

支撑材料

- (一) 教学成果获奖证明 (112项)
- (二) 主要教学改革研究项目 (69项)
- (三) 主要教改研究论文 (59项)
- (四) 指导本科生第一作者发表在 **Nature**、**Science** 等国际重要期刊
发表论文情况 (4 篇)
- (五) 指导本科生第一作者在**SCI**源杂志等国内外重要期刊发表文章
情况 (27篇)
- (六) 指导本科生参与发表**SCI**论文、国家发明专利及软件著作权 (86项)
- (七) 指导本科生大学生创新创业训练项目 (67项)
- (八) 立足于教学的本科生科研训练成果获奖 (80项)
- (九) 出版或获批编著教材 (16项)
- (十) 成果先进事迹宣传与报道 (26项)
- (十一) 毕业本科生代表 (99人)

（一）教学成果获奖证明（112 项）

1. 国家级一流本科课程《植物学 B》，2025 年
2. 国家级一流本科课程《水质工程学》，2025 年
3. 国家级一流本科课程《山野菜认知与开发利用》，2025 年
4. 国家级一流本科课程《动物生理学 A》，2020 年
5. 生物科学拔尖学生培养计划 2.0 基地建设（全国林业院校唯一），2021 年
6. 国家级一流本科专业建设点：给排水科学与工程、信息管理与信息系统，2021 年
7. 国家级一流本科专业建设点：计算机科学与技术、数字媒体技术、食品科学与工程，2020 年
8. 国家级一流本科专业建设点：生物科学、环境工程，2019 年
9. 国家级特色专业：生物学，2008 年
10. 国家生物学理科基地班，1997 年
11. 全国大学生“小平科技创新团队”指导教师，2014 年
12. 全国中学生英才计划导师（6 人次），2025、2024 年
13. 全国高校生命科学类微课教学比赛二等奖，2020 年
14. 北京市级一流本科专业建设点：电子信息科学与技术、环境科学，2021 年
15. 北京市级一流本科专业建设点：数学与应用数学，2020 年
16. 北京市级一流本科专业建设点：计算机科学与技术，2019 年
17. 北京市优秀教师，2022 年
18. 北京市高等学校教学名师奖，2016 年
19. 宝钢优秀教师奖，2021 年
20. 北京市高校优秀本科育人团队，2023、2021、2020 年
21. 北京高校青年教师创新教研工作室，2023 年
22. 北京本科高校产学研深度协同育人平台，2023 年
23. 教育部“长江学者奖励计划”青年学者计划，2022 年
24. 国家林业和草原局青年拔尖人才计划，2020 年
25. 教育部自然科学一等奖（排名第二），2022 年
26. 教育部科技进步一等奖（排名第三），2019 年
27. 北京市科技进步二等奖（排名第二），2024 年
28. 北京高校青年教师教学基本功比赛理科类 A 组一等奖（1 项）、最佳教案奖（1 项）、最佳现场展示奖（1 项）、优秀指导教师奖（1 项），2021 年
29. 首都大中专学生暑期社会实践优秀团队指导教师，2018 年
30. 第二届青年绿色科技创新大赛金奖指导教师，2025 年
31. 北京高校优质本科教材课件，2024、2022 年
32. 北京高校优质本科教案，2022 年
33. 北京市优秀毕业论文指导教师（3 项），2024、2021、2019 年
34. 北京林业大学教学名师（3 项），2024、2022、2017 年
35. 北京林业大学教学成果奖特等奖（2 项）、一等奖（4 项）、二等奖（5 项），2025、2021、2019、2017 年
36. 北京林业大学教师教学创新大赛三等奖（3 项），2023、2021 年
37. 北京林业大学巾帼先锋，2023 年
38. 北京林业大学三八红旗标兵，2021 年
39. 北京林业大学“立德树人优秀教师”，2019 年
40. 北京林业大学十佳研究生导师，2019 年

41. 北京林业大学首届“北林榜样”，2019 年
42. 北京林业大学社会实践优秀指导教师，2018 年
43. 北京林业大学“优秀教师”，2016 年
44. 北京林业大学家骥云龙青年教师教学优秀奖，2016、2013 年
45. 北京林业大学就业创业工作贡献奖，2016 年
46. 北京林业大学优秀班主任（3 项），2021、2019、2018 年
47. 北京林业大学“十佳班主任”提名奖，2020 年
48. 北京林业大学第十九届青年教师教学基本功比赛（实践类）三等奖，2023 年
49. 北京林业大学第十五届青年教师教学基本功比赛三等奖，2019 年
50. 北京林业大学第十四届青年教师教学基本功比赛特色组一等奖、最佳教学演示奖，2018 年
51. 北京林业大学第十二届青年教师教学基本功比赛最佳教学演示奖、最受学生欢迎奖、最佳指导教师奖，2016 年
52. 北京林业大学第十一届青年教师教学基本功比赛二等奖、三等奖，2015、2013 年
53. 北京林业大学第九届青年教师教学基本功比赛三等奖，2012 年
54. 北京林业大学优质本科课件（2 项），2024 年
55. 北京林业大学优质本科课程，2024 年
56. 北京林业大学优质本科教案一等奖（2 项），2020、2018 年
57. 北京林业大学校优秀本科毕业论文指导教师（5 项），2024、2022、2021、2012 年
58. 北京林业大学教育教学改革与研究论文一等奖（1 项）、二等奖（2 项）、三等奖（2 项）、优秀奖（3 项），2022、2020、2018、2017 年
59. 北京林业大学课程思政教学改革优秀案例《动物生理学 A》，2021 年
60. 梁希林业科学技术奖二等奖，2016 年

（二）主要教学改革研究项目（69 项）

1. 面向新工科的计算机专业校企双师建设与实践，国家第二批新工科研究与实践项目，2020 年
2. 新兴技术范式下环境类专业教师教学方法体系构建与实践，国家第二批新工科研究与实践项目，2020 年
3. 林木良种多圃配套育苗技术虚拟仿真实验，国家虚拟仿真实验教学项目，2019 年
4. 专业课发挥思政教育功能教育教学模式研究，北京市高等教育学会面上课题，2023 年
5. “认证标准-思政引领-产学研教”深度融合的给排水专业人才培养模式研究，北京市本科教学改革创新项目，2021 年
6. 新工科背景下环境工程专业课程“理—虚—实”一体化智慧教学模式设计，教育部产学合作协同育人项目，2024 年
7. 《泵与风机》课程数字资源库及教材建设，教育部产学合作协同育人项目，2024 年
8. 北林智慧林草嵌入式实践基地建设，教育部产学合作协同育人项目，2024 年
9. 数字孪生技术融入环境类专业实践教学师资能力建设，教育部产学合作协同育人项目，2023 年
10. “双师型”教师培训与师资队伍建设探索和实践，教育部产学合作协同育人项目，2023 年
11. 基于“思专创”三位一体的农林高校生物类创新创业人才培养路径的探索，教育部产学合作协同育人项目，2023 年
12. 大数据、人工智能与物联网技术应用师资培训，教育部产学合作协同育人项目，2022 年

年

13. 国家级一流本科课程线下课程《动物生理学 A》的虚拟教学资源建设,教育部产学合作协同育人项目,2022 年
14. 基于“科教融合、协同育人”教学理念的动物生理学课程体系改革与实践,教育部产学合作协同育人项目,2021 年
15. 基于虚拟仿真和现场耦合的环境工程专业实习实践课程体系的构建与优化,教育部产学合作协同育人项目,2021 年
16. 新时代环境类专业劳动教育 VR 实践训练体系建设,教育部产学合作协同育人项目,2021 年
17. 北京林业大学嵌入式创新实验室建设,教育部产学合作协同育人项目,2021 年
18. 植物分类的形态术语虚拟仿真实验建设,教育部中国高校产学研创新基金,2023 年
19. 动物学(拔尖班)人工智能示范课程,北京林业大学人工智能示范课试点建设项目,2025 年
20. 动物生理学 A,北京林业大学人工智能示范课试点建设项目,2025 年
21. 国家一流本科课程线下课程《动物生理学》的知识图谱资源建设,北京林业大学知识图谱和数字教材建设专项,2025 年
22. 嘉立创 EDA 在电子电路 CAD 教学中的应用,校级一般项目,2025 年
23. 通信原理强化数理及数智化教学改革研究,校级一般项目,2025 年
24. “五育并举”视域下农林高校新工科专业实践育人体系的探索与研究,北京林业大学五育并举专项,2024 年
25. 基础动物学实验数字资源互动构建与探索,校级一般项目,2024 年
26. 以单片机课程群改革为牵引的新工科人才培养模式探索,校级重点项目,2024 年
27. 电子工艺实习教学改革,校级一般项目,2024 年
28. 生态文明背景下林业特色微生物实验课程的教学改革与创新,校级一般项目,2024 年
29. “五育融合”视域下生物类专业学生创新创业实践育人模式探索与实践,北京林业大学五育并举专项,2023 年
30. 校企协同-产教融合-多元立体化的农林高校新工科专业实践育人体系探索与实践——以给排水科学与工程专业为例,北京林业大学教育教学改革与研究重大项目,2023 年
31. 林业院校“耕读+”劳动教育育人体系的探索与实践,北京林业大学教育教学改革与研究重大项目,2023 年
32. “新工科”背景下环境类课程思政建设的探索与实践,北京林业大学教育教学改革与研究重点项目,2023 年
33. 基于生态教育理念的北林电子编程课教学实践探究——以《Java 开发与实践》为例,北京林业大学教育教学改革与研究一般项目,2023 年
34. 基于雨课堂和项目驱动的《移动软件开发技术》课程教学研究,北京林业大学教育教学改革与研究一般项目,2023 年
35. 拔尖班 2.0 动物学课程创新与深化,北京林业大学教育教学改革与研究一般项目,2023 年
36. 电磁场理论体系构建与实践研究——图解电磁学,校级一般项目,2023 年
37. 嵌入式智能硬件课程及实验室建设,校级一般项目,2023 年
38. 大学基础课思政育人数字信息化教学设计研究,其他项目,2023 年
39. 多维协同、统筹推进本科专业课程思政建设的探索与创新,北京林业大学教育教学改革与研究重大项目,2022 年
40. “新农科”背景下国家线下一流课程思政示范课堂和思政示范课程教学改革与创新,校级

重点项目，2022 年

41. 身心健康的生理学基础，北京林业大学课程思政教研教改专项课题，2021 年
42. 动物生理学 A，北京林业大学课程思政教研专项课题，2021 年
43. 通信原理，北京林业大学课程思政教研专项课题，2021 年
44. 机器学习基础，北京林业大学课程思政教研专项课题，2021 年
45. 基于微信公众号平台的《动物学实验》教学手段和考核方式改革，校级一般项目，2021 年
46. 舌尖上的森林植物，北京林业大学课程思政教研专项课题，2021 年
47. 多维目标体系下环境工程一流专业建设的探索与实践，北京林业大学教育教学改革与研究重大项目，2020 年
48. 动物生理学实验，北京林业大学第三批精品在线开放课程教育教学研究重点项目，2020 年
49. 《基因工程》，北京林业大学课程思政教研教改专项课题，2020 年
50. 《动物改变世界》，北京林业大学课程思政教研教改专项课题，2020 年
51. BOPPPS 教学模式在基础动物学实验教学中的探索与实践，北京林业大学教育教学改革与研究一般项目，2020 年
52. 高频电子技术，北京林业大学课程思政教研教改专项课题，2020 年
53. Java 开发与实践，北京林业大学课程思政教研教改专项课题，2020 年
54. 《移动软件开发技术》课程线上教学方法研究，校级一般项目，2020 年
55. 基于任务驱动的 5G 通信虚拟仿真实践教学研究，校级一般项目，2020 年
56. 虚拟仿真在高频电子线路课堂和实验教学中的应用，校级一般项目，2019 年
57. 基于科教融合理念培养生物类创新创业人才的探索与实践，校级科教融合项目，2019 年
58. 物理学 A，北京林业大学课程思政教研教改专项课题，2019 年
59. 面向新经济的工科专业改造升级路径探索与实践，北京林业大学新工科教改项目，2019 年
60. 本科生毕业设计—社会实践耦合模式探索，北京林业大学教育教学改革与研究重点项目，2019 年
61. 森林生物学创新人才培养模式研究，北京林业大学人才培养共建项目—教学名师项目，2018 年
62. 基于虚拟仿真技术通信原理实验多元化教学探索与实践，校级一般项目，2018 年
63. 基于雨课堂和项目驱动的《移动软件开发技术》课程教学研究，校级一般项目，2018 年
64. 自主学习与创新型森林生物学教学体系与方法研究，北京林业大学教育教学改革与研究一般项目，2017 年
65. 基于创客思维的动物生理学课堂教学模式探索与实践，北京林业大学教育教学改革与研究一般项目，2016 年
66. 大学生自主创新实验室教育探索与实践，北京林业大学教育教学改革与研究一般项目，2015 年
67. 半开放式教学模式在动物组织与胚胎学课程教学中的探索与实践，北京林业大学教育教学改革与研究一般项目，2015 年
68. 《动物生理学》精品课程实验课建设，北京林业大学教育教学改革与研究一般项目，2012 年
69. 《动物生理学》精品课程建设，北京林业大学教育教学改革与研究一般项目，2011 年

（三）主要教改研究论文（59 项）

1. 《动物生理生化大实验》课程思政的改革与探索，中国教育技术装备，2025 年
2. “拔尖计划 2.0”驱动“动物学（拔尖班）”课程教学改革的探索，中国林业教育，2025 年
3. 高等林业院校“植物生理学”课程教学改革的探索—以北京林业大学为例，中国林业教育，2024 年
4. 高校实验室资源开放共享的研究与探索—以北京林业大学生物拔尖创新实验室为例，高校生物学教学研究（电子版），2024 年
5. 依托高校自身特色的 Android 课程教学案例研究—以北京林业大学为例，北京林业大学 2023 年教育教学改革与研究优秀论文选编，2023 年
6. 关于大创项目对生物专业人才培养意义的思考—以北京林业大学生物学院为例，北京林业大学 2023 年教育教学改革与研究优秀论文选编，2023 年
7. 课程思政视角下《基因工程》教学改革措施与成效，北京林业大学 2023 年教育教学改革与研究优秀论文选编，2023 年
8. 融入思政元素的《传感器原理》课程教学改革，北京林业大学 2023 年教育教学改革与研究优秀论文选编，2023 年
9. 课程思政背景下《微生物学》课程数字化资源库建设探索，北京林业大学 2023 年教育教学改革与研究优秀论文选编，2023 年
10. 基于 OBE 理念的《水工艺设备基础》课程教学质量提升实践与思考，北京林业大学 2023 年教育教学改革与研究优秀论文选编，2023 年
11. 动物生理学 A 课程思政案例库建设与实践，高教学刊，2023 年
12. 北京林业大学电子专业实践课程体系改革，北京林业大学教育教学改革研究论文集，2022 年
13. 基于 CDIO 教育模式“双碳—新农科”的《动物生理学》教学，北京林业大学教育教学改革研究论文集，2022 年
14. 新冠肺炎疫情下快速在线翻转课堂教学模式探索与实践—以动物改变世界为例，中国现代教育装备，2022 年
15. 基于虚拟仿真教学模式的“微生物学实验”课程教学改革探索，中国林业教育，2022 年
16. 基于立德树人理念的“动物改变世界”课程思政教学探索，北京地区高校课程思政建设发展论坛集，2021 年
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(七) 指导本科生大学生创新创业训练项目 (67 项)

