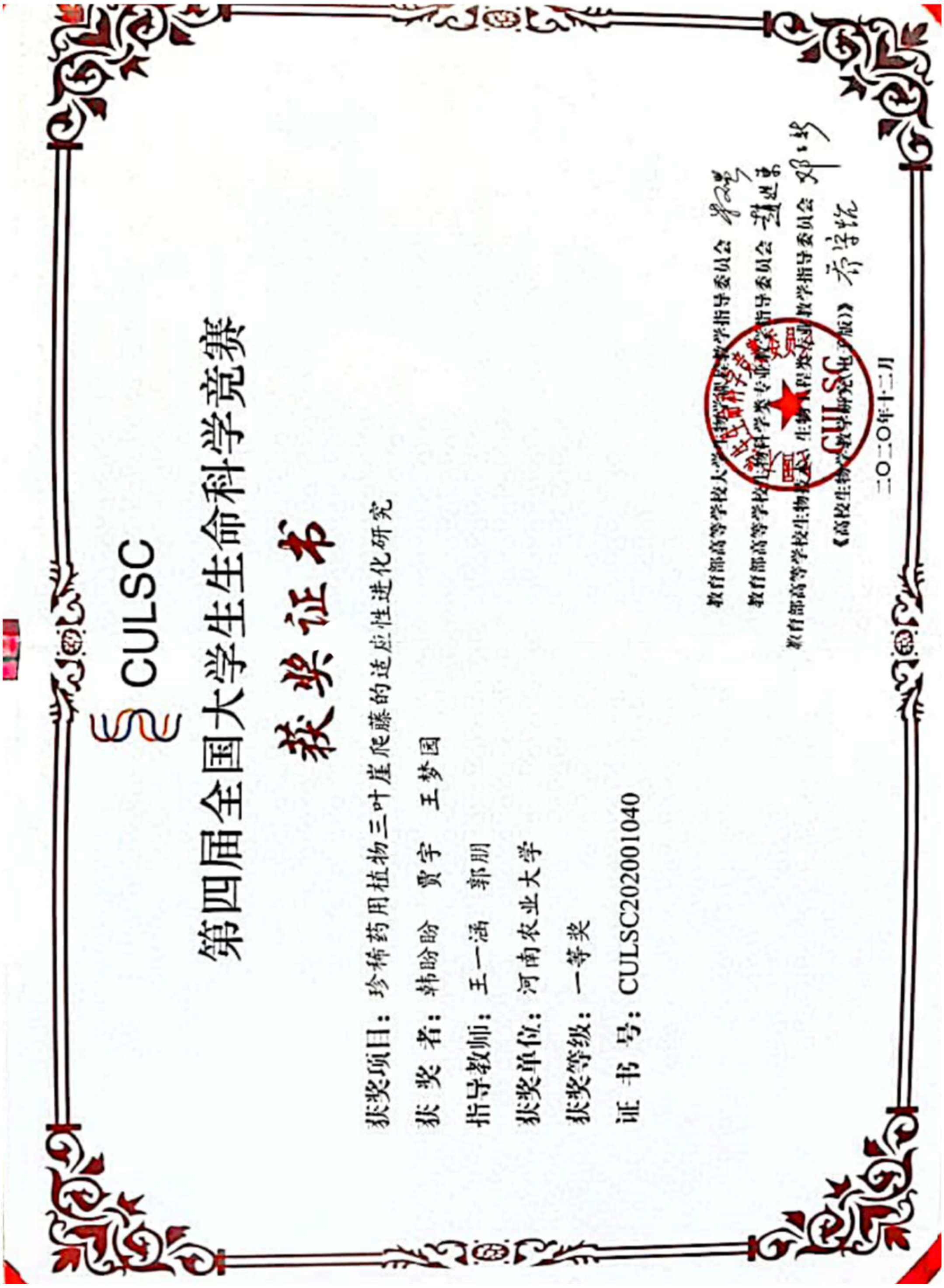
2. 成果受益学生培养成效

2.1 学科竞赛

2.1.1 2020年第四届全国大学生生命科学竞赛一等奖1项



CULSC

第四届全国大学生生命科学竞赛

获奖证书

获奖项目：珍稀药用植物三叶崖爬藤的适应性进化研究

获 奖 者：韩盼盼　贾宇　王梦园

指导教师：王一涵　郭朋

获奖单位：河南农业大学

获奖等级：一等奖

证 书 号：CULSC202001040

教育部高等学校大学生物学课程教学指导委员会

教育部高等学校生物科学类专业教学指导委员会

教育部高等学校生物技术、生物工程类专业教学指导委员会

《高校生物学教学研究（电子版）》

二〇二〇年十二月

2.1.2　2022 年全国大学生生命科学竞赛一等奖 1 项

CULSC

全国大学生生命科学竞赛

2022，科学探究类

获奖项目

高抗白粉病小麦-尾状山羊草7C渐渗系的创制及抗病相关基因挖掘

获奖学生

孙梦欣、张慧颖、宁喜喜、董文婧、智文艳

指导教师

李欢欢、刘文轩

获奖单位

河南农业大学

获奖等级

一等奖

证书编号

CULSC2022KY0113

全国大学生生命科学竞赛委员会
二〇二二年八月

2.1.3 2023 年全国第一届乡村振兴志愿服务技能大赛三等奖 1 项

CPIPC 中国研究生创新实践系列大赛

获奖证书

CERTIFICATE

河南农业大学　刘文新、袁煜翔、刘雯君、李雪盈、郭晟乾

在中国研究生乡村振兴科技强农+创新大赛“欣浩翔杯”第一届乡村振兴志愿服务技能大赛中表现优异，荣获中国研究生乡村振兴科技强农+创新大赛

三等奖

指导教师：陈云、袁志良

中国学位与研究生教育学会　中国科协青少年科技中心

二〇二三年十月

证书编号：2023055O199

2.1.4　2024 年大学生创新创业训练计划项目

河南省教育厅办公室关于开展2024年大学生创新创业训练计划立项和结题验收的通知

[河南省教育厅] 作者：　2024-05-24 09:23:47 | 分享到：

各本科高校：

为贯彻落实《国务院办公厅关于深化高等学校创新创业教育改革的实施意见》，落实《河南省进一步支持大学生创新创业若干措施》，根据《河南省大学生创新创业训练计划管理办法》，按照教育部高等教育司《关于开展2024年国家级大学生创新创业训练计划立项和结题验收工作的通知》要求，现就我省2024年本科高校大学生创新创业训练计划（以下简称“大创计划”）立项及结题验收工作通知如下。

一、立项要求

（一）重点支持项目。面向世界科技前沿、面向经济主战场、面向国家重大需求、面向人民生命健康，鼓励引导大学生围绕基础学科以及新工科、新医科、新农科、新文科等关键领域开展创新实践，设立国家级大学生创新训练计划重点支持项目（以下简称重点支持项目）。

重点支持项目本着“有限领域、有限规模、有限目标”的原则，支持具有一定创新性的基础理论研究项目和有针对性的应用研究项目持续深化研究和实践，鼓励开展新兴边缘学科研究和跨学科的交叉综合研究。研究团队要有效利用高校和社会现有的重点实验室、协同创新中心、工程研究中心、国际科技合作基地、大学科技园、技术中心、技术转移中心、实验教学示范中心等研究平台所拥有的一流学科和科研资源，积极开展前沿性科学研究、颠覆性原创性技术创新、实质性创业实践

