grandinoid hymenial surface, a monomitic hyphal system and ellipsoid to broad ellipsoid basidiospores (4–6 × 3–5 µm). *Lyomyces zhaotongensis* is unique in the grandinoid hymenial surface, a monomitic hyphal system and broadly ellipsoid basidiospores measuring as 2.6–3.5 × 2.5–3 µm. Sequences of ITS and nLSU rDNA markers of the studied samples were generated and phylogenetic analyses were performed using the Maximum Likelihood, Maximum Parsimony and Bayesian Inference methods. The phylogram, based on the ITS+nLSU rDNA gene regions, included three genera within the Schizoporaceae viz. *Fasciodontia*, *Lyomyces* and *Xylodon*, in which the four new species were grouped into *Lyomyces*. The phylogenetic tree inferred from the ITS sequences highlighted that *L. hengduanensis* group with *L. zhaotongensis* and then closely grouped with *L. crustosus*, *L. ochraceoalbus*, and *L. vietnamensis*. The new taxon *L. niveomarginatus* was retrieved as a sister to *L. juniperi*. The new species *L. wumengshanensis* was sister to *L. macrosporus*. The new taxon *L. zhaotongensis* grouped with *L. hengduanensis* and then closely grouped with *L. crustosus*, *L. ochraceoalbus* and *L. vietnamensis*.

Key words: Biodiversity, phylogenetic analyses, taxonomy, Yunnan Province

Introduction

Fungi are one of the most diverse groups of organisms on Earth and play an indispensable role in the forest ecosystem processes and functioning (Hyde 2022; Guan et al. 2023; Deng et al. 2024a). The wood-inhabiting fungal family

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一、项目的技术要求

西南林业大学赵长林发表论文被 SCI 收录、期刊影响因子及中科院 JCR 分区情况。

1. 标题: **Morphology and multigene phylogeny revealed four new species of *Xylodon* (Schizoporaceae, Basidiomycota) from southern China**

作者: Yuan, Q(Yuan, Qi)[1,2];Zhao, CL(Zhao, Changlin)[1,2]

二、情报检索情况:

1. 检索数据库: Science Citation Index Expanded (SCI-E) 网络版
Journal Citation Reports (JCR)
中科院 JCR 分区数据库

2. 检索式: 略

三、检出文献情况 (编号、名称、文献题目及出处)

(一) SCI-E 收录

1. 标题: **Morphology and multigene phylogeny revealed four new species of *Xylodon* (Schizoporaceae, Basidiomycota) from southern China**

作者: Yuan, Q(Yuan, Qi)[1,2];Zhao, CL(Zhao, Changlin)[1,2];

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(二) 期刊影响因子(IF)

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MYCOKEYS	2.8	2.8

(三) 中国科学院 JCR 期刊分区(2023 年)

期刊全称	ISSN	所属大类	大类分区	Top 期刊
MYCOKEYS	1314-4057	生物学	2	否

四、检索结论

依照用户委托，通过国际联机数据库检索，具体结果如下：

(一) SCI 收录：西南林业大学赵长林以通讯作者发表的 1 篇论文已被 SCI-E 收录；

(二) 期刊影响因子见上表；

(三) 中国科学院 JCR 期刊分区见上表。

以上检索结论已经清华大学图书馆信息中心验证，并可在 SCI-E、JCR、中国科学院 JCR 期刊分区数据库中检索、验证。

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检索员职称：助理馆员

审核员（签字）：

审核员职称：副研究馆员

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2024 年 11 月 22 日



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考生类别：	往届毕业生
申请年度：	2025



Article

The Entry of Pollinating Fig Wasps Plays a Pivotal Role in the Developmental Phase and Metabolic Expression Changes in *Ficus hookeriana* Figs

Ying Zhang ^{1,2,†}, Yunfang Guan ^{1,2,†}, Zongbo Li ^{2,3}, Yan Wang ^{1,2}, Changqi Chen ^{1,2}, Xiaoyan Yang ^{1,2} and Yuan Zhang ^{1,2,3,*}