1. 野生达乌尔黄鼠前列腺季节性增生与萎缩过程中上皮细胞内线粒体动态变化的研究, 国家级, 2025 年
2. 维生素 D 通过调节麝鼠泌香腺细胞脂质代谢参与泌香腺性类固醇激素合成, 国家级, 2025 年
3. 不同海拔生境高原鼠兔器官低氧适应调节研究, 国家级, 2025 年
4. 维生素 D 对达乌尔黄鼠肝脏中脂质代谢的季节性调节作用, 国家级, 2025 年
5. 3-甲基-4-硝基苯酚对小鼠卵母细胞 DNA 甲基化水平的影响, 国家级, 2025 年
6. 基于柿子落果提取物的抗氧化特性开发绿色果蔬保鲜膜, 国家级, 2024 年
7. 脱氧地胆草内酯生物活性的功能机制研究, 国家级, 2024 年
8. 麝鼠卵巢线粒体质量控制与性类固醇激素生成的季节性表达, 国家级, 2024 年
9. 林麝泌香腺组织结构及细胞类型分布解析, 国家级, 2024 年
10. 东北林蛙雌雄两性肝脏糖代谢的季节性变化的比较研究, 国家级, 2024 年
11. PtoCOMT2 调控芥子醇合成的分子机制, 国家级, 2023 年
12. 外源性硝酸盐代谢酶在哺乳动物细胞内表达与功能检测, 国家级, 2023 年
13. 白洋淀特色水生植物种质资源调查和综合评价, 国家级, 2023 年
14. 基于基质辅助激光解吸电离质谱成像技术对麝鼠泌香腺内源性脂质分子季节性变化的研究, 国家级, 2022 年
15. 犁鼻器气味受体在雌性麝鼠子宫与卵巢中的季节性表达, 国家级, 2021 年
16. “植物疫苗”防治杨树溃疡病的协同作用机制, 国家级, 2021 年
17. 探究母婴分离对 HPA 轴活性及海马体炎症反应的影响, 国家级, 2021 年
18. 挥发性物质对传粉者行为的影响, 国家级, 2021 年
19. 基于互联网+人工智能的濒危野生动物灭绝风险评估与预警平台设计, 国家级, 2020 年
20. “催产素”通过内分泌、自分泌或旁分泌调节野生达乌尔黄鼠附睾中精子成熟研究, 国家级, 2017 年
21. 睡菜生物学特性及高效繁育技术研究, 北京市级, 2025 年
22. 毛白杨人工林土壤氮素转化相关功能微生物群落分布及组装机制研究, 北京市级, 2025 年
23. 铜死亡调节的结直肠癌分子亚型和预后模型, 北京市级, 2025 年
24. 东北林蛙输卵管季节性代谢的 IGF 通路解析: 从肝脏信号到林蛙油形成, 北京市级, 2025 年

25. 杨树人工林土壤氮素矿化作用及相关功能微生物调节机制, 北京市级, 2025 年
26. 高海拔适应中高原山鹑肝脏的分子适应机制, 北京市级, 2025 年
27. 基于机器学习技术建立双硫死亡相关的肝癌预后模型, 北京市级, 2024 年
28. 饥饿诱导的应激对小鼠肾上腺结构和功能的影响, 北京市级, 2024 年
29. 毛白杨细胞膜锚定转录因子 PtoANAC02 调控水氮耦合效应分子机制研究, 北京市级, 2024 年
30. 铁死亡相关基因在肝细胞癌中的表达及其预后价值, 北京市级, 2023 年
31. 全身及卵巢局部脂肪组织对卵巢代谢及内分泌微环境的影响的比较研究, 北京市级, 2023 年
32. 基于叶片表型及功能分析的 3 种经济灌木抗旱耐盐碱机制研究, 北京市级, 2023 年
33. 多年生杨树人工林土壤微生物的分布及群落组装机制, 北京市级, 2023 年
34. 催产素调控麝鼠香分泌的机制研究, 北京市级, 2023 年
35. 汽车尾气中 3-甲基-4-硝基苯酚暴露干扰节律基因影响小鼠雌性生殖机能的跨代效应, 北京市级, 2023 年
36. AdipoQ 调节卵巢颗粒细胞葡萄糖转运的功能机制研究, 北京市级, 2022 年
37. 柿子皮提取物对乳酸菌冷冻干燥保护效果, 北京市级, 2022 年
38. 杨树抗寒合成菌群诱导杨树抗寒的作用机制, 北京市级, 2022 年
39. 季节性繁殖动物麝鼠睾丸中自噬水平的变化与调控机制研究, 北京市级, 2022 年
40. 冬眠对金仓鼠睾丸内线粒体动态变化及精子发生的影响, 北京市级, 2022 年
41. 维生素 D 受体及其代谢酶在麝鼠睾丸中的季节性表达探究, 北京市级, 2021 年
42. 冬眠对野生达乌尔黄鼠肠道微生物群落变化的影响, 北京市级, 2020 年
43. 重霾污染天气时大气 PM_{2.5} 数浓度谱分布特征研究, 北京市级, 2014 年
44. 麝鼠垂体细胞的季节性变化及其对泌香周期的适应性研究, 校级, 2025 年
45. 野猪和家猪胃壁生理结构及功能的比较研究, 校级, 2025 年
46. 基于微生物组模型杨树促生合成菌群的筛选与构建, 校级, 2025 年
47. 肉牛 TMEM182 基因编辑细胞系构建, 校级, 2024 年
48. 冬眠达乌尔黄鼠睾丸自噬水平的变化与调控机制研究, 校级, 2024 年
49. 杨树人工林土壤氮素转化的关键微生物过程及分子调节, 校级, 2024 年
50. 汽车尾气中 3-甲基-4-硝基苯酚对小鼠卵母细胞基因甲基化影响, 校级, 2024 年
51. 基于高原山鹑探究不同组织器官线粒体特征的高原适应性, 校级, 2024 年
52. 低温对体外培养的达乌尔黄鼠脂肪细胞线粒体功能的影响, 校级, 2024 年
53. 野生达乌尔黄鼠肝脏的季节性变化: 天然的脂肪肝模型?, 校级, 2024 年
54. 基于单细胞转录组测序对麝鼠泌香腺发育和泌香功能调控的研究, 校级, 2023 年
55. m⁶A 甲基化修饰相关基因对犏牛雄性不育的影响, 校级, 2023 年
56. 高通量分离培养和鉴定杨树人工林土壤细菌, 校级, 2023 年
57. 附睾脂肪组织参与 BDE-47 介导的睾丸生殖毒理效应研究, 校级, 2023 年
58. 达乌尔黄鼠前列腺组织上皮细胞异质性分析, 校级, 2023 年
59. 高表达麝香酮合成基因的永生泌香腺细胞的建立, 校级, 2023 年
60. m⁶A 甲基化修饰相关基因在麝鼠睾丸中的季节性表达, 校级, 2022 年
61. 麝鼠肠道微生物对季节性繁殖功能的影响, 校级, 2022 年
62. 复合菌剂厌氧发酵餐厨垃圾产甲烷协同作用机制研究, 校级, 2022 年
63. SOX9 基因及调控通路在麝鼠泌香腺中季节性表达研究, 校级, 2022 年
64. 野生动物原始生殖细胞样细胞 (PGCLC) 体外重构方法建立, 校级, 2021 年
65. 利用酵母进行麝香酮的生物合成的研究, 校级, 2021 年

66. 以冬眠动物为模型研究肥胖对雄性生殖系统的影响, 校级, 2016 年
67. 催乳素调节雄性麝鼠泌香腺分泌麝香功能研究, 校级, 2015 年

(八) 立足于教学的本科生科研训练成果获奖 (80 项)

1. 第十届全国大学生生命科学竞赛 (科学探究类) 三等奖 (2 项), 2025 年
2. 第二届青年绿色科技创新大赛金奖, 2025 年
3. 中国国际大学生创新大赛北京赛区二等奖, 2025 年
4. “挑战杯”首都大学生课外学术科技作品竞赛一等奖, 2025 年
5. 第十一届北京市大学生生物学竞赛, 奇思妙想竞赛单元, 二等奖, 2025 年
6. 北京科学传播大赛二等奖, 2025 年
7. 第二届北京林业大学“勉励杯”大学生创新创业大赛优秀奖, 2025 年
8. 第四届森林生物学国际论坛青年学术“玉兰奖”评选活动三等奖, 2024 年
9. 第九届全国大学生生命科学竞赛 (科学探究类) 一等奖 (1 项)、三等奖 (1 项), 2024 年
10. 第十届北京市大学生生物学竞赛一等奖 (2 项)、二等奖 (1 项), 2024 年
11. 中国国际大学生创新大赛北京林业大学校赛二等奖, 2024 年
12. 北京林业大学首届“勉励杯”大学生创新创业大赛优秀奖, 2024 年
13. 第十五届北京市大学生化学实验竞赛一等奖, 2024 年
14. 第八届中国国际“互联网+”大学生创新创业大赛总决赛铜奖, 2023 年
15. 第九届中国国际“互联网+”大学生创新创业大赛北京市三等奖, 2023 年
16. “挑战杯”首都大学生课外学术科技作品竞赛主体赛二等奖 (1 项)、三等奖 (1 项), 2023 年
17. 北京林业大学第十三届“梁希杯”大学生课外学术科技作品竞赛银奖 (1 项)、铜奖 (1 项)、优秀奖 (1 项), 2023 年
18. 第九届中国国际“互联网+”大赛北京林业大学校赛优秀奖, 2023 年
19. 第五届全国高校计算机能力挑战赛人工智能挑战赛本研组全国决赛一等奖, 2023 年
20. 华北五省(市、自治区)及港澳台大学生计算机应用大赛本科组二等奖, 2022 年
21. 第八届中国国际“互联网+”大学生创新创业大赛北京赛区一等奖, 2022 年
22. 第八届北京市大学生生物学竞赛一等奖 (1 项)、二等奖 (1 项)、三等奖 (2 项), 2022 年
23. 第七届全国大学生生命科学竞赛二等奖, 2022 年
24. 北京市大学生节能节水低碳减排社会实践与科技竞赛一等奖, 2021 年
25. 全国大学生软件测试大赛总决赛开发者测试个人赛三等奖, 2021 年
26. 第六届全国大学生生命科学竞赛一等奖 (1 项)、三等奖 (2 项), 2021 年
27. 第十一届“挑战杯”首都大学生课外学术科技作品竞赛二等奖, 2021 年
28. 第七届北京市大学生生物学竞赛二等奖 (1 项)、三等奖 (1 项), 2021 年
29. 第六届北京市大学生生物学竞赛一等奖 (1 项)、二等奖 (1 项), 三等奖 (1 项), 2020 年
30. 北京林业大学第六届“互联网+”大赛校赛优秀奖, 2020 年
31. 第五届全国大学生生命科学创新创业大赛一等奖 (2 项), 2020 年
32. 第四届全国大学生生命科学创新创业大赛一等奖 (1 项)、二等奖 (1 项)、三等奖 (1 项), 2019 年
33. 第五届北京市大学生生物学竞赛二等奖 (2 项)、三等奖 (1 项), 2019 年
34. 第十届“挑战杯”首都大学生课外学术科技作品竞赛二等奖 (1 项)、三等奖 (2 项), 2019 年

年

35. 北京林业大学第十一届“梁希杯”大学生课外学术科技作品竞赛一等奖（3项），2019年
36. 第二届全国大学生生命科学竞赛三等奖（2项），2018年
37. 第四届北京市大学生生物学竞赛之生物学实验设计竞赛一等奖（2项），2018年
38. 第十五届“挑战杯”全国大学生课外学术科技作品竞赛三等奖（1项），2017年
39. 第九届“挑战杯”首都大学生课外学术科技作品竞赛一等奖（1项）、二等奖（1项）、三等奖（1项），2017年
40. 北京林业大学第十届“梁希杯”大学生课外学术科技作品竞赛一等奖（2项）、二等奖（1项），2017年
41. 北京市大学生生物学竞赛之生物学实验技能竞赛三等奖，2016年
42. “挑战杯”首都大学生课外学术科技作品竞赛一等奖（1项）、三等奖（2项），2015年
43. 大学生“小平科技创新团队”，2014年
44. 第十三届“挑战杯”全国大学生课外学术科技作品竞赛三等奖，2013年
45. 第七届“挑战杯”首都大学生课外学术科技作品竞赛一等奖（1项）、二等奖（1项），2013年
46. 北京林业大学第八届“挑战杯”大学生课外学术科技作品大赛三等奖（2项），2013年
47. 中国林学会梁希科学技术奖梁希优秀学子奖，2012年

（九）出版或获批编著教材（16项）

1. 《智慧林业学》，高等农林院校智慧林业专业系列教材，中国林业出版社，2025年
2. 《数据库原理及应用教程》第4版 微课版，“十二五”普通高等教育本科国家级规划教材，人民邮电出版社，2024年
3. 《城市环境生物》，教育部战略性新兴产业“十四五”高等教育教材，2024年
4. 《乡土植物资源调查与评价》，“十四五”高等教育教材，2024年
5. 《比较动物生理学》，首批普通高等农林院校“十四五”规划教材，2024年
6. 《动物行为与福利学》，农业农村部“十三五”规划教材，2024年
7. 《植物细胞壁与木材形成》，高等教育出版社，2023年
8. 《Java基础实践教程》，西安电子科技大学出版社，2023年
9. 《生殖内分泌》，国家林业和草原局研究生教育“十四五”规划教材项目，2021年
10. 《食品微生物学》，普通高等教育“十三五”规划教材，中国轻工业出版社，2017年
11. 《有机固体废物资源化利用》，普通高等教育“十三五”规划教材，2017年
12. 《现代食品加工技术》，中国农业科学技术出版社，2015年
13. 《数据库原理及应用教程（第3版）》，“十二五”普通高等教育国家级规划教材，人民邮电出版社，2014年
14. 《观赏植物种质资源学》，教育部特色专业教材，2012年
15. 《VISUAL C++程序设计技巧与实例》，中国铁道出版社，2003年
16. 《VISUAL C# 2005 技术内幕》，机械工业出版社，2002年

（十）成果先进事迹宣传与报道（26项）

1. 新华网、中国网专题报道团队育人成果：“师心如风育新苗 科教融合铸匠魂”，2025年7月16日
2. 北京信息科技大学新闻网报道：校工会赴兄弟高校调研学习北京市青教赛、青管赛组织和参赛经验，2025年6月23日
3. 《人民日报》“民生无小事”栏目关于北京通州张家湾集体林场的科技小院生物多样性实