热点资讯
- 2024年河南省普通高校招生本科一批院校平行
- 内乡县第七小学：尊重教师权益 彰显人文关怀
- 2024年濮阳市普通高中招生录取最低控制分数
- 平顶山市2024年中招统招批次正录投档线（市
- 关于本科提前批、国家专项计划本科批、对口
- 本科一批、艺术本科批、地方专项计划本科批
- 中招录取分数线公布！涉及洛阳这些高中
- 商丘市教育体育局关于2024年普通高中招生录

微信
- @河南高考生，投档、进档、预录、退档、征
- 河南多所高校2024年招生计划公布！专业、人
- 2024年河南本科提前批等批次今日开始填报志
- 河南省2024年高招一分一段表出炉！
- 河南2024年高考分数线公布！附志愿填报及录

项目编号	学院	项目名称	项目类型	项目负责人	指导教师
2023CX099	园艺学院	CO2在果蔬保鲜中的作用机理初探及应用研究	创新训练项目	刘怡萌	胡青霞
2023CX100	园艺学院	辣椒耐热相关基因功能分析	创新训练项目	宋云慧	刘珂珂
2023CX101	园艺学院	基于甜瓜核心种质的耐冷性GWAS分析及优异育种材料的创制	创新训练项目	周然然	李琼
2023CX102	园艺学院	生物菌肥改良菜田土壤重金属污染	创新训练项目	李鹏举	董韩、朴凤植
2023CX103	园艺学院	紫斑牡丹种子发育特性及其产量构成因子研究	创新训练项目	杨甜甜	郭鑫、娄雪源
2023CX104	园艺学院	功能性芽菜生物活性成分富集技术研究	创新训练项目	张恩	王凡、李阳
2023CX105	园艺学院	光敏色素作用因子*CsPIF7b*调控茶树低温胁迫的分子机制研究	创新训练项目	赵洋	班秋艳
2023CX106	园艺学院	黄瓜矮化基因*dw-2*的图位克隆和功能验证	创新训练项目	卢志林	杨森
2023CX107	信息与管理科学学院	“双碳”目标下河南省数字乡村发展赋能农业碳生产率增长的机制研究	创新训练项目	盛德青	侯建、沙德春
2023CX108	信息与管理科学学院	“农乡视联”可视农业创新技术开发与应用	创新训练项目	李安迪	汪强、乔红波
2023CX109	信息与管理科学学院	基于量本利分析的生猪养殖项目的经济评价研究	创新训练项目	邓宏灿	马巧云
2023CX110	信息与管理科学学院	边缘计算环境下资源分配模型及算法研究	创新训练项目	马擎智	刘冰杰、董萍
2023CX111	信息与管理科学学院	计算机代数系统与非线性扩散方程的条件Lie-Bäcklund对称	创新训练项目	王一铭	汪松玉、姬利娜
2023CX112	生命科学学院	重要资源植物苍山冷杉的种质资源评价与保护	创新训练项目	刘佳雨	邵毅贞、刘凤琴
2023CX113	生命科学学院	糖基转移酶ZmXYXT2调控玉米拟轮枝镰孢菌抗性的作用机制解析	创新训练项目	李玉坤	徐玉芳，张会勇
2023CX114	生命科学学院	桂花幼枝^{60}Co-γ 射线辐照诱变及表型变异研究	创新训练项目	杨佳豪	王一涵、郭明
2023CX115	生命科学学院	大豆高油基因的图位克隆及功能初探	创新训练项目	刘梦雨	岳岩磊、李涛