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Abstract: The fig (the syconium of the *Ficus* tree) and its pollinating fig wasp represent exceptional examples for researching plant–insect interactions due to their remarkable specificity in species interaction and mutually beneficial symbiotic relationship. However, the mechanisms underlying the developmental process of monoecious figs in response to the entry of pollinating fig wasps (pollinators) and the metabolic changes occurring during this process remain elusive. Our study employed a combination of controlled experiments in the field and LC–MS methods to investigate the impact of pollinating fig wasp entry on the developmental phase of figs, as well as the metabolic alterations occurring during this process. A total of 381 metabolites and 155 differential metabolites were identified, with the predominant classes of metabolites being organic acids, lipids, and benzene aromatic compounds. The results suggest that in the absence of wasp entry, the receptive phase of fig would exhibit an extended duration. However, upon the entry of fig wasps, the receptive phase of figs would terminate within a span of 1 to 2 days, concomitant with substantial fluctuations in the composition and proportions of metabolites within the fig. Our research focuses on the analysis of linoleic acid metabolism, phenylpropanoid biosynthesis, and flavonoid biosynthesis pathways. Our findings suggest that the entry of wasps triggers alterations in the metabolic regulatory mechanisms of figs. Prior to wasp entry, metabolites primarily regulate fig growth and development. However, after wasp entry, metabolites predominantly govern lipid accumulation and the establishment of defense mechanisms, indicating a transition in fig development. This metabolic perspective explains why figs promptly enter an interflower phase that is not attractive to pollinating fig wasps after their entry, and how figs achieve reproductive balance through the regulation of different metabolic pathways. This study provides scientific evidence for elucidating the stability mechanism of the fig wasp mutualistic system.

Keywords: pollinating fig wasp; monoecious; symbiosis; receptive phase; syconium

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5、学术能力证明材料



forests



Article

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不同外源激素处理对榕属植物种子萌发和幼苗生长的影响

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(1.西南林业大学生物多样性保护学院, 昆明 650224;

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摘要:为探究植物外源激素对榕树种子萌发及幼苗生长的影响,采用3种传统激素(IAA、GA、6-BA)的5个浓度(0(ck), 10, 20, 40, 80 mg/L),分别对雌雄同株榕树桑叶榕和雌雄异株榕树小叶榕进行处理,研究各处理对种子萌发及幼苗生长的影响。结果表明,3种外源激素对榕树种子萌发和幼苗生长均具有一定的促进效应,但不同激素的促进效应存在差异,同一激素的不同浓度对种子萌发和幼苗生长的影响不同,相同浓度的同一激素对不同的榕树种子萌发和幼苗生长影响也不同。总体来说,3种激素的一定浓度范围对榕树种子萌发率及种子活力的提高、萌发时间的缩短有一定的促进作用,能够促进生根、拓展根系生长,促进根系的生长,但两种榕属植物种子的萌发和幼苗生长及对激素的响应不同。

关键词: 外源激素; 榕属植物; 种子萌发; 萌发特性; 幼苗生长

DOI: 10.16590/j.cnki.1001-4705.2023.06.080

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Effects of Different Exogenous Hormone Treatments on Seed Germination and Seedling Growth of *Ficus* Plant

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Abstract: In order to explore the effects of exogenous plant hormones on seed germination and seedling growth of *Ficus* tree, five concentrations of 3 traditional hormones such as auxin (IAA), gibberellin (GA) and cytokinin (6-BA) at 0 mg/L (control group), 10 mg/L, 20 mg/L, 40 mg/L and 80 mg/L, were carried out on monoecious *Ficus benjamina* and dioecious *Ficus hispida*, respectively, to explore effect of each treatment on seed germination and seedlings. Research results showed that the three kinds of exogenous hormones on *Ficus* tree seed germination and seedling growth had certain stimulative effect, while different hormones had different promoting effects on seeds and seedlings of *Ficus* trees. Different concentrations of the same hormone had different effects on seed germination and seedling growth, and the same concentration of the same hormone had different effects on seed germination and seedling growth of different *Ficus* trees. Generally speaking, the three hormones in different concentration ranges could promote the *Ficus* tree seed germination rate and seed vigor, shorten the germination time to a certain extent, could promote rooting, extending rhizoid growth, or promote root growth, but the responses of seed germination and seedling of two *Ficus* plants to hormones were different.

Key words: exogenous hormone; *Ficus* plants; germination of seed; germinating characteristic; seedling growth

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