验室的报道，2025 年 6 月 18 日

4. 《中国环境报》报道：“种子银行”为物种延续提供保障 | 科技助力，守护多样之美，2025 年 5 月 22 日
5. 《人民日报》报道团队古树鉴定系统开发成果：“让古树与人和谐共生”，2025 年 4 月 28 日
6. 新华网、中国科学院昆明分院报道 2025 腾冲科学家论坛·生物多样性保护与区域高质量发展（怒江）专题活动，2025 年 4 月 19 日
7. 《北京青年报》关于国家林业和草原局应急揭榜挂帅项目“野生动植物和古树名木鉴定技术及系统研发”验收会举行的报道，2025 年 3 月 26 日
8. 央广网《校招直通车》我的大学：走进北京林业大学节目中，团队教师参与直播报道，2024 年 6 月 14 日
9. 科技日报《科普一下》栏目报道团队教师开展的关于兰花螳螂伪装能力与滑翔能力科普，2023 年 12 月 8 日
10. 南开融媒报道：“乡村振兴 南开力量 | 科技帮扶助力夏河畜牧业高质量发展”，2023 年 8 月 27 日
11. 北京林业大学绿色新闻网报道生物学院“北京高校青年教师创新教研工作室”揭牌，2023 年 7 月 27 日
12. 中国教育电视台 1 频道《育见》播出的《一颗种子的“太空之旅”》节目，2023 年 6 月 29 日
13. 《副中心新闻》媒体采访介绍团队教师带领学生开展生物多样性保护工作及副中心生物多样性保护成效，2023 年 6 月 6 日
14. 国家林业与草原局《中国绿色守望者》栏目、《中国绿色时报》关于北京城市副中心打造“生物天堂”的报道，2023 年 5 月 19 日
15. CCTV-17 农业农村频道《致富经》栏目报道关于鳄鱼美食：夏日里的“冷”美食，2022 年 7 月 12 日
16. 《新周刊》采访团队教师，从植物的角度谈谈中国城市绿化中的植物、城市与人之间共生共存的关系，2022 年 3 月 29 日
17. CCTV-17 农业农村频道《致富经》栏目报道关于鳄鱼养殖：南鳄北养 多样赚钱，2021 年 9 月 3 日
18. 湖南卫视《新闻大求真》栏目介绍团队教师带领学生开展珍稀濒危兰花的保护生物学研究，2021 年 7 月 23 日
19. 中央教育电视台在全国教育新闻联播节目报道课程思政成果：“以榜样的力量引领人 着眼国家战略需求培养人”，2020 年 11 月 18 日
20. 澎湃新闻、全国教育新闻联播报道团队教师赴科右前旗支教并成立“北林大和科右前旗教学名师工作坊联合工作站”，为学生讲授植物学相关知识，2020 年 6 月 8 日
21. 北京林业大学绿色新闻网报道团队教师参加青年教师基本功大赛，2019 年 4 月 11 日
22. 《北林报》报道成果完成人科教融合教书育人的先进事迹：“我与学生共成长”，2018 年 11 月 15 日
23. 第二届北京林业大学大学生创新创业训练成果展示与经验交流会做《“创新活动”之花》的主题发言，宣传和介绍了科教融合协同育人取得的成绩和经验，2015 年 6 月 15 日
24. 《中国绿色时报》报道团队成果指导的大学生入选科技创新团队，2014 年 5 月 8 日
25. 《中国绿色时报》报道团队成果培养生物学创新人才，2014 年 3 月 21 日
26. 《北林报》报道团队成果培养创新人才的“样板田”，2013 年 9 月 16 日

（十一）毕业本科生代表（99人）

郭子铭、史可、徐义舒、张玉蛟、毛馨艺、莫岚、刘诗佳、宋宗胜、邱万理、宋语涵、常琮朝、王天宇、许升、李宇宸、严梦灿、宋丰成、穆圣衡、郑然希、于越、闫凌霄、许照乘、李宏旭、周健、陈森达、赵文斯、李懿帆、刘艾琳、袁毅慧、赵美琪、周兆福、谈天柱子、谢宜珊、王梓源、张艺涵、赵东辰、冯子阳、武玲、孙语泽、刘博、韩用功、席紫藤、米永艺、陈一凡、陈天厚、刘旭豪、张雪莹、安晓宇、陈颖铎、周粤、曹泽昊、张宇哲、姜文娟、瞿小龙、胡若涵、刘方舟、杜泽涛、蒋妙妙、王祺、崔可、郭诗曼、宋悦、闫帅廷、刘昊、杨楚峤、谢艺嘉、王冰蓉、谭金宜、王艺、齐鸿煜、范思洁、郭桐、刘霏霏、吴宇晴、张晓璇、张雨薇、王福琳、蔡高辕、许哲楠、王子谊、张书豪、翟浩铭、黄逸凯、刘天禹、滑蕊、唐瑶、卜郁、莫丽红、吕卿毓、纳静、张硕、刘佳琪、郑倩雯、杨文、张亦藜、席丽琴、徐小牧、孙中恩、崔雁翔、高艳珊

教学成果获奖证明（112 项）



中华人民共和国教育部

Ministry of Education of the People's Republic of China

Language

语言

无障碍浏览

登录

注册

当前位置: 首页 > 公示

关于第三批国家级一流本科课程认定结果的公示

根据《教育部关于一流本科课程建设的实施意见》（教高〔2019〕8号）和《教育部办公厅关于开展第三批国家级一流本科课程认定工作的通知》（教高厅函〔2023〕24号）的有关要求，经有关部门（单位）教育司（局）、各省级教育行政部门和高校申报推荐，我部组织网络评审和会议评审，拟认定5999门课程为第三批国家级一流本科课程（名单见附件）。其中，线上课程1000门，虚拟仿真实验教学课程500门，线下课程1842门，线

124	兽医公共卫生学	孙英健	史晓敏、李秋明	北京农学院
125	作物昆虫学	郭洪刚	覃晓春、杜艳丽	北京农学院
126	机械原理	康峰	袁湘月、王亚雄、王猛猛、付建蓉	北京林业大学
127	水质工程学	张立秋	曲丹、程翔、封莉、张盼月	北京林业大学
128	植物学 B	程瑾	刘忠华、郭惠红、王若涵、李晓娟	北京林业大学
129	现代物流与供应链管理	张名扬	马宁、胡明彤、尤薇佳	北京林业大学

74	食品微生物学	陈晶瑜	李平兰、赵亮、郑浩	中国农业大学	智慧树网
75	微生物及植物病原学	周涛	张燕、张力群、范在丰	中国农业大学	智慧树网
76	家畜解剖及组织学	匡宇	常建宇	中国农业大学	智慧树网
77	计算机辅助设计	漆楚生	张宗玲、荀进胜	北京林业大学	爱课程(中国大学 MOOC)
78	风景园林规划设计——城市滨水景观	李惊	吴丹子、张诗阳、李慧、钱云	北京林业大学	爱课程(中国大学 MOOC)
79	动植物检疫	石娟	刘树强、梁特	北京林业大学	爱课程(中国大学 MOOC)
80	山野菜认知与开发利用	陈玉珍	李慧、赵宏飞、薛华	北京林业大学	学堂在线

国家级一流本科课程

证书

课程类别: 线下一流课程

课程名称: 动物生理学 A

课程负责人: 翁强

课程团队其他主要成员: 袁峥嵘、韩莹莹、张浩林

主要建设单位: 北京林业大学

★ ★ ★ ★ ★

教育部
2020 年 11 月

证书编号: 2020130115

教育部办公厅

教高厅函〔2019〕46号

教育部办公厅关于公布 2019 年度国家级和 省级一流本科专业建设点名单的通知

3、2019年度北京林业大学一流本科专业建设点名单（国家级+市级）

北京林业大学2019年度国家级一流本科专业建设点名单	
序号	专业名称
1	生物科学
2	木材科学与工程
3	林产化工
4	环境工程
5	风景园林
6	园艺
7	水土保持与荒漠化防治
8	林学
9	园林
10	森林保护
11	草业科学
12	农林经济管理



教育部财政部关于批准第三批高等学校特色专业建设点的通知

教高函〔2008〕21号

各省、自治区、直辖市教育厅(教委)、财政厅(局)，新疆生产建设兵团教育局、财务局，有关部门(单位)教育司(局)、财务司(局)，教育部直属各高等学校：

第三批高等学校特色专业建设点名单			
项目编号	学校名称	专业名称	备注
TS10591	北京大学	汉语言文学	
TS10620	北京农学院	园艺	
TS10621	北京林业大学	生物科学	
TS10622	首都医科大学	生物医学工程	



荣誉证书

北京林业大学“北林”野生动物生殖奥秘探索创新团队：

大学生“小平科技创新团队”称号



二〇一四年八月

证书

编号：2020015

北京林业大学 袁峥嵘、张浩林、韩莹莹、翁强：

作品脑的高级功能——睡眠在2020年全国高校
生命科学类微课教学比赛中，荣获二等奖。

特颁此证，以资鼓励。

全国高校生命科学类微课教学比赛组委会
《高校生物学教学研究（电子版）》编辑部（代章）

二〇二〇年四月

荣誉证书

翁 强同志：

在教育教学工作中成绩优异，授予
北京市优秀教师称号。



2022年9月

荣誉证书

翁 强同志：

在北京市高等学校教学名师奖评选中，您
荣获第十二届北京市高等学校教学名师奖。
特发此证

北京市教育委员会
二〇一六年九月

宝钢教育奖证书



翁强老师荣获二〇二一年度

宝钢优秀教师奖。特颁此证。

学校 北京林业大学

宝字第 202110530号

宝钢教育基金会理事长 **胡望明**

2021 年 11 月

荣誉证书

北京林业大学森林生物学校尖学生培养团队：

在北京高校优质本科育人团队评选中，贵团队
被评为2023年度“北京高校优秀本科育人团队”。

特发此证。

北京市教育委员会
二〇二三年八月



荣誉证书

北京林业大学环境科学与环境工程专业“三全育人”团队：

在北京高校优质本科育人团队评选中，
贵团队被评为2021年度“北京高校优秀本科育人团队”。

特发此证！

北京市教育委员会
二〇二一年九月



荣誉证书

北京林业大学森林植物学卓越人才联合培养平台：

在北京本科高校产学研深度协同育人平台评选中，被评为2023年度“北京本科高校产学研深度协同育人平台”。

特发此证。

北京市教育委员会
二〇二三年八月

長江學者獎勵計劃

CHANG JIANG SCHOLARS PROGRAM

青 年 学 者
Chang Jiang Scholars

兹批准北京林业大学
聘任 宋跃朋 为教育部
2022 年度“长江学者奖励
计划”青年学者，支持期 3
年。



中华人民共和国教育部
MINISTRY OF EDUCATION, PEOPLE'S REPUBLIC OF CHINA
编号: Q2022232 2023 年 8 月

证 书

第 2020BJ006 号

宋跃朋同志：

入选为全国林草科技创新人才计划
青年拔尖人才，特发此证。

国家林业和草原局
2020 年 8 月 4 日



高等学校科学研究优秀成果奖
(科学技术)

证 书

项目名称: 杨树基因组功能元件适应性演化与遗传
调控机制

奖励类别: 自然科学奖

奖励等级: 一等奖

获 奖 者: 宋跃朋



证书编号: 2022-030-R02

高等学校科学研究优秀成果奖
(科学技术)

证 书

项目名称: 杨树分子育种技术体系创新与优良品种
创制

奖励类别: 科学技术进步奖

奖励等级: 一等奖

获 奖 者: 宋跃朋



证书编号: 2019-172-R03



北京市科学技术奖 科学技术进步奖 证书

为表彰北京市科学技术奖获得者，
特颁发此证书。

项目名称：抗旱节水杨树新品种定向创制与示范
应用

奖励等级：二等奖

获奖者：宋跃朋



2024年4月24日

No.2023-J12-2-03-R02







青年服务国家
Youth Serve China

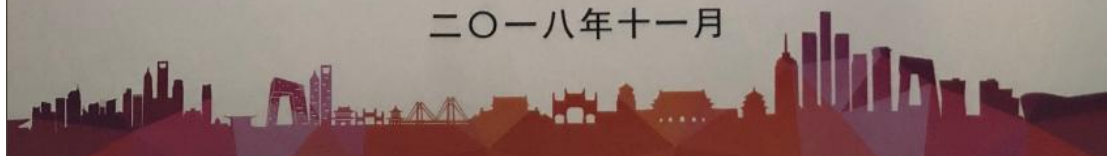
在2018年首都大中专学生暑期社会
实践工作中表现突出、成绩显著、被评
为“2018年度首都大中专学生暑期社
会实践优秀团队”。

团队：华夏龙吟奥森水碧蓝湖团

队员：刘源 王薇 刘震旦 蓝宝良 陈玲慧 杨韫瞳
刘思宇 张国慧 冯清 张宇潇

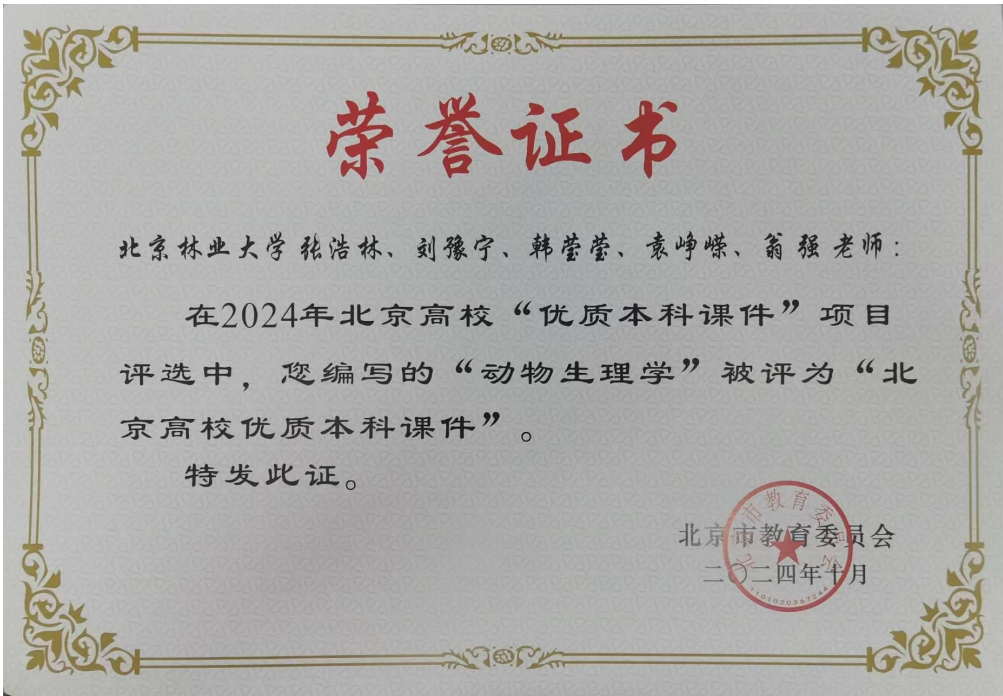


二〇一八年十一月



第二届青年绿色科技创新大赛获奖名单
(按首字母排序)