2.1.5　2021 年全国大学生生命科学竞赛河南省赛区一等奖 1 项

CULSC　HEN-CULSC

全国大学生生命科学竞赛(2021,科学探究类)河南省赛区

获奖证书

获奖项目：基于时间分化假说的大型真菌物种多样性维持机制分析

获奖等级：一等奖　　**获 奖 者：**陈云、张梦帆、张潇瑜、杜苗、刘意帆

指导教师：陈云、袁志良　　**获奖单位：**河南农业大学

全国大学生生命科学竞赛河南省赛区委员会

2021 年 11 月

证书号：HA-CULSC2021KY0011

2.1.6　2022 年全国大学生生命科学竞赛河南省赛区二等奖 5 项

CULSC　HEN-CULSC

全国大学生生命科学竞赛(2022,科学探究类)河南省赛区

获奖证书

获奖项目：基于代谢组解析彩叶桂彩叶呈色机制

获奖等级：二等奖　　获 奖 者：轩雨蒙、张欣欣、刘丰赫

指导教师：郭朋、王一涵　　获奖单位：河南农业大学

全国大学生生命科学竞赛河南省赛区委员会

2022 年 8 月

证书号：HA-CULSC2022KE0071

CULSC HEN-CULSC

全国大学生生命科学竞赛(2022,科学探究类)河南省赛区

获奖证书

获奖项目：玉米磷素感应蛋白 SPXs 与 PHR1 蛋白的分子互作研究

获奖等级：二等奖

获 奖 者：贾小洁、楚舒雅、郭林峰、张文顺、孙雨晴

指导教师：刘娜

获奖单位：河南农业大学

全国大学生生命科学竞赛河南省赛区委员会

2022 年 8 月

CULSC HEN-CULSC

全国大学生生命科学竞赛(2022,科学探究类)河南省赛区

获奖证书

获奖项目： 重要资源植物苍山冷杉复合体的保护遗传学研究

获奖等级： 二等奖

获 奖 者： 王伟、滕汝鑫、王宗帆

指导教师： 邵毅贞、陈云

获奖单位： 河南农业大学

全国大学生生命科学竞赛河南省赛区委员会
2022年8月

证书号：HA-CULSC2022KE0068

CULSC HEN-CULSC

全国大学生生命科学竞赛(2022,科学探究类)河南省赛区

获奖证书

获奖项目：基于浅层测序的世界榆属（Ulmus）DNA 条形码研究

获奖等级：二等奖

获 奖 者：王贝、白凯博、马玉凡、张晓康、叶子怡

指导教师：林楠、刘燕培

获奖单位：河南农业大学

全国大学生生命科学竞赛河南省赛区委员会

2022 年 8 月

证书号：HA-CULSC2022KE0113

CULSC HEN-CULSC

全国大学生生命科学竞赛(2022,科学探究类)河南省赛区

获奖证书

获奖项目： 单加氧酶 HhMO 催化烯烃不对称环氧化的立体控制机制研究

获奖等级： 二等奖

获 奖 者： 刘倩、袁子豪、帅文通、刘琰

指导教师： 林晖、陈红歌

获奖单位： 河南农业大学

全国大学生生命科学竞赛河南省赛区委员会

2022年8月

证书号： HA-CULSC2022KE0106

2.1.7　2021 年全国大学生生命科学竞赛河南省赛区二等奖 1 项

CULSC　HEN-CULSC

全国大学生生命科学竞赛(2021,科学探究类)河南省赛区

获奖证书

获奖项目：花粉管萌发蛋白 PsiP 在提高玉米耐热性中的作用机制

获奖等级：二等奖　　**获 奖 者：**谢长龙、宋豪淇、刘颂、刘梦真、

指导教师：胡秀丽，赵玉龙　　**获奖单位：**河南农业大学

全国大学生生命科学竞赛河南省赛区委员会

2021 年 11 月

证书号：HA-CULSC2021KE0066

2.1.8　2022 年全国大学生生命科学竞赛河南省赛区三等奖 3 项

CULSC　HEN-CULSC

全国大学生生命科学竞赛(2022,科学探究类)河南省赛区

获奖证书

获奖项目：ShinyCircos：交互式创建 Circos 图的 R/Shiny 应用程序

获奖等级：三等奖　　　获 奖 者：王亚洲、张潇、董依涵、田格、邓兆龙

指导教师：姚文、李阳　　　获奖单位：河南农业大学

全国大学生生命科学竞赛河南省赛区委员会

2022 年 8 月

证书号：HA-CULSC2022KE0202

CULSC HEN-CULSC

全国大学生生命科学竞赛(2022,科学探究类)河南省赛区

获奖证书

获奖项目： 亲环素 A 通过调控 Twist1 稳定性调节 A549 细胞凋亡

获奖等级： 三等奖

获 奖 者： 张艳艳、李文青、李梦瑶、梁泽阳、杨雨

指导教师： 刘薇、岳岩磊

获奖单位： 河南农业大学

全国大学生生命科学竞赛河南省赛区委员会

2022 年 8 月

证书号：HA-CULSC2022KE0175

CULSC HEN-CULSC

全国大学生生命科学竞赛(2022,科学探究类)河南省赛区

获奖证书

获奖项目：呋喃醛耐受酵母中功能基因簇的发掘鉴定

获奖等级：三等奖

获 奖 者：李世文、朱添添、熊萌萌、李若楠、范崇政

指导教师：王旭、刘娜

获奖单位：河南农业大学

全国大学生生命科学竞赛河南省赛区委员会

2022年8月

证书号：HA-CULSC2022KE0227

2.1.9 2021年全国大学生生命科学竞赛河南省赛区三等奖3项

CULSC HEN-CULSC

全国大学生生命科学竞赛(2021,科学探究类)河南省赛区

获奖证书

获奖项目：酪蛋白激酶2（CK2）在增强玉米高温胁迫中的作用机制

获奖等级：三等奖

获 奖 者：宋鲁豫、杜涛、邓宏旭

指导教师：刘燕培、杨浩

获奖单位：河南农业大学

全国大学生生命科学竞赛河南省赛区委员会

2021年11月

证书号：HA-CULSC2021KS0054

CULSC 全国大学生生命科学竞赛（2021，创新创业类）

获奖证书

获奖项目： 抗白粉病小麦-高大山羊草3Sl易位系的创制及3Sl染色体特异分子标记的开发

获 奖 者： 裴少龙、付巧、卞翔、崔天庆、刘璐

指导老师： 李欢欢、刘文轩

获奖单位： 河南农业大学

获奖类型： 三等奖（创新类）

证 书 号： CULSC2021CS0050

全国大学生生命科学竞赛委员会

二〇二一年十一月

CULSC 全国大学生生命科学竞赛（2021，科学探究类）

获奖证书

获奖项目： 高大山羊草广谱抗白粉病基因*Pm13a*的精细定位与候选基因挖掘

获 奖 者： 裴少龙 付巧 卞翔 吴希凡 孙正好

指导教师： 李欢欢 刘文轩

获奖单位： 河南农业大学

获奖类型： 三等奖

证 书 号： CULSC2021KS0106

全国大学生生命科学竞赛委员会
二〇二一年十一月

2.2 发表论文

2.2.1　本科生王亚洲以第一作者在 iMeTa（IF=27.3）发表论文，指导老师：姚文，2023 年

Received: 23 February 2023 | Revised: 1 April 2023 | Accepted: 13 April 2023
DOI: 10.1002/imt2.109

PROTOCOL

iMeta WILEY

shinyCircos-V2.0: Leveraging the creation of Circos plot with enhanced usability and advanced features

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Abstract

We previously developed shinyCircos, an interactive web application for creating Circos diagrams, which has been widely recognized for its graphical user interface and ease of use. Here, we introduce shinyCircos-V2.0, an upgraded version of shinyCircos that includes a new user interface with enhanced usability and many new features for creating advanced Circos plots. To help users get started with shinyCircos-V2.0, we provide detailed tutorials and example input data sets. The application is available online at https://venyao.xyz/shinyCircos/ and https://asiawang.shinyapps.io/shinyCircos/, or can be installed locally using the source code deposited in GitHub (https://github.com/YaoLab-Bioinfo/shinyCircos-V2.0).

KEYWORDS
Circos, data visualization, R/Shiny, shinyCircos, web application

Highlights

- We presented a web application shinyCircos-V2.0 for creation of a Circos plot.
- shinyCircos-V2.0 is an upgraded version of shinyCircos with a more user-friendly interface and many new features.
- Detailed tutorials and example input data sets are provided to enhance the usability of shinyCircos-V2.0.

INTRODUCTION

Circos [1] is a visualization tool developed by Krzywinski et al. in 2009 for comparative genomics, which has become an indispensable tool for newly sequenced genomes and other genomic studies. It enables the visualization of various types of genomic data, including single nucleotide polymorphisms, InDels, genes, DNA methylation, and others, in a circular format. Since its development, the Circos plot has been frequently utilized to demonstrate similarities or differences among diverse genomic features associated with the same genomic regions. A typical Circos plot consists of

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Yazhou Wang and Lihua Jia contributed equally to this study.

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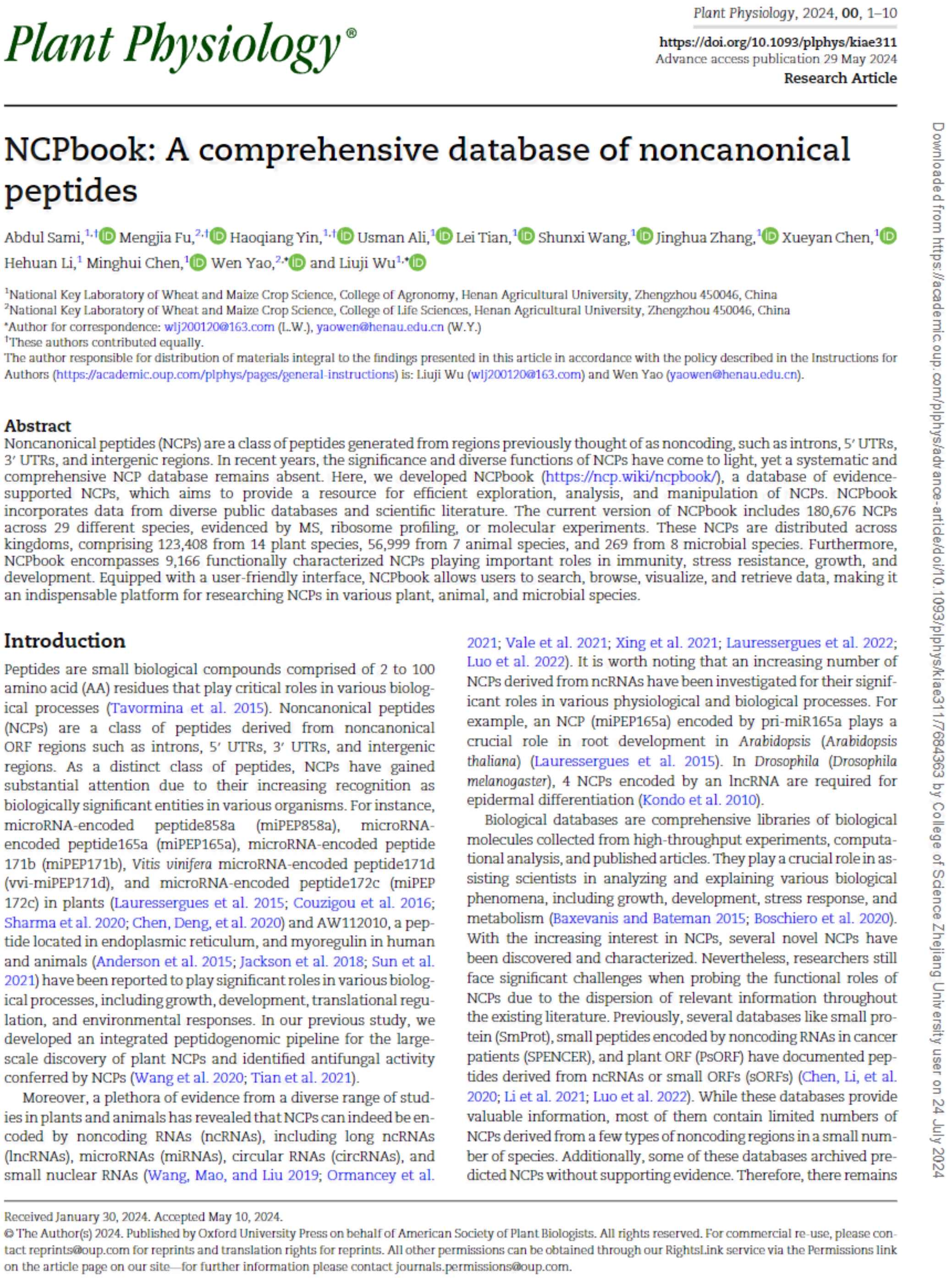
2.2.2　本科生付梦镓以第二作者在 Plant Physiology（中科院 1 区，IF=8.0）发表论文，指导老师：姚文，2024 年



Plant Physiology

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Research Article

NCPbook: A comprehensive database of noncanonical peptides

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Abstract

Noncanonical peptides (NCPs) are a class of peptides generated from regions previously thought of as noncoding, such as introns, 5′ UTRs, 3′ UTRs, and intergenic regions. In recent years, the significance and diverse functions of NCPs have come to light, yet a systematic and comprehensive NCP database remains absent. Here, we developed NCPbook (https://ncp.wiki/ncpbook/), a database of evidence-supported NCPs, which aims to provide a resource for efficient exploration, analysis, and manipulation of NCPs. NCPbook incorporates data from diverse public databases and scientific literature. The current version of NCPbook includes 180,676 NCPs across 29 different species, evidenced by MS, ribosome profiling, or molecular experiments. These NCPs are distributed across kingdoms, comprising 123,408 from 14 plant species, 56,999 from 7 animal species, and 269 from 8 microbial species. Furthermore, NCPbook encompasses 9,166 functionally characterized NCPs playing important roles in immunity, stress resistance, growth, and development. Equipped with a user-friendly interface, NCPbook allows users to search, browse, visualize, and retrieve data, making it an indispensable platform for researching NCPs in various plant, animal, and microbial species.

Introduction

Peptides are small biological compounds comprised of 2 to 100 amino acid (AA) residues that play critical roles in various biological processes (Tavormina et al. 2015). Noncanonical peptides (NCPs) are a class of peptides derived from noncanonical ORF regions such as introns, 5′ UTRs, 3′ UTRs, and intergenic regions. As a distinct class of peptides, NCPs have gained substantial attention due to their increasing recognition as biologically significant entities in various organisms. For instance, microRNA-encoded peptide858a (miPEP858a), microRNA-encoded peptide165a (miPEP165a), microRNA-encoded peptide 171b (miPEP171b), *Vitis vinifera* microRNA-encoded peptide171d (vvi-miPEP171d), and microRNA-encoded peptide172c (miPEP 172c) in plants (Lauressergues et al. 2015; Couzigou et al. 2016; Sharma et al. 2020; Chen, Deng, et al. 2020) and AW112010, a peptide located in endoplasmic reticulum, and myoregulin in human and animals (Anderson et al. 2015; Jackson et al. 2018; Sun et al. 2021) have been reported to play significant roles in various biological processes, including growth, development, translational regulation, and environmental responses. In our previous study, we developed an integrated peptidogenomic pipeline for the large-scale discovery of plant NCPs and identified antifungal activity conferred by NCPs (Wang et al. 2020; Tian et al. 2021).

Moreover, a plethora of evidence from a diverse range of studies in plants and animals has revealed that NCPs can indeed be encoded by noncoding RNAs (ncRNAs), including long ncRNAs (lncRNAs), microRNAs (miRNAs), circular RNAs (circRNAs), and small nuclear RNAs (Wang, Mao, and Liu 2019; Ormancey et al. 2021; Vale et al. 2021; Xing et al. 2021; Lauressergues et al. 2022; Luo et al. 2022). It is worth noting that an increasing number of NCPs derived from ncRNAs have been investigated for their significant roles in various physiological and biological processes. For example, an NCP (miPEP165a) encoded by pri-miR165a plays a crucial role in root development in *Arabidopsis* (*Arabidopsis thaliana*) (Lauressergues et al. 2015). In *Drosophila* (*Drosophila melanogaster*), 4 NCPs encoded by an lncRNA are required for epidermal differentiation (Kondo et al. 2010).

Biological databases are comprehensive libraries of biological molecules collected from high-throughput experiments, computational analysis, and published articles. They play a crucial role in assisting scientists in analyzing and explaining various biological phenomena, including growth, development, stress response, and metabolism (Baxevanis and Bateman 2015; Boschiero et al. 2020). With the increasing interest in NCPs, several novel NCPs have been discovered and characterized. Nevertheless, researchers still face significant challenges when probing the functional roles of NCPs due to the dispersion of relevant information throughout the existing literature. Previously, several databases like small protein (SmProt), small peptides encoded by noncoding RNAs in cancer patients (SPENCER), and plant ORF (PsORF) have documented peptides derived from ncRNAs or small ORFs (sORFs) (Chen, Li, et al. 2020; Li et al. 2021; Luo et al. 2022). While these databases provide valuable information, most of them contain limited numbers of NCPs derived from a few types of noncoding regions in a small number of species. Additionally, some of these databases archived predicted NCPs without supporting evidence. Therefore, there remains

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2.2.3　2019 级本科生周宇朝在 Frontiers in Genetics（JCR Q2）发表论文

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Using landscape genomics to assess local adaptation and genomic vulnerability of a perennial herb *Tetrastigma hemsleyanum* (Vitaceae) in subtropical China