金奖		
1	储“液”拔萃基于沿海绿色能源的全液冷储能技术 领军者	广东海洋大学
2	醇真——基于新型工程菌构建的紫杉醇绿色高效生 产技术	山东中医药大学
3	基于“炭-菌协同”机制的生态修复材料设计与水体 净化性能优化研究	扬州职业技术大学
4	基于农业废弃物的耐候型粉体蛋白胶黏剂创新研发	山东农业大学
5	净益求禽——禽白血病病毒磁微粒化学发光抗原检 测首创者	山东农业大学
6	粮安无忧——鸟害智能防护装置	河套学院
7	“零醇π动力”基于传质-反应耦合的无醇啤酒乙醇 脱除与风味物质保留技术研究	湖南农业大学
8	秦风绿账：咸阳生态家底精算与乡村振兴新引擎	咸阳市规划设计研 究院
9	水智瞳——合成生物学赋能环境治理：基于工程酵 母的水体新型污染物检测仪器研发	北京林业大学



关于公布2022年优质本科课程和 优质本科教材课件遴选结果的通知

发布时间: 2022-09-19 来源: 北京市教育委员会

分享:   

京教函〔2022〕394号

各本科高等学校:

根据《北京市教育委员会关于开展2022年北京高校“优质本科课程”和“优质本科教材课件”建设的通知》(京教函〔2022〕143号),市教委组织了“优质本科课程”和“优质本科教材课件”的申报和评选工作,现将2022年遴选结果予以公布。

对于获评北京高校“优质本科课程”的主讲教师,认定为“北京高等学校优秀专业课(公共课)主讲教师”,我委将颁发证书以资鼓励,并给予相应政策支持。

各高校要进一步加强本科课程及教材课件建设,充分发挥“优质本科课程”和“优质本科教材课件”的引导和示范作用,进一步激发教师对本科教学的积极性,不断更新教学理念,推进课程创新与课程建设,提高教材课件的规范性和前沿性,有力支撑高校专业发展建设和实践创新教育改革,不断提升北京高等教育人才培养质量。

附件:

- 1、[2022年北京高校优质本科课程名单](#)
- 2、[2022年北京高校优质本科教材课件名单](#)

北京市教育委员会

2022年9月16日

附件 2

2022 年北京高校“优质本科教材课件”名单

序号	学校名称	项目名称	主 编	出版社	类型	项目类型
74	北京林业大学	数据库原理及应用教程（第四版）	陈志泊	人民邮电出版社	教材	

ID	奖项名称	奖励类型（新）	获奖年度	获奖级别（新）	本科教学获奖成员信息
2248	数据库原理及应用教程（第四版）	北京高校优质本科教材课件	2022	省部级其他	序号 1 陈志泊 2 #19670103 3 许福 4 #19790706



荣誉证书

北京林业大学韩莹莹老师：

在2022年北京高校“优质本科教案”项目评选中，您编写的“动物生理学A”课程教案被评为“北京高等学校优质本科教案”。

特发此证。

北京市教育委员会
二〇二三年一月

荣誉证书

韩莹莹同志：

您指导的本科毕业设计（论文）《野生达乌尔黄鼠卵巢血管内皮生长因子季节性表达调控及功能研究》，获评为2024年北京市普通高校优秀本科毕业设计（论文），您获评为优秀指导教师。

特发此证，以资鼓励。

北京市教育委员会
2024年11月

荣誉证书

张浩林同志：

您指导的本科毕业设计（论文）《低温诱导对达乌尔黄鼠掌丸功能的影响》，获评为2021年北京市普通高校优秀本科毕业设计（论文），您获评为优秀指导教师。

特发此证，以资鼓励。



荣誉证书

韩莹莹同志：

您指导的本科毕业设计（论文）《脂联素介导急性饥饿诱导卵巢损伤机制研究》，获评为2019年北京市普通高校优秀本科毕业设计（论文），您获评为优秀指导教师。

特发此证，以资鼓励。



北京林业大学
第十一届“教学名师奖”评选结果
(按姓氏笔画排序)

姓 名	学 院
马 岚	水土保持学院
苏晓慧	信息学院
苏淑钗	林学院
宋 卓	体育教学部
陈文汇	经济管理学院
姚 朋	园林学院
黄 河	园林学院
韩莹莹	生物科学与技术学院
韩静华	艺术设计学院
漆楚生	材料科学与技术学院



荣誉证书

程瑾老师：

经评选，您被评为

北京林业大学教学名师

北京林业大学

二〇一七年五月

关于2025年校级本科教育教学成果奖评选结果的公示

[发布日期：2025-09-25 点击数：6]

近日，学校开展2025年校级本科教育教学成果奖评审工作。经教师申请、学院初评推荐、校级专家评审，确定“‘科教融汇、数智赋能、成长领航’卓越拔尖人才培养模式改革与实践”等15项成果为特等奖，“‘121’协同推进学生体质健康促进的探索与实践”等30项成果为一等奖，“‘产教双融·赛研双驱’，面向人居环境治理的园林管理课程创新与实践”等25项成果为二等奖。现将名单予以公示（各等级内按照成果名称拼音排序）：

特等奖（15项）

序号	成果名称	成果完成单位
1	“科教融汇、数智赋能、成长领航”卓越拔尖人才培养模式改革与实践	袁峥嵘、程瑾、许福、程翔、宋跃朋、韩莹莹、张浩林、赵宏飞、刘豫宁、国辉、李鑫伟、翁强、徐桂娟
2	“认知、认同、践行”三阶递进构建习近平生态文明思想铸魂育人的北林模式	王洪元、张志强、刘广超、张秀芹、林震、马静、吴健、蔡紫薇、谭文斌
3	“三课联动·三实贯通·三加赋能”风景园林实践育人模式的创新与实践	赵晶、郑曦、吴丹子、郝培亮、马嘉、王晔月、林辰松、段威、张诗阳、黄河、黄更、李剑
4	“生态‘拓’维-产教融‘通’-数智‘铸’能”水土保持与荒漠化防治一流专业建设与实践	王云琦、王彬、程金花、王依涵、吕立群、王玉杰、张守红、许行、张帆、于明合
5	“四维三阶”服务生态文明建设：林工育人团队的建设与实践	唐峰、马尔妮、李艳洁、张建、王猛、袁湘月、韩巧玲、王亚雄、付建蓉、张成、彭亮、李亚棋
13	五大体系 五个面向 五种能力：森林生物学拔尖创新人才培养模式实践之路	安黎哲、付玉杰、程瑾、张浩林、翁强、钮世辉、李晓娟、申磊、徐桂娟、高雨菲

一等奖（30项）

序号	成果名称	成果完成单位
29	植物学课程的深耕与辐射：支撑生态文明建设高素质人才培养的基石工程	程瑾、刘忠华、郭惠红、李晓娟、高宏波、刘迪、王若涵、董树斌、刘平丽、刘小敏、胡青、张贵芳、禹瑞敏、王诗俊

二等奖（25项）

序号	成果名称	成果完成单位
5	“智慧强基、两维联动、三融赋能”的理学素养协同提质教学体系改革与实践	汪沛、张艺潇、丰全东、张立、李莉、岳瑞峰、张晓宇、陈菁、田慧、孙阳、吴昊林、章娟、李鑫伟、姚宇峰、李由
20	新农科背景下林学通识课“林学概论”三维融合教学体系构建与创新实践	敖妍、彭祚登、陈仲、马履一、贾忠奎、孙永江、张新娜、王佳茜、段昉、席本野
21	新农科背景下生态文明引领的大学英语“五位一体”育人体系创新与实践	李芝、吴增欣、冯强、姜瑞娟、白雪莲、朱丽轩、王雪梅、刘真、梁艳春
22	需求导向 数智赋能 理实融合：国贸专业人才培养模式研究	吴成亮、张洋、侯方森
23	一核两翼三融四发展：创新教研工作室驱动新农科创新人才培养的探索与实践	韩莹莹、翁强、张浩林、马超、袁峥嵘、刘豫宁、霍星辰、张路路

荣誉证书

翁 强 张浩林 袁峥嵘 韩莹莹 徐桂娟:

国家级一流本科线下课程教学改革示范, 获
2021 年北京林业大学教学成果奖一等奖。

北京林业大学
二〇二一年九月

荣誉证书

孙德智 王毅力 王强 程翔 李敏 邱斌 张盼月
曲丹 王辉 党岩 豆小敏 洪喻 王春梅:

专业思政同行-产生导向驱动-科教融合助力”
模式推动环境专业人才高质量培养, 获 2021 年北京
林业大学教学成果奖二等奖。

北京林业大学
二〇二一年九月

荣誉证书

陈玉珍 李 慧 马 超 赵宏飞 薛华
史玲玲:

打造精品《山野菜认知与开发利用》在线开
放课程的探索与实践,获 2021 年北京林业大学
教学成果奖二等奖。

北京林业大学
二〇二一年九月

荣誉证书

翁强 韩莹莹 袁峥嵘 张浩林 徐桂娟:

科教融合协同育人培养生物类创新型人才探
索与实践,获 2019 年北京林业大学教学成果奖二
等奖。

北京林业大学
二〇二一年二月

荣誉证书

翁强 袁峥嵘 韩莹莹 徐桂娟 张浩林：

经评选，《大学生创新实验室人才培养模式的研究与实践》获二〇一七年校级教育教学成果

一等奖

北京林业大学
二〇一七年七月

荣誉证书

程翔 王毅力 卢振雷 李敏 张立秋 曲丹 张盼月
梁文艳 齐飞：

经评选，《基于工程教育认证的环境工程专业人才培养模式创新与实践》获二〇一七年校级教育教学成果

一等奖

北京林业大学
二〇一七年七月

荣誉证书

HONORARY CREDENTIAL

为表彰北京林业大学第三届教师教学创新大赛获奖者，特颁发此证书。

获奖课程：动物生理学 A

主讲教师：张浩林

团队成员：袁峥嵘、韩莹莹、刘豫宁

获奖等级：三等奖



荣誉证书

HONORARY CREDENTIAL

为表彰北京林业大学第三届教师教学创新大赛获奖者，特颁发此证书。

获奖课程：环境微生物学（双语）

主讲教师：程翔

团队成员：胡潜

获奖等级：三等奖



荣誉证书

生物科学与技术学院 韩莹莹团队，荣获第一届北京林业大学
教师教学创新大赛 副高 组

三等奖

特颁此证。

参赛课程：身心健康的生理学基础

团队成员：张浩林、袁峥嵘、翁强



荣誉证书

HONORARY CERTIFICATE

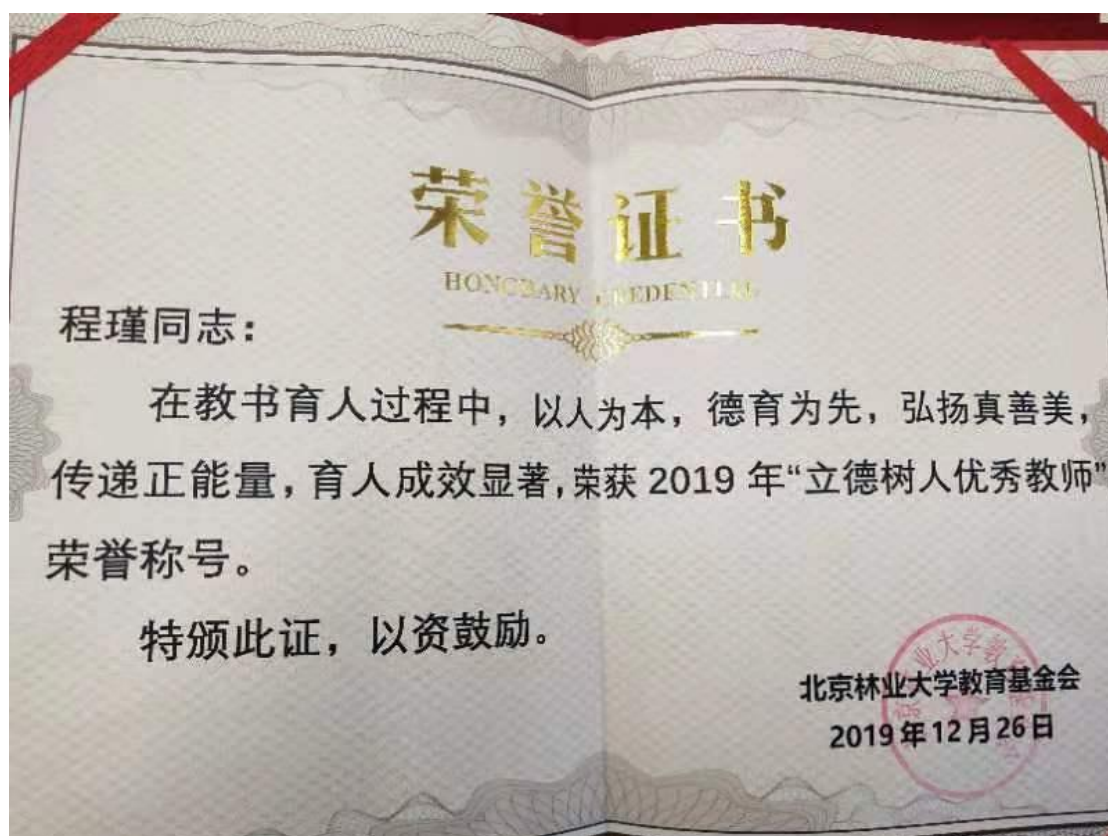
授予 程瑾 同志：

北京林业大学巾帼先锋荣誉称号

中国教育工会北京林业大学委员会

二〇二三年三月







言传身教、勇于创新，带领学生科技创新的好老师翁强；



荣誉证书

袁峥嵘：

荣获北京林业大学 2018 年社会实践

优秀指导教师

特颁此证，以资鼓励。

共青团北京林业大学委员会
二〇一八年十一月

荣誉证书

程翔同志：

在2016年北京林业大学“优秀教师”、“先进工作者”评选活动中，被评为“优秀教师”称号，特发此证，以资鼓励。

北京林业大学

2016年4月29日

荣誉证书

HONORARY CREDENTIAL

程瑾 同志：

荣获 2013 年家骥云龙青年教师教学优秀奖，
特发此证，以资奖励。

北京林业大学

北京林业大学教育基金会

二〇一三年九月

荣誉证书

程翔 同志：

荣获 2016 年家骥云龙青年教师教学优秀奖，
特发此证，以资奖励。

北京林业大学

北京林业大学教育基金会

二〇一六年九月

荣誉证书

程翔同志：

在北京林业大学 2016 年就业创业工作中表现突出，被评为

就业创业工作贡献奖

特发此证，以资鼓励。

北京林业大学

二〇一六年十二月

北京林业大学

Beijing Forestry University

荣誉证书

程翔 同志：

在二〇一 一 至二〇一 二 学年度

被评为 优秀班主任 。

特此证明，以资鼓励。

北京林业大学

二零一二年十一月九日



北京林业大学
BEIJING FORESTRY UNIVERSITY

荣誉证书

刘豫宁老师:

在北京林业大学第十九届青年教师
教学基本功比赛（实践类）中荣获:

三等奖

特发此证，以资鼓励。



荣誉证书

张浩林 老师：

荣获北京林业大学第十五届青年教师教学基本功比赛“三等奖”。

特颁此证，以资鼓励。



荣誉证书

韩莹莹 老师：

在北京林业大学第十四届青年教师教学基本功比赛中荣获“一等奖”。

特颁此证，以资鼓励。



荣誉证书

韩莹莹 老师：

在北京林业大学第十四届青年教师教学基本功比赛中荣获“最佳教学演示奖”。

特颁此证，以资鼓励。

北京林业大学
二〇一八年十一月

荣誉证书

袁峥嵘 老师：

在北京林业大学第十四届青年教师教学基本功比赛中荣获“最佳指导教师奖”。

特颁此证，以资鼓励。

北京林业大学
二〇一八年十一月

荣誉证书

袁峥嵘 老师：

在北京林业大学第十二届青年教师教学基本功比赛中荣获“二等奖”。

特颁此证，以资鼓励。

北京林业大学
二〇一六年十二月

荣誉证书

程瑾 老师：

在北京林业大学第十二届青年教师教学基本功比赛中荣获“最佳教学演示奖”。

特颁此证，以资鼓励。

北京林业大学
二〇一六年十二月

荣誉证书

程瑾 老师：

在北京林业大学第十二届青年教师教学基本功比赛中荣获“最受学生欢迎奖”。

特颁此证，以资鼓励。

北京林业大学
二〇一六年十二月

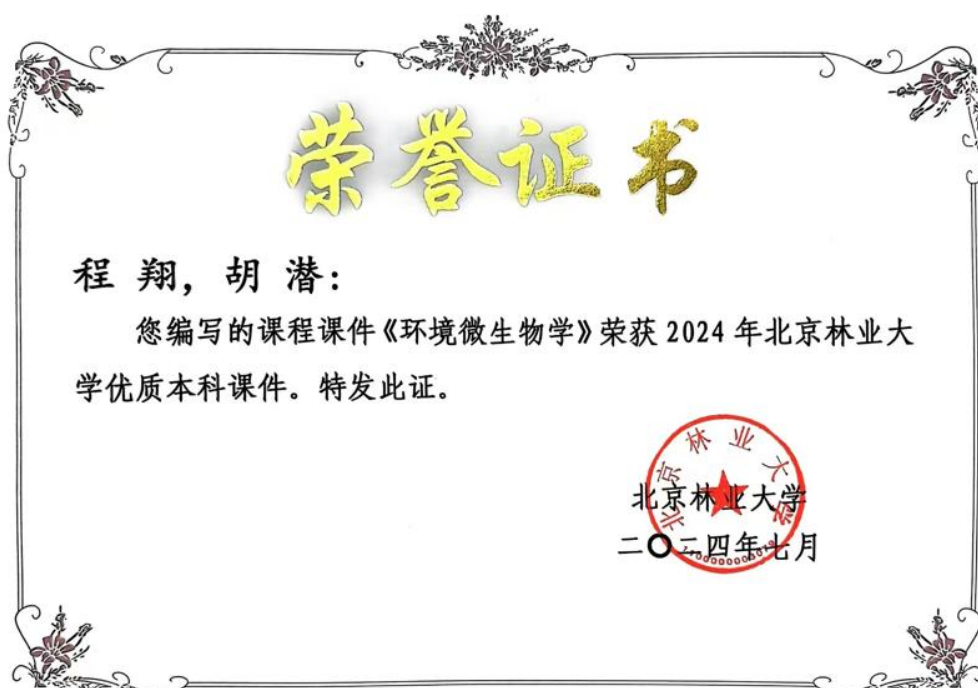
荣誉证书

宋跃朋 老师：

在北京林业大学第十一届青年教师教学基本功比赛中荣获“二等奖”。

特颁此证，以资鼓励。

北京林业大学
二〇一五年十二月



2024 年北京林业大学优质本科课程名单

(按照课程名称笔画数排序列出)

序号	课程名称	负责人	所在单位
1	日语翻译理论与实践	魏萍	外语学院
2	水土保持工程学	周金星	水土保持学院
3	水分析化学	齐飞	环境科学与工程学院
4	生态与环境心理学	田浩	人文社会科学学院
5	动物学实验	张东	生态与自然保护学院
6	动植物检疫	石娟	林学院
7	机械原理 A	康峰	工学院
8	城乡绿地系统规划 A	李方正	园林学院
9	恢复生态学	董世魁	草业与草原学院
10	高等数学	李扉	理学院
11	虚拟商业社会跨专业综合实训	薛永基	经济管理学院
12	植物学 B	程瑾	生物科学与技术学院
13	数据结构	李冬梅	信息学院

2024 年北京林业大学优质本科教案课件名单

(按照教案课件名称笔画数排序列出)

序号	教案课件名称	负责人	所在单位	类别
1	人工智能与创业智慧	李华晶	经济管理学院	课件
2	中外装饰艺术史	辛贝妮	艺术设计学院	教案
3	中国古代木结构建筑	戴璐	材料科学与技术学院	教案
4	风景园林设计思维	张诗阳	园林学院	课件
5	心理学研究方法	于晓	人文社会科学学院	教案
6	心理学研究方法	于晓	人文社会科学学院	课件
7	电工电子技术 A	王凡	工学院	教案
8	动物生理学	张浩林	生物科学与技术学院	课件
9	动物学实验	张东	生态与自然保护学院	教案

附件

2020年北京林业大学本科课程优秀教案获奖名单

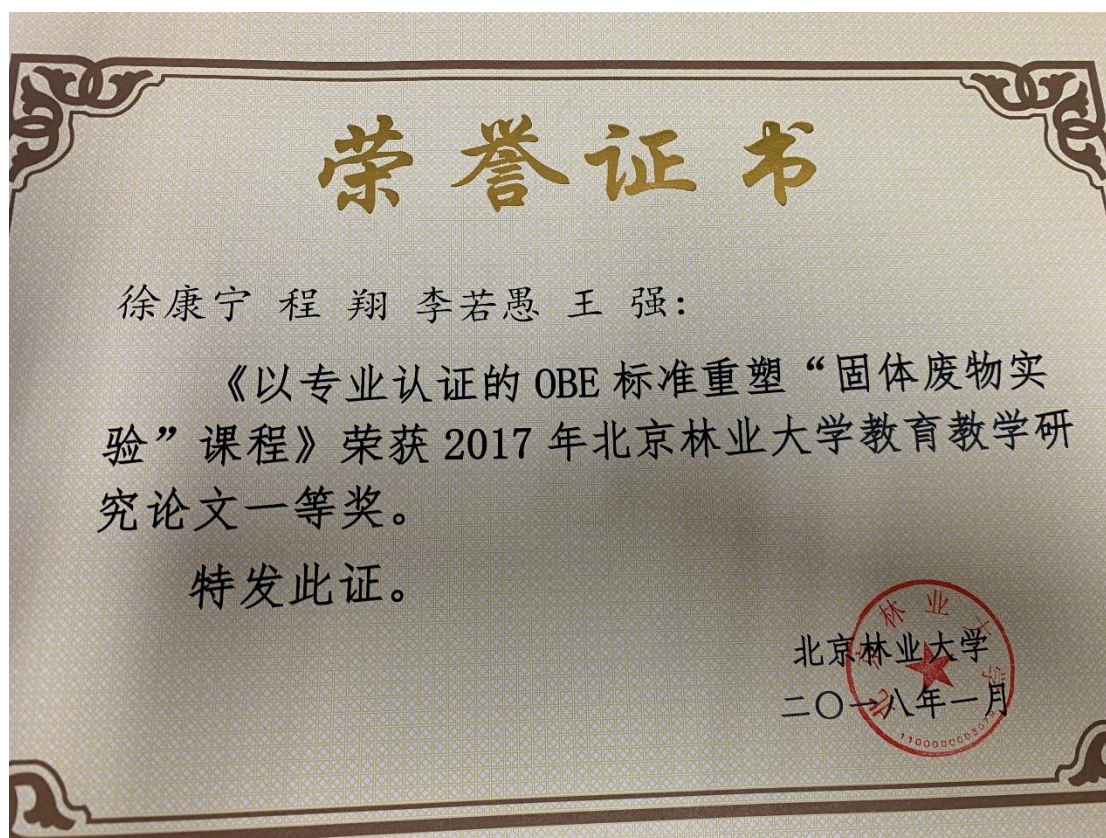
序号	课程名称	教师姓名	所在单位	获奖等奖
1	人造板工艺学	唐睿琳	材料科学与技术学院	一等奖
2	大学英语	梁艳春	外语学院	一等奖
3	木材学A	马尔妮 曹金珍	材料科学与技术学院	一等奖
4	免疫学	张浩林	生物科学与技术学院	一等奖
5	思想道德修养与法律基础	朱 红	马克思主义学院	一等奖
6	食品工程原理	任迪峰	生物科学与技术学院	一等奖
7	微生物学	郑 菲	生物科学与技术学院	一等奖

附件

2018年北京林业大学本科课程优秀教案获奖名单

序号	教师姓名	参评教案课程名称	所在学院	获奖等级
1	马超	食品毒理学	生物学院	一等奖
2	邓晓	羽毛球	体育部	
3	张学霞	资源环境遥感	水保学院	
4	赵媛媛	风沙物理学	水保学院	
5	郭允倩	细胞生物学	生物学院	
6	韩莹莹	身心健康的生理学基础	生物学院	





北京林业大学2022年教育教学改革与研究优秀论文奖获奖名单

(同一等级内以第一作者姓氏笔画为序)

序号	论文题目	第一作者	获奖等级	所在单位
105	课程思政背景下“现代微生物学实验技术”教学改革及思考	国辉	二等奖	生物科学与技术学院

荣誉证书

徐康宁 李若愚 程翔:

《自主学习在线上教学中的作用初探——以北京林业大学环境工程专业必修课“固体废物处理处》荣获 2020 年北京林业大学教育教学研究论文二等奖。

特发此证。

北京林业大学

二〇二一年一月

荣誉证书

张浩林 韩莹莹 袁峥嵘 高福利 翁强:

《疫情新常态下本科生创新实验室的安全管理工作探讨》荣获 2020 年北京林业大学教育教学研究论文三等奖。

特发此证。

北京林业大学

二〇二一年一月

荣誉证书

张浩林 韩莹莹 高福利 袁峥嵘 翁强：

《VR全景视频在“免疫学实验”课程教学中的应用探索》荣获2019年北京林业大学教育教学研究论文三等奖。

特发此证。

北京林业大学
二〇二〇年五月

荣誉证书

袁峥嵘，高福利，韩莹莹，张浩林，翁强：

《新冠肺炎疫情下快速在线翻转课堂教学模式探索与实践——以“动物改变世界”为例》荣获北京林业大学2022年教育教学改革与研究优秀论文优秀奖。

特发此证。

北京林业大学
二〇二三年三月

荣誉证书

袁峥嵘 韩莹莹 张浩林 翁强：

《“创客教学法”在动物生理学教学中的创新探索与实践》荣获 2018 年北京林业大学教育教学研究论文优秀奖。

特发此证。

北京林业大学

二〇一八年三月

荣誉证书

张浩林 韩莹莹 袁峥嵘 翁强：

《为学生扣好专业基础课程的“纽扣”——以“动物组织与胚胎学”为例》荣获 2017 年北京林业大学教育教学研究论文优秀奖。

特发此证。

北京林业大学

二〇一八年一月

荣誉证书

袁峥嵘 张浩林 韩莹莹 翁强 高福利：

案例胰岛素的发现与应用——医学界的重要里程碑荣获 2021 年北京林业大学“课程思政”教学改革优秀案例。

特发此证。

北京林业大学
二〇二一年十二月

动物生理生化大实验课程思政改革与探索*

——以北京林业大学为例

袁峥嵘 翁强 韩莹莹 张浩林 刘豫宁

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摘 要:为落实立德树人根本任务,将思政教育贯穿教育教学全过程,开展课程思政,以满足培育高素质、复合型、创新型人才的需求。以动物生理生化大实验课程为例,阐述课程教学现状,从提升授课教师课程思政意识和育人水平、明确课程思政建设目标、深度挖掘思政元素、改进教学方法、丰富教学载体途径和完善多元教学评价考核机制等方面,探讨课程思政改革与实践,旨在为推动高校实验课程思政建设,提高教育教学质量,培育高素质、复合型、创新型人才提供参考和借鉴。

关键词:课程思政;动物生理生化大实验;教学改革;思政教育;实验课

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0 引言

在新时代背景下,为落实立德树人根本任务,必须将思政教育贯穿教育教学全过程,开展课程思政。要切实推进高校课程思政与思政课程同向同行,充分发挥课程改革的“主战场”作用、课堂教学的“主渠道”作用和教师队伍的“主力军”作用,做到门门课程有思政,发挥协同效应,构建“全员育人、全过程育人、全方位育人”的“三全育人”大格局^[1-3]。

在高校人才培养过程中,将专业实践课程与思政教育紧密融合,已成为一种必然趋势^[4]。动物生理生化大实验课程主要面向动物学相关专业的研究生。该课程通过基础和综合性生理生化实验,对学生进行实验基本技能训练,旨在培养学生系统掌握现代生物学研究中动物生理生化相关研究方法。课程综合利用动物学、动物生理学、生物化学与分子生物学的实验技术和方法,主要开展基因 mRNA 表达、蛋白质免疫印迹、免疫组织化学、免疫荧光等实验,高通量多组学数据生信处理与分析,以及相关合成生物学、基因编辑技术等新技术和国家“双碳”战略与生态文明建设相结合的开放设计性实验等,培养学生的攻坚克难力和团队精神,提升学生自主、系统探索动物学相关研究的能力,增强学生的独立动手能力、分析解决问题能力和科学思维。通过这些教学内容,学生在知识层面、能力层面和思政层面均有提升,提高了综合素质,为后续科学研究打下坚实基础。

究打下坚实基础。

在动物生理生化大实验这门专业课的课堂教学中,北京林业大学课程教学团队积极开展课程思政改革与探索,主要目标是提升教师的思政素质和育人能力,提高学生的思政素养,激发学生对科学研究的热爱与重视,引导学生服务国家战略目标,树立科技强国理念,增强学生对祖国的热爱之情,鼓励学生投身社会主义科技建设事业。通过这些举措,致力于综合提高实验教学质量,增强教学效果,落实立德树人,实现课程教学与思政教育同向同行,培养高素质、复合型、创新型人才。

1 动物生理生化大实验课程教学现状

目前,北京林业大学动物生理生化大实验课程教学团队由教授二人(其中一人为北京市教学名师)、副教授二人、讲师一人和实验师一人组成。在北京市教学名师的示范引领和“传、帮、带”作用下,教学团队成员长期从事一线教学与科研工作,积累了丰富的教学经验,打下了深厚的工作基础。教学团队现承担动物生理学国家级线下一流本科课程,曾获北京市高等教育教学成果二等奖一项、校级教学成果奖一等奖两项和二等奖一项等荣誉。教学团队成员在教学竞赛中屡获佳绩,包括北京市青年教师基本功比赛一等奖、北京林业大学青年教师基本功比赛一等奖和二等奖等,并多次指导学生在各类学科竞赛中获奖,如全国大学生生命科学创新创业大赛一等奖、二等奖,中国国际“互联网+”

*项目来源:北京林业大学研究生课程建设项目和教学改革研究项目“《动物生理生化大实验 I》课程思政教学改革与探索”(KCSZ23027);北京市高等教育学会 2023 年立项面上课题“专业课发挥思政教育功能教育教学模式研究”(MS2023016);作者简介:袁峥嵘、翁强,教授;韩莹莹、张浩林,副教授;刘豫宁,讲师。

“拔尖计划 2.0”驱动“动物学(拔尖班)” 课程教学改革的探索

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(北京林业大学生物科学与技术学院, 北京 100083)

摘要:“动物学”课程是高校生物类专业的重要基础课程。当前课程教学面临教材内容滞后、教学时数紧张、教学方法单一化以及考核评价体系局限性的多重挑战,这些问题严重制约了学生能力与视野的全面培养。为满足“基础学科拔尖学生培养计划 2.0 基地”的需求,对北京林业大学生物科学(拔尖班)的“动物学(拔尖班)”课程进行了教学改革。课程实施双语教学,优化教材内容。以全英文教材为主导,以动物进化为核心脉络,确保知识的前沿性,拓宽学生的国际学术视野;通过 BOPPPS 教学法增加课堂互动,促进深度学习。课程还增设了学术墙报汇报(poster presentation)环节,锻炼学生科研表达与学术创新能力。学生认为双语教学、poster presentation 等改革措施拓宽了知识视野、增强科研素养、深化对动物学的理解。结果表明,改革措施不仅提升了学生的学习成效,更为“拔尖班 2.0”背景下的“动物学”课程持续优化提供支持,为培养具有国际视野与创新能力的生物科学拔尖人才奠定基础。

关键词:拔尖计划 2.0; 动物学; 教学方法; 双语教学; 学术墙报汇报

高等林业院校“植物生理学”课程教学改革的探索 ——以北京林业大学为例

王厚领 赵媛媛 赵 瑞 程 瑾 夏新莉

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摘要:“植物生理学”课程与农林业基础研究和生产实践应用研究紧密相关。随着现代植物生理研究前沿理论和技术迅速发展,植物生理学已和其他多个学科如细胞生物学、分子生物学、生物化学、结构生物学等产生交叉,给课程教学带来了较大挑战。传统的“植物生理学”课程存在教学内容需要优化、授课模式较为单一、学生学习效率和效果需要提高、实验设备落后于实验教学要求等问题,使得学生的学习主动性不高,学习效率较低,并且影响了学生用高精度、高效率实验仪器研究探索未知科学真理的欲望和创新思维的训练。提出了“植物生理学”课程优化授课内容素材增强逻辑性和系统性、多种授课模式并用增强“教”与“学”的效果、更新整合实验仪器设备等改革措施,提高了学生学习积极性和主动性、增加了学习兴趣和求知欲,课程的实验精确性和效率也得到提高。

关键词:植物生理学; 问题导向; 教学改革; 实验效率

[编者按]

党的二十大报告强调,教育、科技、人才是全面建设社会主义现代化国家的基础性、战略性支撑。推进中国式现代化建设,必须提高基础研究人才自主培养能力质量,努力造就一大批国家创新发展急需的基础研究人才,切实提升基础研究的支撑能力和保障水平。本期聚焦“提高基础研究人才自主培养能力质量”,从建设基础研究高水平支撑平台、加强基础研究人才队伍建设等角度刊登 2 篇专题论文,可为广大一线教育工作者提供切实可行的教学改革思路与方法借鉴。

高校实验室资源开放共享的研究与探索

——以北京林业大学生物拔尖创新实验室为例

宋涵,付玉杰,李瑞丽,程瑾^(✉)

北京林业大学生物科学与技术学院,北京,100083

摘要:高校实验室开放共享可优化资源配置,提高实验室资源利用效率。本文针对实验室资源开放共享过程中存在的问题,从共享理念、制度建设、信息化平台搭建和培训考核评价体系四个方面提出了具体建议与方法,介绍了北京林业大学生物科学与技术学院拔尖创新实验室开放共享的具体实施方案,为高校实验室资源的共享机制建设提供有效参考。

关键词:高校实验室,开放共享,创新管理

北京林业大学 2023 年教育教学改革与研究优秀论文选编

依托高校自身特色的 Android 课程 教学案例研究¹

——以北京林业大学为例

李鑫伟 张立 孙阳²

(北京林业大学理学院,北京 100083)

摘要:十四五规划明确提出“推动互联网、大数据、人工智能等同各产业深度融合”,Android 开发作为智能终端主流支撑技术之一,已成为高校信息类课程教育改革的研究热点。Android 课程教学案例设计不恰当会降低学生的课程期望和学习兴趣,直接影响教学效果。为此,以“依托高校自身特色”“与学生需求紧密结合”“研以致用”为理念,讨论了 Android 课程教学案例设计方法,并以北京林业大学为例,设计了一个“北林大一新生校园掌中宝 APP”教学案例,该案例的成功实

关于大创项目对生物专业人才培养意义的思考¹

——以北京林业大学生物学院为例

史玲玲 徐桂娟 付玉杰 程瑾²

(北京林业大学生物科学与技术学院 北京 100083)

摘要:大学生创新创业训练计划项目强调学生的自主性和创新性,在解决实际问题中培养大学生的创新思维和团队合作能力。

本文在分析北京林业大学及其二级学院生物学院的政策和服务机制对大创项目的组织引导作用的基础上,介绍了“双一流”背景下大创项目对生物类专业人才培养的意义,并以见证者和亲历者的身份指出了大创项目在运行中存在的问题并提出了解决措施。大创项目的运行改变了传统的教学模式,提高了教学质量和人才培养质量,推动了整个教育环境的创新和改变。

关键字:双一流;大创项目;创新能力;生物类;人才培养。

课程思政视角下《基因工程》 教学改革措施与成效¹

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摘要:课程思政是将各类课程与思想政治理论课同向同行,形成协同效应的综合性教育教学理念。“基因工程”是集生命科学前沿科学理论与技术于一体的专业基础课程,该课程内容涉及的转基因研究内容一直是我国学术界和社会议论的热点内容,使其成为课程思政改革的优良载体。因此,我们将课堂中转基因理论知识与我国转基因产业相关政策、科技前沿以及发展现状紧密联系起来,形成从基础理论研究到实际生产一线工作的完整映射,将为培养能够熟练利用专业知识科学普及转基因技术的人才队伍提供一个良好的示范。

关键词:基因工程;转基因;课程思政

融入思政元素的《传感器原理》课程教学改革¹

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摘 要:《传感器原理》课程是当今信息技术领域中的重要学科,在自动化、通信、医疗等领域发挥着重要作用。如何将《传感器原理》课程与思想政治教育相结合,提高《传感器原理》课程的教学效果和思想政治教育水平,是当前亟待解决的问题。本文提出了一种全新的课程思政教育模式,将思政元素贯穿于专业教育的各个环节,聚焦在知识传授、技能培养和思想传承三个方面的探索。通过将专业教育与思政教育自然地结合起来,确保专业课程与思想政治课程同向同行,形成协同效应,为《传感器原理》课程的教学改革提供一定的借鉴和参考。

关键词: 传感器原理; 思想政治教育; 教学设计; 教学实践; 教学改革

课程思政背景下《微生物学》课程 数字化资源库建设探索¹

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摘 要:课程思政是落实立德树人根本任务的关键,数字化资源是实施数字化学习的必要条件。课程思政背景下草业科学专业《微生物学》课程数字化资源建设,不仅丰富和更新了课程教学资源,而且将思政理念贯彻于传统教学内容,同时扩大了学生获取知识的途径,使学生对课程的学习和教师的指导时间和范围扩大到课堂和教室以外的时间和空间,改进学生的学习方式,满足多元化的学习需求,提高学生的学习兴趣和效率,尤其符合后疫情时代对学生线上授课资源的需求。本文通过分析目前草业科学专业《微生物学》教学中存在的问题、《微生物学》数字化资源建设的必要性和意义,提出课程思政背景下数字化课程建设的思路,及数字化资源建设的具体内容。

关键词: 草业科学; 微生物学; 数字化资源; 课程建设; 课程思政

基于 OBE 理念的《水工艺设备基础》课程教学质量提升实践与思考¹

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摘要: 工程教育认证是提升给排水科学与工程专业人才培养质量的重要保障。然而, 依据工程教育认证标准, 《水工艺设备基础》课程由于开设时间较晚、涉及内容复杂等问题, 教学质量难以保证。基于学习产出导向教育(OBE)理念, 本文对课程重要性、存在问题和解决建议等方面进行探讨分析, 为该课程教学质量提升提供可行的思路。

关键词: 工程教育认证; OBE 理念; 水工艺设备基础; 教学质量; 对策建议

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动物生理学 A 课程思政案例库建设与实践

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摘要: 利用专业知识教学进行课程思政教育是高校开展立德树人教育的重要举措。课程思政是高校实现全程育人、全方位育人, 促进学生全面发展的重要途径。思政案例库建设是课程思政的前提和保障。该文从“家国情怀、科学精神、文化自信、爱国主义”四个方面探索生物科学专业动物生理学 A 课程思政案例库建设, 挖掘蕴含于动物生理学 A 课程中的显性及隐性的德育元素, 为在专业知识传授中有机融入思想政治教育, 实现全方位育人奠定基础。

关键词: 动物生理学 A; 课程思政; 思政案例库; 教学改革; 德育元素

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北京林业大学电子专业实践课程体系改革

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摘要: 新农科和新工科为农林高校电子信息类专业的发展指明了方向, 同时对电子专业实践课程体系的建设和提出了更高的要求。本文立足于北京林业大学理学院电子信息科学与技术专业, 系统阐述了北林电子专业实践课程体系“一创一促”的改革理念、“八维、五步、两抓手”的改革举措、阶段性改革成效和未来规划。以更好的迎合新农科和新工科建设, 培养家国情怀深、信息电子工程应用能力强、高素质林草类复合创新人才。

关键词: 新农科; 新工科; 电子信息专业; 实践课程体系; 改革

截止 2022 年 8 月, 全国共有农林类院校 40 所, 其中设置了电子信息科学与技术专业/电子信息工程专业的院校共计 32 所。“新农科”和“新工科”建设已成为农林院校电子信息类专业的改革抓手^[1-2]。在农林院校电子信息类专业的人才培养过程中, 实践育人既能够有效推进工农学科交叉融合, 又能够促使电子信息类专业的特色化发展^[3-4]。因此, 实践课程体系建设一直是农林院校电子专业改革的重头戏。

基于CDIO教育模式“双碳-新农科”的“动物生理学”教学改革与探索

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摘要: 为适应“30·60”双碳目标形势下生物专业发展对“新农科”生物科学高素质创新型专业人才的需求, 本文采用CDIO教育理念对“动物生理学”课程从教学模式、教学内容、教师能力提升、学生综合素质提高、教学考核模式、课程思政教学等方面进行教育教学改革与实践, 探索“动物生理学”课程服务于“双碳”背景下高素质创新型人才培养和“新农科”建设的创新改革方式, 旨在进一步提高教学质量和教学效果, 为培养高素质创新型人才提供参考和借鉴。

关键词: CDIO教育理念; “双碳”; “新农科”; “动物生理学”; 教学改革

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疫情下在线翻转课堂教学模式探索与实践 ——以动物改变世界为例

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摘要: 在教育部“停课不停教、停课不停学”的号召下, 探索与实践动物改变世界课程的“两平台、两主体、三环节”互动式在线翻转课堂教学模式。通过在线翻转课堂, 学生自主学习能力、参与课堂互动意识、学习体验及效果得到有效提升, 实现了教学相长。

关键词: 在线翻转课堂; 动物改变世界; 视频会议

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基于虚拟仿真教学模式的“微生物学实验”课程教学改革探索

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摘要: “微生物学实验”课程具有很强的实践性和应用性。作为微生物学教学的重要环节, “微生物学实验”课程是培养学生创新能力和实践能力的必要手段, 对微生物学理论知识的巩固和加深具有重要意义。分析目前“微生物学实验”课程教学中存在的主要问题, 包括没有实物操作的情况下学生预习抽象, 课堂上很难实现一对多维度的展示, 不利于微生物学知识点之间的贯通、拓展等。针对该课程课堂教学受相关条件限制的主要问题, 同时结合新冠肺炎疫情防控常态化的相关要求, 提出引入虚拟仿真教学平台, 构建“多媒体+虚拟仿真+课堂训练”多元结合的“微生物学实验”课程教学模式。“微生物学实验”虚拟仿真教学可将抽象的知识具体化, 将知识点和主要实验技术多维度交叉融合, 有利于学生课前课后反复学习巩固知识并拓展应用, 有效提高学生的实践操作能力和创新思维能力。在此基础上, 从教学设备改善、在线资源优化、实验内容交叉融合以及实验考核全面化等方面提出了“微生物学实验”课程改革的具体举措。最后, 从促进专业知识和信息技术的有效结合、促进自主学习的可控性、促进教学质量和效率的提高、促进课堂操作与虚拟教学的有机结合等方面分析了“微生物学实验”课程改革的效果, 以期改革创新本科实践教学策略、加速课程现代化建设和提高人才培养质量提供有益参考。

关键词: 微生物学实验; 虚拟仿真教学; 课程改革

基于立德树人理念的“动物改变世界”课程思政教学探索

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摘 要

立德树人是教育的根本任务。本文深入挖掘《动物改变世界》课程中所蕴含的思想政治教育元素,从课程思政目标、教育理念、育人目标、教师课程思政教学能力、教学模式、教学内容、教学考核与评价等方面探索实践了《动物改变世界》课程“课程思政立德树人”的措施和途径,为其它课程思政立德树人教育教学改革提供参考和借鉴。

关键词 立德树人; 动物改变世界; 课程思政; 课程思政教学探索

基于“科教融合、协同育人”理念的新时代农林高校 本科毕业设计(论文)工作探索与实践

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摘 要: 高校本科毕业设计(论文)是本科教育中特别重要的教学环节之一,是衡量本科生是否符合毕业资格的重要标准,同时也是反映高校本科教育教学质量的重要指标。本文分析了目前高校本科毕业设计(论文)存在的主要问题,并探索与实践了基于“科教融合、协同育人”理念的新时代农林高校本科毕业设计(论文)的具体措施,旨在有效提升新时代农林高校本科教育教学质量、增强学生的综合素质和可持续发展能力。

关键词: 本科毕业设计(论文); “科教融合、协同育人”; 本科教育; 人才培养模式

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新工科背景下环境工程专业科技创新实践课程建设探索*

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摘 要: 基于新工科环境类专业对应用型人才和创新型人才的培养要求,探索了由学生掌握课程主动权,教师辅助的科技创新实践教学模式。学生将全流程参与实验调研、设计、操作、总结及成果展示环节,充分锻炼信息获取能力、专业文本撰写能力、动手能力、沟通交流能力,以获得综合素质的提升。研究成果有助于提升环境类专业人才培养质量,提高毕业生综合素质,培养满足我国生态文明建设战略需求的环境工程专业人才。