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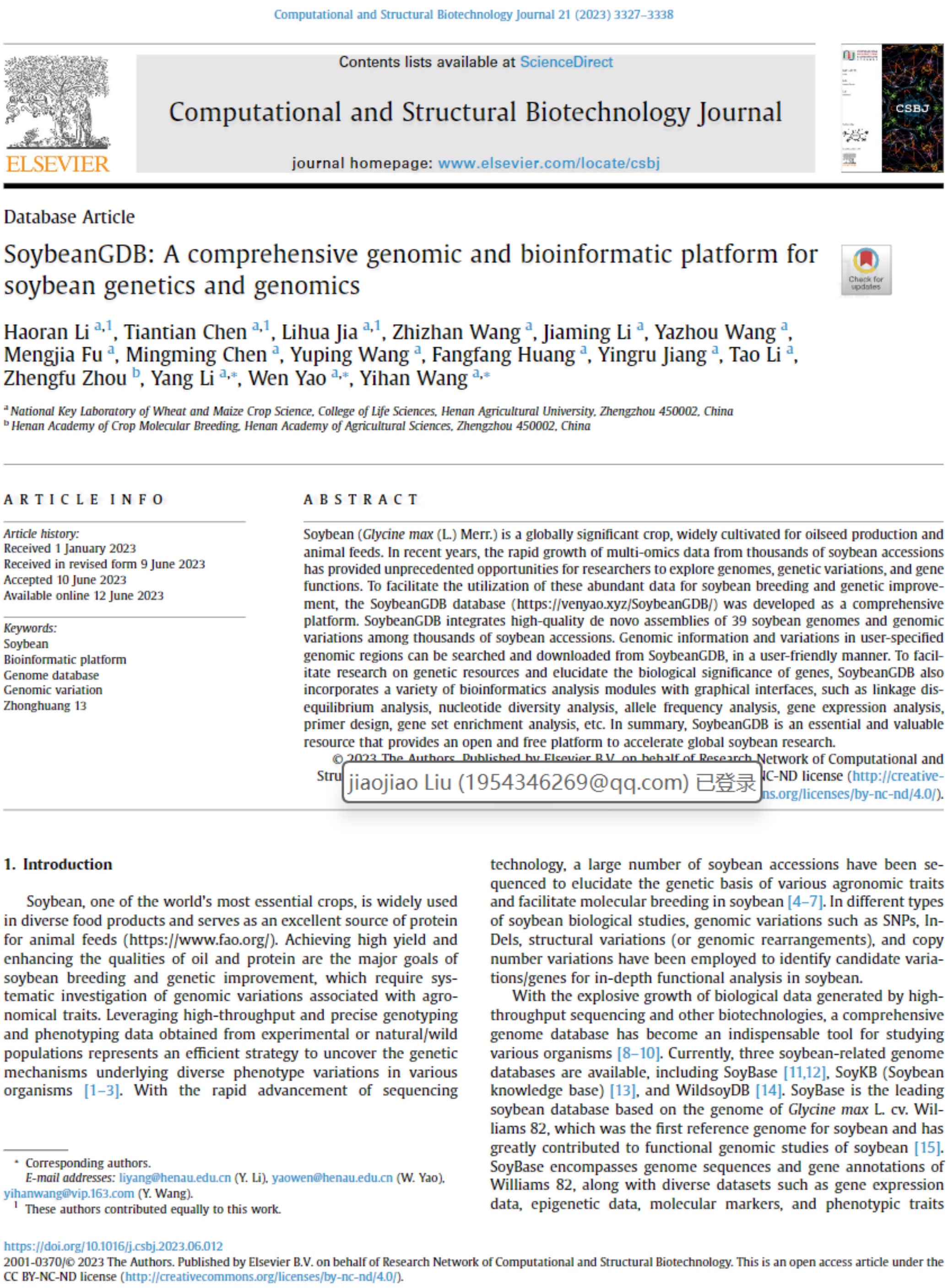
Understanding adaptive genetic variation of plant populations and their vulnerabilities to climate change are critical to preserve biodiversity and subsequent management interventions. To this end, landscape genomics may represent a cost-efficient approach for investigating molecular signatures underlying local adaptation. *Tetrastigma hemsleyanum* is, in its native habitat, a widespread perennial herb of warm-temperate evergreen forest in subtropical China. Its ecological and medicinal values constitute a significant revenue for local human populations and ecosystem. Using 30,252 single nucleotide polymorphisms (SNPs) derived from reduced-representation genome sequencing in 156 samples from 24 sites, we conducted a landscape genomics study of the *T. hemsleyanum* to elucidate its genomic variation across multiple climate gradients and genomic vulnerability to future climate change. Multivariate methods identified that climatic variation explained more genomic variation than that of geographical distance, which implied that local adaptation to heterogeneous environment might represent an important source of genomic variation. Among these climate variables, winter precipitation was the strongest predictor of the contemporary genetic structure. F_{ST} outlier tests and environment association analysis totally identified 275 candidate adaptive SNPs along the genetic and environmental gradients. SNP annotations of these putatively adaptive loci uncovered gene functions associated with modulating flowering time and regulating plant response to abiotic stresses, which have implications for breeding and other special agricultural aims on the basis of these selection signatures. Critically, modelling revealed that the high genomic vulnerability of our focal species via a mismatch between current and future genotype-environment relationships located in central-northern region of the *T. hemsleyanum*'s range, where populations require proactive management efforts such as assistant adaptation to cope with ongoing climate change. Taken together, our results provide robust evidence of local climate adaption

2.2.4 2019 级本科生陈甜甜在 Computational and Structural Biotechnology Journal（JCR Q2）发表论文



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Database Article

SoybeanGDB: A comprehensive genomic and bioinformatic platform for soybean genetics and genomics

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A B S T R A C T

Soybean (*Glycine max* (L.) Merr.) is a globally significant crop, widely cultivated for oilseed production and animal feeds. In recent years, the rapid growth of multi-omics data from thousands of soybean accessions has provided unprecedented opportunities for researchers to explore genomes, genetic variations, and gene functions. To facilitate the utilization of these abundant data for soybean breeding and genetic improvement, the SoybeanGDB database (https://venyao.xyz/SoybeanGDB/) was developed as a comprehensive platform. SoybeanGDB integrates high-quality de novo assemblies of 39 soybean genomes and genomic variations among thousands of soybean accessions. Genomic information and variations in user-specified genomic regions can be searched and downloaded from SoybeanGDB, in a user-friendly manner. To facilitate research on genetic resources and elucidate the biological significance of genes, SoybeanGDB also incorporates a variety of bioinformatics analysis modules with graphical interfaces, such as linkage disequilibrium analysis, nucleotide diversity analysis, allele frequency analysis, gene expression analysis, primer design, gene set enrichment analysis, etc. In summary, SoybeanGDB is an essential and valuable resource that provides an open and free platform to accelerate global soybean research.

1. Introduction

Soybean, one of the world's most essential crops, is widely used in diverse food products and serves as an excellent source of protein for animal feeds (https://www.fao.org/). Achieving high yield and enhancing the qualities of oil and protein are the major goals of soybean breeding and genetic improvement, which require systematic investigation of genomic variations associated with agronomical traits. Leveraging high-throughput and precise genotyping and phenotyping data obtained from experimental or natural/wild populations represents an efficient strategy to uncover the genetic mechanisms underlying diverse phenotype variations in various organisms [1–3]. With the rapid advancement of sequencing technology, a large number of soybean accessions have been sequenced to elucidate the genetic basis of various agronomic traits and facilitate molecular breeding in soybean [4–7]. In different types of soybean biological studies, genomic variations such as SNPs, InDels, structural variations (or genomic rearrangements), and copy number variations have been employed to identify candidate variations/genes for in-depth functional analysis in soybean.

With the explosive growth of biological data generated by high-throughput sequencing and other biotechnologies, a comprehensive genome database has become an indispensable tool for studying various organisms [8–10]. Currently, three soybean-related genome databases are available, including SoyBase [11,12], SoyKB (Soybean knowledge base) [13], and WildsoyDB [14]. SoyBase is the leading soybean database based on the genome of *Glycine max* L. cv. Williams 82, which was the first reference genome for soybean and has greatly contributed to functional genomic studies of soybean [15]. SoyBase encompasses genome sequences and gene annotations of Williams 82, along with diverse datasets such as gene expression data, epigenetic data, molecular markers, and phenotypic traits

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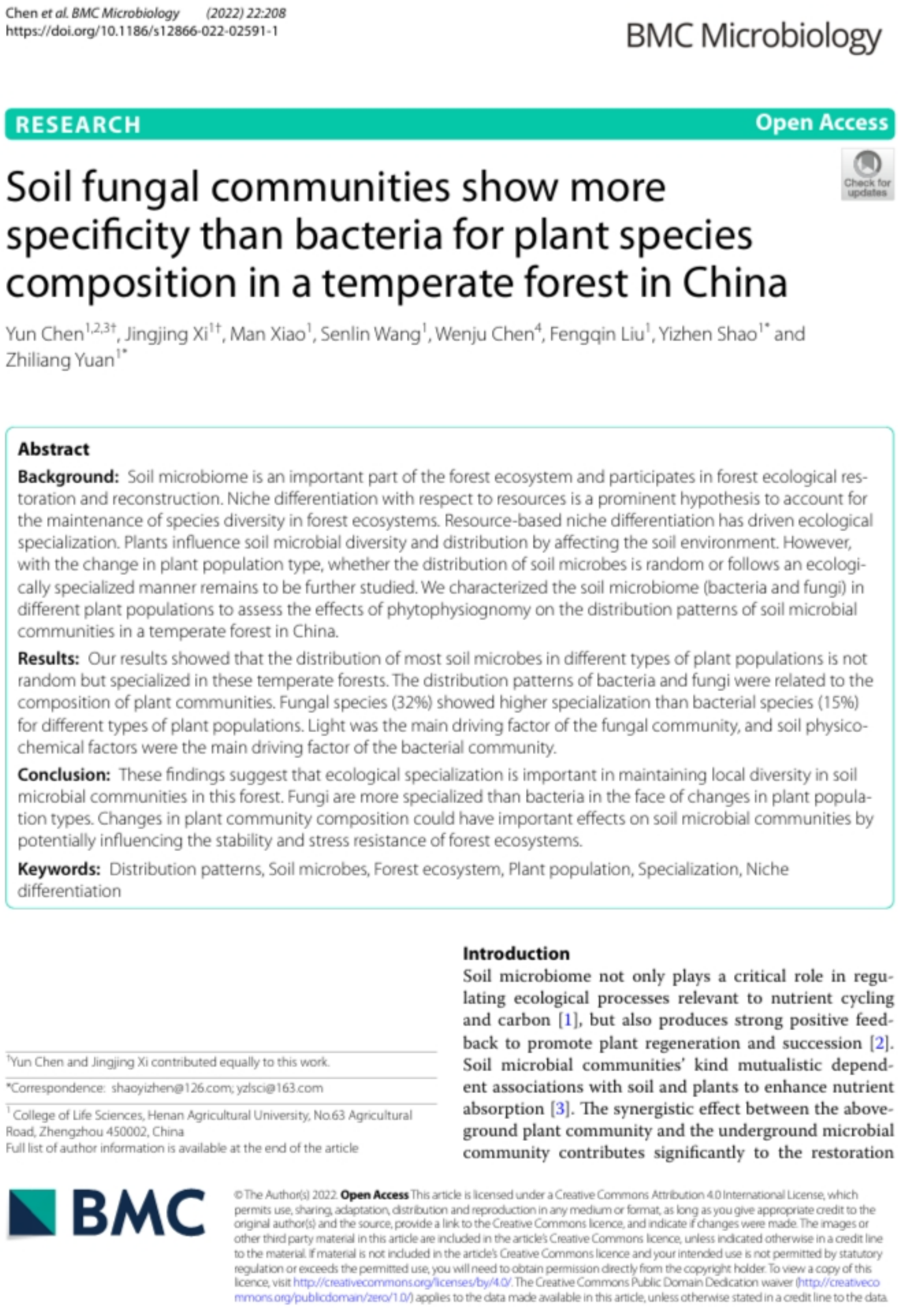
2.2.5　2018级本科生肖曼、习靓靓在 BMC Microbiology（JCR Q2）发表论文



Chen *et al. BMC Microbiology* (2022) 22:208
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BMC Microbiology

RESEARCH **Open Access**

Soil fungal communities show more specificity than bacteria for plant species composition in a temperate forest in China

Yun Chen[1,2,3†], Jingjing Xi[1†], Man Xiao[1], Senlin Wang[1], Wenju Chen[4], Fengqin Liu[1], Yizhen Shao[1*] and Zhiliang Yuan[1*]

Abstract

Background: Soil microbiome is an important part of the forest ecosystem and participates in forest ecological restoration and reconstruction. Niche differentiation with respect to resources is a prominent hypothesis to account for the maintenance of species diversity in forest ecosystems. Resource-based niche differentiation has driven ecological specialization. Plants influence soil microbial diversity and distribution by affecting the soil environment. However, with the change in plant population type, whether the distribution of soil microbes is random or follows an ecologically specialized manner remains to be further studied. We characterized the soil microbiome (bacteria and fungi) in different plant populations to assess the effects of phytophysiognomy on the distribution patterns of soil microbial communities in a temperate forest in China.

Results: Our results showed that the distribution of most soil microbes in different types of plant populations is not random but specialized in these temperate forests. The distribution patterns of bacteria and fungi were related to the composition of plant communities. Fungal species (32%) showed higher specialization than bacterial species (15%) for different types of plant populations. Light was the main driving factor of the fungal community, and soil physicochemical factors were the main driving factor of the bacterial community.

Conclusion: These findings suggest that ecological specialization is important in maintaining local diversity in soil microbial communities in this forest. Fungi are more specialized than bacteria in the face of changes in plant population types. Changes in plant community composition could have important effects on soil microbial communities by potentially influencing the stability and stress resistance of forest ecosystems.