关键词: 新工科; 环境工程; 教学; 创新实践

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碳中和视角下面向三全育人的农林高校 本科毕业论文质量提升途径

——以北京林业大学环境专业为例

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摘要: 习总书记在联合国大会上提出了碳达峰碳中和目标, 这对我国农林高校环境专业人才培养提出了新的要求。本科毕业论文是本科生培养的最后环节, 也是最重要的一环。我院尝试在农林高校环境专业本科毕业论文全过程中加强质量管理, 在选题、开题、中期检查、答辩、后期检查等各个环节, 紧密结合碳达峰、碳中和要求, 切实履行全员、全过程、全方位的三全育人理念, 从而全面提高了本科毕业论文的质量, 在已举办的 4 届全国高校环境类专业本科生优秀毕业论文(设计)评比中连续获奖, 提升了农林高校环境专业人才水平。

关键词: 碳中和; 三全育人; 农林高校; 环境专业; 本科毕业论文

以 OBE 为导向的环境工程专业本科毕业 论文(设计)管理工作探索

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摘要: 工程教育认证是保障我国高等工程教育质量的重要举措, 本文以我校环境工程专业认证工作为案例, 探讨了产出导向型教育引导下环境工程专业毕业论文(设计)的改革举措, 从本科毕业论文(设计)对毕业要求指标点的支撑、毕业论文(设计)的题目顶层设计、科教结合、产教融合和过程质量监控几个方面总结了环境工程专业毕业论文(设计)工作对学生解决复杂环境工程问题能力达成的支撑, 并提出了采用层次分析法改进本科生毕业论文(设计)支撑能力达成的总体评价的建议。

关键词: OBE; 环境工程专业; 本科毕业论文(设计); 能力达成; 层次分析法

基于创新实验教学的实验室管理改革探索

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摘要:实验教学在综合素质人才培养中发挥着重要作用,实验室是开展实验教学和科研训练的主要阵地。创新实验教学的开展对实验室的硬件配置和管理模式提出了更高要求。以北京林业大学为例,阐述了在创新实验教学开展过程中遇到的挑战和问题;硬件上对先进设备需求迫切;教学管理上监管工作量增大,安全秩序和卫生维护及设备使用管理难度加大;学生主体上也显露出一些问题亟待改善,比如安全意识不强、自律性不足、组内参与度不一等。针对这些问题,从实验室育人的角度,提出了教学实验室管理改革的一些举措:①细化实验室安全制度,创建安全实验环境;②让学生参与实验室管理,培养学生主人翁责任意识;③注重植入环保理念,营造绿色实验室环境;④借助新媒体,形成优秀的实验室文化;⑤把立德树人教育融入实验课堂,培养学生优秀品质。教学实践收到了很好的效果:①显著提高了学生的安全意识,实验室环境显著改善;②增强了学生的科学求知欲,促进了每一位同学的进步;③将课程思政引入实验课堂,提升了学生的思想政治素养。

关键词:创新性实验教学;实验室管理;实验室文化;综合素质;人才培养

高等农林院校实验室生物安全问题 及其应对策略的探讨 ——以北京林业大学为例

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摘要:生物类实验室安全是高等院校安全工作的重要组成部分,是创建和谐校园与避免出现安全事故的重要保障。生物类实验室是进行生物技术试验的重要场所,具有较高的潜在安全风险。针对我国高等农林院校生物类实验室生物安全所面临的硬件条件比较薄弱,实验室管理机构运行不畅、安全管理经费不足,检查、督查、奖惩机制不完善及风险评估机制未形成,安全教育浮于表面等问题,依据新实施的国家生物安全法及北京林业大学实验室生物安全管理的实践,提出如下安全管理的对策:①健全生物安全管理制度体系;②完成实验室的生物安全分级;③强化生物安全教育,提升自我防护意识;④加强生物安全操作与防护;⑤规范生物废弃物管理,以为高等农林院校实验室生物安全提供保障。

关键词:实验室;生物安全;问题与对策

国家级线下一流本科课程建设与改革实践研究*

——以动物生理学课程为例

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摘要: 双一流背景下全面开展一流本科课程建设的“双万计划”实施促进了各高等院校一流本科课程建设的高潮。本文以获得首批国家级线下一流本科课程《动物生理学》课程为例, 分别从引入课程思政, 坚持立德树人, 课程内容体现时代性, 前沿性, 实用性和创新性, 教学过程中融入现代信息技术, 不断改进教学方法, 始终强调以学生为中心, 以学生全面发展为核心, 突出学生主体地位, 创新考核评价机制, 促进教学相长, 不断加强教师队伍及教育教学能力建设, 强化课程实践教学改革等方面进行了阐述, 希望可以为其它本科课程建设与改革实践提供参考和借鉴。

关键词: 一流本科课程; 一流本科专业; 双一流; 动物生理学; 课程建设与改革实践

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基于项目驱动的android课程研究

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摘要: 基于android系统的移动终端设备在智能终端市场上占据了主导地位, 国内高校纷纷开设了android课程, 以满足日益增长的社会需求。由于android知识体系庞杂, 实践性强, 传统的教学模式以知识点讲授为主, 实践教学环节薄弱, 已不能满足社会对android人才的需求。将android课程知识与生动活泼的APP项目融合能够很好地激发学生兴趣, 提高学生动手实践能力, 是当前android课程改革的研究热点之一。文章以“基于语音识别的智能记事本APP设计”项目为例, 探讨了基于项目驱动的android课程设计和实施方案。

关键词: android课程; 项目驱动; 语音识别

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以学生为中心的“环境微生物学实验” 教学改革与实践

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“环境微生物学实验”是高等理工学校环境科学与工程及相关专业本科学生的专业核心课，本课程以微生物学为理论基础，是生命科学和环境科学与工程学的交叉学科，具有较强的实践性和应用性。“环境微生物学实验”配合“环境微生物学”课程学习而设置，是理论课的延伸，是环境类工科人才培养过程中的重要实践性教学环节，培养学生运用中所学的微生物学知识解决实际环境问题的能力，对于工程实践能力的培养至关重要^[1]。

“以学生为中心”是一种基于能力范式的教学理念，是指以学生的学习和发展为中心，教学过程从“教师、课堂、教材”的教师“传授模式”向“学生、学习、学习过程”的学生“学习模式”转变，从而使学生的知识、能力和素质获得全面的提升^[2]。本教学团队在“环境微生物学实验”课程教学实践中，开展了基于“以学生为中心”理念的课程教学改革，重点培养学生的自主学习能力、实践动手能力和创新意识，取得了一定的成效。

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北京林业大学第十四届青年教师教学基本功比赛最佳指导教师(2018年)

教师简介:副教授,生物科学与技术学院动物学教研室教师。2014年7月至北京林业大学工作,2018—2019年于美国普渡大学访问学习。主讲“动物生理学”“免疫学”“动物改变世界”等课程。2016年获北京林业大学第十二届青年教师教学基本功比赛特色组二等奖;2018年获北京林业大学第十四届青年教师教学基本功比赛最佳指导教师奖。曾获北京市高等教育教学成果奖二等奖1项,校级教学成果奖一等奖1项。

教学感悟:学生与我共同成长!

青年教师教学基本功比赛与日常教学实践结合之路

摘要:实践经验表明青年教师教学基本功比赛有助于提升高校青年教师教学能力。本文结合自身参加及指导青年教师参加教学基本功比赛的经历与体会,探索和实践了将青年教师教学基本功比赛与日常教学实践结合的有效方法。以期与大家分享经验,共同助力提高青年教师素质及教学能力。

关键词:青年教师;教学基本功比赛;日常教学;教学能力

近年来,各高校将举办青年教师教学基本功比赛作为提高青年教师教学能力的重要途径,探索“以赛促教”,助力教育质量提升。北京林业大学已成功举办十四届青年教师教学基本功比赛,为广大青年教师搭建了一个相互交流学习、相互促进、全面提高教学能力的成长平台。笔者参加了我校第十二届青年教师教学基本功比赛,并获得特色组二等奖。两年后作为指导教师,帮助青年教师斩获我校第十四届青年

“互联网+大学物理实验”课程教学改革的探索

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摘要:随着“新工科”教育的深入发展,加强“互联网+大学物理实验”课程建设已成为当前高等院校教育改革的一个重要方面。在深入剖析了“互联网+大学物理实验”课程教学特点的基础上,针对当前课程教学出现的实验数据无人工处理、缺少实验报告、实验成绩仅由预习成绩和实验数据决定的问题,探讨了“互联网+大学物理实验”课程教学管理平台的改革方案,其核心内容包括:学生应在课堂上完成数据处理并提交系统,完成由模块化在线填写和完整纸质版撰写两种模式相结合的实验报告,实验成绩由教师和“互联网+大学物理实验”课程管理系统进行综合评分。教学结果表明,通过教学改革,学生的学习积极性和学习效果均有明显的提高。

关键词:大学物理实验;互联网+;教学管理平台;课程建设

环境微生物学实验教学内容和考核方式的改革与探索

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摘 要：环境微生物实验是环境工程专业的一门重要基础实验课程。针对本门实验课教学内容缺乏环境工程专业特色，综合设计型实验内容较少，实验成绩考核单一等方面所存在的问题与不足，对教学内容和考核方式进行了改革。通过增加专业特色内容、构建设计性实验和增强能力考核等方面的改革，使环境微生物学实验达到培养学生实践动手能力和运用知识解决实际工程问题能力的目的。

关键词：环境微生物学实验；教学内容；考核方式

一、引言

环境微生物学是北京林业大学（以下简称我校）环境工程专业的专业基础课，是我校环境工程、给排水科学与工程等专业的必修专业课，环境微生物学实验是支撑环境微生物学的实验课程，其课程是强化巩固环境微生物的基本理论知识、锻炼学生观察能力和操作能力、培养学生创新性和技术探索思维及解决实际环境问题的重要环节^[1]。

环境微生物学实验以普通微生物学为基础，研究微生物的一般规律，微生物与环境间的相互作用，微生物活动对环境产生的影响，以及在环境污染控制工程中有关的微生物学原理^[2]。学生主要学习和掌握微生物的观察、培养、分离、灭菌、无菌操作等基本的微生物学实验研究方法 & 环境微生物的应用技术等。目前，我校环境微生物学实验面向环境类专业大学三年级本科生开设，学生人数约 120 人，主要由 6 个实验构成，共 16 个学时。2018 年，我校环境工程专业第二次通过了中国工程教育认证协会（CEEAA）工程教育专业认证，我校环境微生物学不断融入专业认证的 OBE（Outcome-Based Education）理念，并在学时精简的大背景下，结合近年来实验教学存在的问题，从教学内容和考核方式方面进行了改革的探索与实践，重新梳理了 6 个环境微生物学实验，使得实验内容不仅保留了基础性实验，又丰富了综合性实验，取得了较好的效果。本文根据改革的体会，总结了环境微生物学实验教学中存在的问题，介绍了改革的一些具体做法，以期达到提高实验课教学效果，培养学生实践动手能力和运用知识解决实际工程问题能力的目的。

论文名称	作者	学校
基于“教赛融合”模式的创新教育新思考	韩莹莹、张浩林、袁峥嵘、 鲍伟东、翁强	北京林业大学
新时代农科类大学生创新创业实践能力提升路径研究	王亚南、冯国营、薛松、李庆亮	山东农业大学
基于 CNN 的遥感图像建筑物自动提取方法研究	余安祺、任芳语、肖扬	吉林建筑大学
互联网+背景下高校创新创业教育育人新方法	赵芷莹	东北大学
美国创业教育及启示与建议	赵明家	吉林农业大学
大学生创新创业教育模式探索——以内蒙古民族大学计算机科学与技术学院为例	邵飞飞	内蒙古民族大学
少数民族学生创新创业能力培养研究	通拉嘎	内蒙古民族大学

校友企业家创业历程的质性研究	邵敏、翟洪江、邹良影、王杜春	温州科技职业学院
创新创业人才培养体系的建设与实践	徐丽丽、郑灵翔、石江宏、谢火木、钟杰	厦门大学
专创融合路径研究：能力素质的视角	朱翠兰	东北大学
“导师制课题式”科研创新人才培养模式	张浩林、韩莹莹、袁峥嵘、高福利、翁强	北京林业大学
新时代中医药院校大学生创新创业能力培养路径研究	杨利利、方雅玲、徐伟	福建中医药大学
中心复合设计优化硝酸咪康唑缓释给药系统	李国华	辽宁科技学院
浅谈化工类本科创新创业型人才培养模式研究	李韵捷	广东工业大学
创新思维意识与能力培养——课程学习体会	王丹、韦龙明	桂林理工大学

“山野菜认知与开发利用”课程的慕课建设

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摘 要: 慕课是大规模开放的在线课程。“山野菜认知与开发利用”课程的慕课建设依靠学校的政策支持和团队的共同努力。“山野菜认知与开发利用”课程慕课建设主要包括慕课建设背景、课程特色和预期目标、课程内容设计、课程视频拍摄与制作、课程运行等,并提出学术性、普适性、趣味性、应用性、灵活性、可视性的教学定位,同时对线上与线下混合式教学模式进行了探索,旨在为方兴未艾的其他课程慕课建设提供思路和启示。

关键词: 慕课建设;山野菜认知与开发利用;在线开放课程;教学探索

创客教学法在“动物生理学”教学中的 创新探索与实践

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摘要: 基于创客教育探索与实践的创客教学法是一种鼓励学生在探索、发明和创造过程中主动与协作学习的教学方法,主要包括有启发创意—设计创意—制作创意—分享创意—评价创意5个关键步骤。通过“创客教学法”在“动物生理学”中的教学实践,学生自主设计并制作了灭虫灯、测谎仪等实用的创意作品。创客教学法充分调动了学生的学习兴趣 and 主动性,培养了学生的创客思维,实现了线上线下融合学习方式,提高了学生的创新能力和实践能力,教学效果明显提升,为改革创新本科学生人才培养模式和提高人才培养质量提供了有益借鉴。

关键词: 创客教育;创客教学法;动物生理学;创意;实践能力

本硕联动的产学研联合人才培养模式研究

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摘 要: 总结目前的研究生产学研联合培养方法, 指出当前联合培养过程中存在的典型问题, 阐述北京林业大学全日制工程硕士专业学位研究生的产学研联合培养模式, 说明实践结果。

关键词: 产学研联合; 工程硕士; 专业学位; 研究生培养

“食品质量与安全”课程教学改革的探索

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摘 要: “食品质量与安全”是食品科学与工程专业的主干课程之一, 也是一门具有较强实践性和应用性的课程。根据课程的特点与定位, 分析了课程教学改革的必要性, 针对教学内容陈旧、重点不突出, 教学方法单一, 实验、实践课程缺乏创新性等问题, 提出了教学改革措施: 首先优化课程教学内容, 增加食品科技前沿知识; 其次采用多媒体等现代化教学手段, 增加案例教学; 第三, 改革传统的实验、实习及课程设计环节, 弱化以教师为主导的教学模式, 突出学生的主体作用, 培养学生综合运用知识的能力。通过课程教学改革, 培养了学生学习的主动性, 强化了学生的实践能力, 提高了教学质量。