Keywords: Distribution patterns, Soil microbes, Forest ecosystem, Plant population, Specialization, Niche differentiation

Introduction

Soil microbiome not only plays a critical role in regulating ecological processes relevant to nutrient cycling and carbon [1], but also produces strong positive feedback to promote plant regeneration and succession [2]. Soil microbial communities' kind mutualistic dependent associations with soil and plants to enhance nutrient absorption [3]. The synergistic effect between the aboveground plant community and the underground microbial community contributes significantly to the restoration

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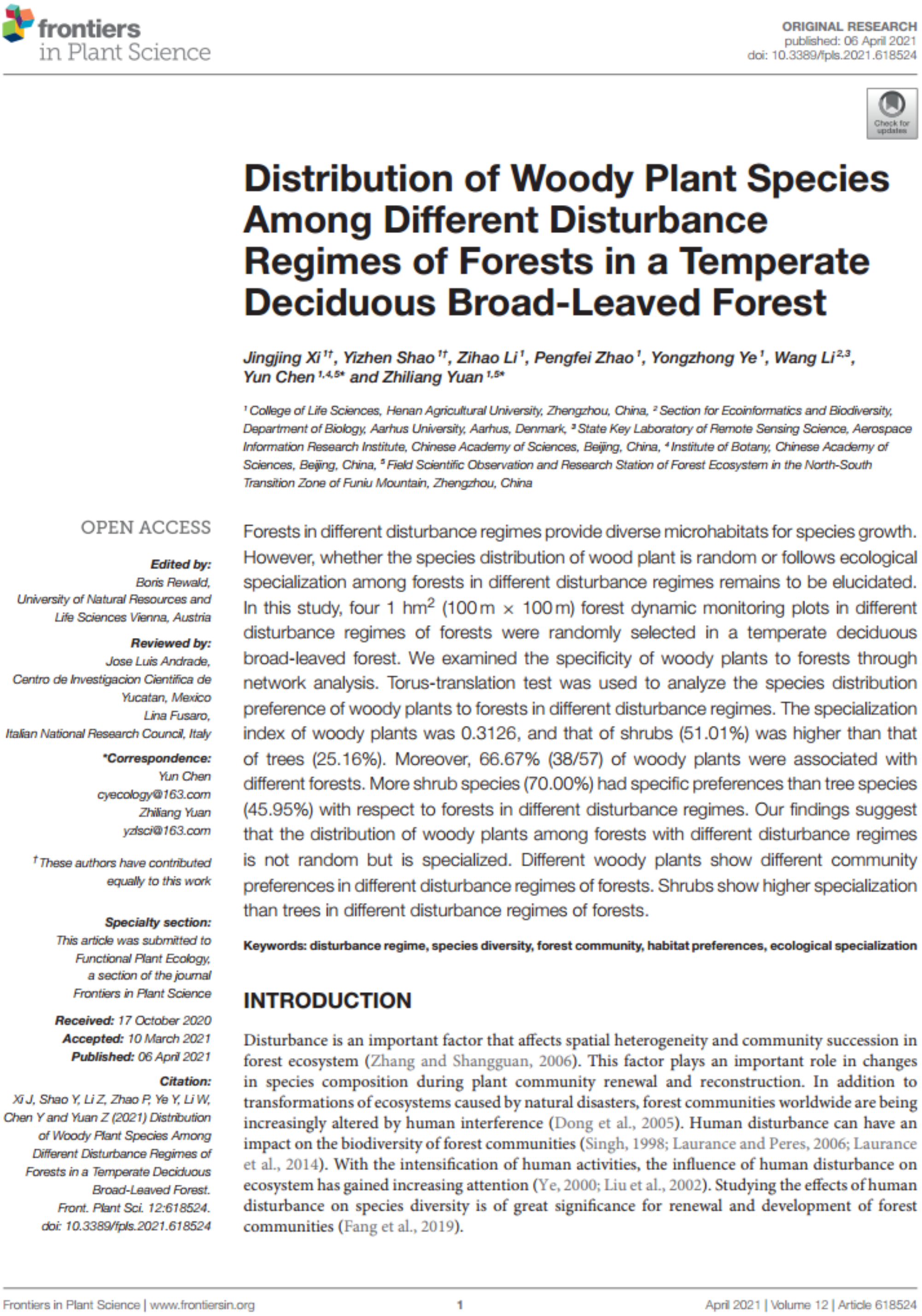
2.2.6 2018 级本科生习靓靓、李子豪在 Frontiers in Plant Science（JCR Q1）发表论文



frontiers
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ORIGINAL RESEARCH
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Distribution of Woody Plant Species Among Different Disturbance Regimes of Forests in a Temperate Deciduous Broad-Leaved Forest

Jingjing Xi[1†], **Yizhen Shao**[1†], **Zihao Li**[1], **Pengfei Zhao**[1], **Yongzhong Ye**[1], **Wang Li**[2,3], **Yun Chen**[1,4,5*] and **Zhiliang Yuan**[1,5*]

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Forests in different disturbance regimes provide diverse microhabitats for species growth. However, whether the species distribution of wood plant is random or follows ecological specialization among forests in different disturbance regimes remains to be elucidated. In this study, four 1 hm^2 (100 m × 100 m) forest dynamic monitoring plots in different disturbance regimes of forests were randomly selected in a temperate deciduous broad-leaved forest. We examined the specificity of woody plants to forests through network analysis. Torus-translation test was used to analyze the species distribution preference of woody plants to forests in different disturbance regimes. The specialization index of woody plants was 0.3126, and that of shrubs (51.01%) was higher than that of trees (25.16%). Moreover, 66.67% (38/57) of woody plants were associated with different forests. More shrub species (70.00%) had specific preferences than tree species (45.95%) with respect to forests in different disturbance regimes. Our findings suggest that the distribution of woody plants among forests with different disturbance regimes is not random but is specialized. Different woody plants show different community preferences in different disturbance regimes of forests. Shrubs show higher specialization than trees in different disturbance regimes of forests.

Keywords: disturbance regime, species diversity, forest community, habitat preferences, ecological specialization

INTRODUCTION

Disturbance is an important factor that affects spatial heterogeneity and community succession in forest ecosystem (Zhang and Shangguan, 2006). This factor plays an important role in changes in species composition during plant community renewal and reconstruction. In addition to transformations of ecosystems caused by natural disasters, forest communities worldwide are being increasingly altered by human interference (Dong et al., 2005). Human disturbance can have an impact on the biodiversity of forest communities (Singh, 1998; Laurance and Peres, 2006; Laurance et al., 2014). With the intensification of human activities, the influence of human disturbance on ecosystem has gained increasing attention (Ye, 2000; Liu et al., 2002). Studying the effects of human disturbance on species diversity is of great significance for renewal and development of forest communities (Fang et al., 2019).

2.2.7 本科生王贝以第二作者在分子植物育种（北大核心）发表论文，指导老师：林楠，2023 年

分子植物育种
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作者：　　刘蕊，王贝，郭朋，刘燕培，王一涵，尚富德，林楠
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研究报告
Research Report

木犀科叶绿体基因组比较及 DNA 条形码分析

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摘　要　木犀科 (Oleaceae) 隶属于双子叶植物纲唇形目 (Lamiales)，该科植物因具有良好的经济价值和较高的园林观赏价值而被广泛栽培，但传统的分类学对其准确鉴定存在困难，严重阻碍了木犀科植物资源的保护和利用。本研究从 NCBI 下载了 27 个木犀科叶绿体基因组序列，涵盖了木犀科 5 个族 4 个亚族 19 个属 8 个组 27 个种，对其进行叶绿体基因组比较及 DNA 条形码分析。结果表明 (1) 木犀科植物的叶绿体基因组均为典型的四分体结构，大小在 154 kb~159 kb，包含 80 个蛋白编码基因，30 个 tRNA 及 4 个 rRNA；(2) 四分体结构比较发现，LSC 与 IRb 及 SSC 与 IRa 区域的边界基因分别为 *rpl2* 和 *ycf1*，但在族间呈现不同程度的收缩和扩张。共线性分析发现木犀科 5 个族中仅在素馨族 (Jasmineae) 中发生~20 kb 的倒位和 *accD* 基因的丢失，明显区别于其他族；(3) 相较于国际通用条形码，我们筛选到的高变异片段和叶绿体基因组数据对木犀科物种的鉴定能力大幅度提升；(4) 基于不同矩阵构建木犀科系统发育树，结果支持将木犀科划分为 5 个族 4 个亚族，与前人结果基本一致。因此，本研究证实了叶绿体基因组在木犀科植物的鉴定中具有重要作用，为未来木犀科植物的系统发育及遗传多样性的相关研究奠定理论基础。

关键词　木犀科; 叶绿体基因组; 四分体结构比较; DNA 条形码; 系统发育

Comparison and DNA Barcoding Analysis of Chloroplast Genomes in Oleaceae

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College of Life Sciences, Henan Agricultural University, Zhengzhou, 450002
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Abstract　Oleaceae, one of typical family within Lamiales, is widely cultivated in the world due to the high ornamental and economic value. The definition and discrimination have been challenging based on traditional taxonomy, which highly impedes the protection and utilization of Oleaceae plants. In the current study, 27 chloroplast genomes were downloaded from NCBI, covering 5 tribes, 4 subtribes, 19 genera, 8 sections and 27 species of Oleaceae. We are aiming to explore the comparison and DNA barcoding of chloroplast genomes in Oleaceae, and our results showed that (1) the chloroplast genomes of Oleaceae exhibited a typical quadripartite structure, and the length of chloroplast genomes of Oleaceae ranged from 154 kb to 159 kb, including 80 protein-coding genes, 30 tRNA, and 4 rRNA; (2) comparison of quadripartite structure found the boundary genes of LSC/IRb and SSC/IRa were *rpl2* and *ycf1*, respectively, but degrees of gene expansion and contraction have been various among different tribes of Oleaceae. Meanwhile, synteny analysis revealed that Jasmineae was distinct from other tribes of Oleaceae by ~20 kb inversion and the loss of *accD* gene; (3) compared to international universal barcodes, variable hotpot regions and chloroplast genomes greatly improved the identification rate of Oleaceae species; (4) our phylogenetic trees based on different matrixes were highly consistent and supported Oleaceae divided into 5 tribes and 4 subtribes, the result was basically consistent with previous studies. Therefore, this study confirmed that chloroplast genomes play an important role in the identification of plants in Oleaceae, and our study will lay a theoretical foundation in promoting phylogeny and the research of genetic diversity in Oleaceae.

Keywords　Oleaceae; Chloroplast genome; Comparison of quadripartite structure; DNA barcoding; Phylogeny

木犀科 (Oleaceae) 隶属于双子叶植物纲唇形目 (Lamiales)，木犀科植物主要分布在热带和温带地区，

2.2.8 本科生王志飞以第三作者在植物学报（北大核心）发表论文，指导老师：杨浩，2019 年

植物学报 *Chinese Bulletin of Botany* 2019, **54** (2): 157–167, www.chinbullbotany.com
doi: 10.11983/CBB18133

· 特邀综述 ·

作物花粉高温应答机制研究进展

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摘要 随着全球气候变暖加剧, 农作物面临更加严峻的高温威胁。高温胁迫影响作物生长发育各个阶段, 其中花粉发育过程对高温胁迫最为敏感, 因此花粉高温应答机制成为当前植物学研究热点。研究表明, 花粉可以通过质膜上的钙离子通道、内质网中的未折叠蛋白反应、活性氧积累以及H2A.Z等机制感知高温胁迫, 并通过调控热激蛋白表达、糖代谢、激素水平及活性氧清除能力适应高温胁迫。该文从高温对花粉发育的影响、花粉高温胁迫应答机制以及花粉高温胁迫研究的实验设计等方面进行综述, 旨在为相关研究提供借鉴。

关键词 作物, 花粉, 高温, 应答机制

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随着全球气候逐渐变暖, 温度变化对生态环境的影响日益明显(Hansen, 2015)。IPCC (Intergovernmental Panel on Climate Change)研究报告指出, 相比20世纪末, 目前全球气温已经增加约4°C, 而温度升高将严重影响农作物生长, 威胁粮食安全(Lobell et al., 2011)。因此, 开展作物的高温胁迫研究具有重要意义。花粉作为一种具有特殊结构和功能的微小生命有机体, 包含父本基因组信息, 是种子植物有性生殖的重要调控者。由于花粉结构简单, 因此成为研究植物细胞极性、命运分化和发育的理想体系(鲁云龙等, 2014)。在生产实践中, 雄蕊产生有活性的花粉是作物形成种子和果实的前提。花粉发育过程对高温非常敏感, 高温导致花粉活性降低甚至失活, 使作物穗粒数和坐果率显著降低, 最终导致粮食减产。因此, 花粉高温应答机制研究成为植物学家关注的重点。

通常情况下, 在高于最适温度5°C以上的环境下, 花粉就会遭受高温伤害。许多重要作物如小麦(*Triticum aestivum*)、水稻(*Oryza sativa*)和玉米(*Zea mays*), 其开花期均集中在夏季, 极易遭遇连续或严重的高温天气, 从而导致花粉发育异常(Barnabás et al., 2008)。水稻散粉时环境温度通常在28°C以上, 温度每升高1°C, 就会造成水稻减产约8%。如果温度升高到33°C, 会导致花粉产量降低到13%; 而温度升高到39°C, 就会导致花粉完全丧失活性, 落在柱头上的花粉无法萌发(Prasad et al., 2006; Endo et al., 2009)。高温对小麦影响更为严重, 在小孢子形成期, 环境温度达30°C时就会造成小孢子发育异常; 而在小花发育阶段, 长期温和高温(25°C, 白天)也会影响小麦的花粉发育(Farooq et al., 2011)。此外, 对玉米、高粱(*Sorghum bicolor*)和大麦(*Hordeum vulgare*)等的研究表明, 白天温度高于32°C会对花粉发育造成不同程度的影响(Lyakh et al., 1991; Liu et al., 2015)。

由于花粉取材相对困难, 因此针对花粉高温应答机制的研究相对较少。但随着分离技术的发展以及多种组学技术的应用, 人们对花粉的高温应答机制已有一定认识(Qin et al., 2008; Jagadish et al., 2010; Yang et al., 2015; González-Schain et al., 2016; Keller et al., 2017, 2018)。本文针对高温对作物花粉发育过程的影响、花粉高温胁迫应答机制, 以及花粉高温胁迫研究实验设计进行综述, 以期为相关研究提供借鉴。

1 高温对花粉发育的影响

花粉作为植物高度特化的雄配子体, 其发育过程既短

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