关键词: 生物科学与技术; 食品质量与安全; 教学改革与实践

指导大学生“小平科技创新团队”创新实践的几点体会

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摘 要: 大学生“小平科技创新团队”的宗旨是倡导以学生为主体的本科人才培养和创新性研究学习, 带动广大学生在本科阶段得到科学研究与发明创造的初步训练。北京林业大学生物科学与技术学院以大学生“小平科技创新团队”为依托, 开展大学生创新实践活动, 促进探索创新性人才培养的新模式, 推进大学生创新实践平台建设, 提高大学生培养质量。在指导大学生创新实践过程中, 注重调动大学生学习的主动性、积极性和创造性, 激发大学生的创新思维和创新意识, 注重培养大学生的团队协作精神, 塑造大学生良好的个性人格和综合素质。

关键词: 小平科技创新团队; 创新教育; 学习主动性; 实践教学; 教育改革

微生物发酵工程学结合“实践教学”的探索^①

——以北京林业大学为例^①

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摘要: 微生物发酵工程学是北京林业大学生物科学与技术学院本科生的重要专业基础课, 主要介绍微生物发酵工程的发展前沿及相关重要技术的应用。课程要求学生系统掌握发酵工程的基本理论、基本知识和基本技能, 建立较深刻的微生物学观点, 形成科学的思维方式。本文从该课程所面临的问题出发, 提出理论知识结合实践教学的探索思路, 从优化课程内容、丰富教学方法、改革考核方式三个方面探讨理论知识如何与实践教学法有效结合, 并总结了这种方式所取得的成效, 为培养社会所需的多元化高级应用型人才提供保障。^①

关键词: 微生物发酵工程学; 实践教学; 网络化模式; 理论教学^①

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基于工程教育认证标准的环境工程专业课程教学体系的构建

——以北京林业大学为例

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摘 要: 目前, 国际上关于工程教育学历互认的 3 个协议中,《华盛顿协议》知名度最高, 具有着重要和广泛的影响。2013 年中国作为预备成员, 成功加入《华盛顿协议》, 这意味着中国开展的工程教育认证工作得到签约国家的普遍认可, 这也是我国高校工科专业本科教育走向国际化的必由之路。在系统分析了《工程教育认证标准》对环境工程专业课程体系各项要求的基础上, 以北京林业大学环境工程专业为例, 探讨了基于工程教育认证标准的环境工程专业课程体系的构建方法; 首先, 课程体系的构建应体现专业特色; 其次, 应将认证标准逐项落实在课程教学的各个环节; 第三, 改进课程考核方式。通过环境工程专业课程体系的构建, 为工科专业人才培养质量的快速提升提供借鉴。

关键词: 工程教育认证; 环境工程专业; 课程体系构建

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高等林业院校“微生物学”课程教学改革的思考

——以北京林业大学为例

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摘 要: “微生物学”课程是北京林业大学生物科学与技术学院面向全校开设的一门重要的专业基础课。该课程采取理论教学与实践研究相结合的方式, 对于培养学生正确地认识微生物, 并将其应用在食品、抗生素、酶制剂等生产上具有重要意义。分析了目前“微生物学”课程教学中面临的问题, 提出了教学改革的思路, 并从教学内容、教学手段、考核方式等方面进行了探讨, 指出高等林业院校要结合不同专业的需求设置不同类型(包括内容和课时)的课程, 积极开展实践教学, 发掘学生创新性思维能力, 以期有效改善教学效果, 提高学生学习的主动性和能动性, 进而培养出符合社会需求的专业化人才。

关键词: 高等林业院校; 微生物; 教学改革

教育信息化背景下高校师生关系的新思考

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摘 要: 随着信息科技的飞速发展,“云计算”“大数据”“物联网”“互联网+”等概念应运而生,并强有力地渗透到各行各业,更是创造性地触及教育领域的各个角落。大数据时代的到来,使我国高校教育信息化呈现融合与创新的新趋势。这对我国高校师生关系的演化及发展产生了重大影响。为此,在对教育信息化的内涵及特征、师生关系在教育教学过程中的重要地位、我国传统师生关系的演化及发展等进行阐述的基础上,指出教育信息化背景下我国传统的高校师生关系已经不能够完全适应时代发展的需求,正面临着转型挑战。教育信息化不仅对我国高校教师的“教”提出新要求,即打破传统思想束缚、转变教育观念,通过自主学习提高信息技术素养,利用信息资源促进自身专业能力发展;而且对学生的“学”也提出新要求,即提高信息化的自主学习能力、培养信息化的合作学习能力、开展信息化的探究性学习等。因此,教育信息化背景下我国高校师生关系发展的新方向是建立平等、民主的师生关系,构建协作、互动的师生关系,从学校层面推动和谐师生关系的发展。

关键词: 高校;教育信息化;教与学;师生关系

中外合作办学项目运行机制的建设

——以北京林业大学生物技术专业中加合作办学项目为例

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摘 要: 自 2013 年开始,北京林业大学与加拿大不列颠哥伦比亚大学联合实施生物技术专业本科教育项目,经过几年的实践,目前在中外合作办学项目运行机制建设方面已取得以下成效。一是人才培养机制建设方面,在实施“3+2”培养模式的基础上,形成人才培养特色。二是教学运行机制建设方面,科学设计教学计划,优化教学大纲和课程内容,丰富授课方式,引进新型教学方式,以强化学生的专业素养。三是项目管理机制建设方面,建立专门的中外合作办学项目管理机构、适应中外合作办学项目特点的服务机制和中外合作办学项目学分互认制度,以保障中外合作办学项目的顺利实施。四是教学质量监督机制建设方面,建立“教学标准、教学督导、教学反馈与改进”三位一体的教学质量监督体系,以教学标准体系规范整个教学过程,通过建立期中检查和听课制度对教学过程进行监督和指导,基于教学状况调查和畅通的信息沟通渠道及时进行教学信息反馈和教学改进,以促进教学质量的不断提高。

关键词: 中外合作办学;运行机制;生物技术专业;人才培养;项目管理

刚柔相济的教学管理模式在 二级学院教学管理中的应用 ——以北京林业大学生物科学与技术学院为例

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摘要: 教学管理是大学日常工作的核心,是人才培养的重要保障。在大众化教育、个性化需求形势下,传统的刚性管理模式已经不适应多样化和创新型人才发展的需要,必须引入柔性管理概念,做到刚柔并济,使教学管理工作有序、高效地开展。分析刚柔并济教学管理理念的合理性,并以北京林业大学生物科学与技术学院为例,从教学管理理念、教学管理制度、教学管理方法等几个方面浅析了刚柔并济的教学管理模式在院级教学管理中的应用。

关键词: 刚性管理;柔性管理;教学管理模式

创客教育背景下大学生创新精神和实践能力的培养

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摘要: 全球创客教育的兴起为创新型人才培养提供了一条新途径。创客教育的核心理念在于动手实践和创新精神。传统教育观念、人才培养模式、教学内容与方法、创新与科研机制、激励评价机制等因素制约了大学生创新精神和实践能力的培养,增强创客教育观念、开设创客课程、改革教学方式、加强实验教学与社会实践活动、建立科研创新平台、构建创客组织、培养创客型师资、培育崇尚创新的创客文化氛围是培养大学生创新精神和实践能力的有效途径。

关键词: 创客;创客教育;大学生;创新精神;实践能力

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实践教学

浅谈创新实验室中大学生创新能力的培养

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摘要: 许多高校的教学改革都以培养和增强学生的实验能力、创新能力和创新精神为目标。以北京林业大学生物科学与技术学院大学生创新实验室为例,探讨了创新实验室中提高大学生实验能力、创新精神和创新能力的有效方法。该创新实验室主要由生物科学类专业本科生参与,大学生通过科研立项等项目进入创新实验室,在指导教师的亲自指导下进行相关科研训练。实践证明大学生在本科阶段的实验能力、创新能力和创新精神得到显著提高。

关键词: 创新实验室, 大学生, 创新能力, 导师负责制

浅谈野生动物生殖生理学大学生创新型实验室 在本科人才培养中的引领作用

——以北京林业大学为例

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摘要: 在生物学专业的本科教学中培养具有创新能力的大学生是我国生物科学发展的需要,也是提高生物学专业本科生就业的需要。总结了北京林业大学生物科学与技术学院野生动物生殖生理学大学生创新型实验室的建设、运行管理和创新实践的经验。教学实践表明,创新型实验室为大学生创新意识和创新能力的培养提供了一个良好的环境和基础平台,是培养和提高大学生创新意识和创新能力的一种有效途径。

关键词: 创新型实验室;科研创新;创新人才培养;生物科学;实验室建设与管理

基于微信平台的“园林植物”课程 辅助性学习方法的探讨

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摘要: 微信(Wechat)是一款具有通讯、社交和平台化功能的手机软件,是一种重要的移动互联网入口。微信的通信功能和社交功能提升了微信用户间的互动交流,同时它的平台化功能也提供了一种新的移动应用方式,为网络环境下的学习注入了新的力量。借助微信平台,探讨了“园林植物”课程辅助性学习的方法:首先,可以利用微信演示“园林植物”课程的教学内容;其次,可以利用微信拓展“园林植物”课程的教学内容的范围。教师通过微信平台,将有关“园林植物”课程的文字、语音、图片、视频等融入其中,突破了课程教学时间和空间的限制,促进了学生与学生之间的合作学习,调动了学生学习的兴趣和积极性,为学生营造了个性化学习的环境。

关键词: 微信平台;园林植物;辅助性学习

MOOC模式下的微生物发酵工程学教学改革探索

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摘 要: 微生物发酵工程学是北京林业大学生物理科基地专业本科生重要的一门专业基础课, 该课程采取教学与实践相结合的方式, 着重介绍微生物发酵工程的发展前沿及相关重要技术的应用。在总结北京林业大学生物理科基地微生物发酵工程教学经验的基础上, 从教学内容、教学方式、教学成果以及考核方式等方面探讨了MOOC模式下的微生物发酵工程学教学改革探索。

关键词: 微生物发酵工程学; 慕课模式; 教学改革

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Teaching Reform in Microbial Fermentation Engineering under the MOOC Model

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教改纵横

因“材”施教在植物学教学中的具象延伸

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摘 要: 专业基础课程的开设必须服务于林业院校特色专业创新型人才的培养目标, 这一教学理念已成为各林业院校和专任教师的共识。植物学知识是林业院校各专业核心课程的重要基础, 在植物学教学过程中开展“因材施教”是这一教育理念的具体贯彻和体现, 具体包括因“教学对象”不同施教和用不同“教材”施教两个层面。教学过程中既关注于受教对象的知识能力差异和专业需求差别, 又注重特色教材的建设和针对性辅助性教学内容的选择, 使植物学课程教学服务于各专业核心课程的学习, 服务于高等林业教育人才培养中应用型人才的需求。

关键词: 植物学, 专业基础课程, 专业核心课程, 因材施教

Competency-based Instructing System in Botany

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提高大学生创新性科研训练效果的探索 ——以“重霾污染天气时大气 PM_{2.5} 数浓度谱分布特征研究”实验为例

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摘要: 为了培养大学生的科研意识和动手能力, 激发大学生的创新思维, 结合当前环境领域的热点问题, 申请并执行了大学生创新性科研训练项目——重霾污染天气时大气 PM_{2.5} 数浓度谱分布特征研究。该文阐述了大学生在创新科研训练中可能遇到的问题及解决方法, 提出了提高本类项目实施效果的途径: 首先应确立可行的创新性实验项目的选题; 其次要多途径激发学生的科研潜能; 第三, 用学术论文巩固科研训练的成果。大学生创新性实验项目不仅锻炼了学生的创新思维, 提高了实际动手能力, 而且还培养了本科生的科研素养, 有利于养成独立思考的好习惯。同时, 将大学生科研训练与本科生毕业论文相结合, 提高了本科毕业论文的水平, 锻炼了学生专业论文的写作能力。

关键词: 科研训练; 创新思维; 实践能力

“环境工程微生物学”课程教学的几个重要问题

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摘要: 为适应环境工程学科和环境工程微生物学的快速发展, 对北京林业大学“环境工程微生物学”课程几年来的教学经验和存在的问题进行了总结和分析, 指出新形势下“环境工程微生物学”的教学工作应通过准确理解课程的定位和目标, 优化设置课程的核心内容并紧密结合环境学科的新进展, 充分借助多媒体信息要素与最新的科研成果和成功的工程实例, 注重不同层次的实验训练等方面来丰富教学内容和形式, 提高教学的效率和效果, 从而满足当前环境工程领域对创新性人才的培养要求。

关键词: 环境工程微生物学; 课程定位; 教学内容; 教学方法; 实验设置

“科研式”教学法在动物生理学 教学过程中的探索与实践

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关键词: 动物生理学 “科研式”教学法; 科研创新; 教学改革; 人才培养教学方法; 教学效果

摘要: 文章在介绍动物生理学课程的基础上,结合现代高等教育需要培养具有良好科研素质和创新能力的高素质人才要求,提出将“科研式”教学法应用于动物生理学课程教学中,对“科研式”教学法的理论内涵、教学方式、教学手段和应用效果进行了研究和探索,不仅培养了学生严谨的科学态度,较强的科研意识,较大的科研发展潜力和创造精神,同时也提升了教师自身的专业水平和科研素养,总体教学效果良好,教学水平得到显著提高。教学实践表明“科研式”教学法具有较好的可行性和有效性。

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【探索与实践】

给水排水工程专业实践教学模式及考核方法探究

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摘要: 为适应给水排水工程专业对学生实践能力的高要求,分析了当前高等院校在实践课程设置及教学和考核中存在的不足,针对实践教学环节涉及的实验、实习和设计三大部分,结合北京林业大学“给排水专业实践教学”课程几年来的经验与问题进行总结和分析,指出新形势下,实践教学应通过准确把握目前社会对专业实践能力要求定位和目标,优化设置课程的核心内容,并紧密结合给排水工程学科的最新研究进展与科研成果及工程案例,通过大学生科技创新等不同层次的实验科研训练等方面来丰富实践教学内容和形式,建立水处理全流程实验设计及盲样考核、管网制作及压力实验考核、实际水厂设计及设计运行核心参数考核的多途径教学模式及考核渠道探索,充分调动了学生的能动性,提高了教学的效率和效果,从而满足当前给排水工程领域对创新性实践人才的培养要求。

关键词: 给排水实践课程; 课程定位; 教学内容; 考核方法

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“环境工程微生物学”课程教学的几个重要问题

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摘要: 为适应环境工程学科和环境工程微生物学的快速发展,对北京林业大学“环境工程微生物学”课程几年来的教学经验和存在的问题进行了总结和分析,指出新形势下“环境工程微生物学”的教学工作应通过准确理解课程的定位和目标,优化设置课程的核心内容并紧密结合环境学科的新进展,充分借助多媒体信息要素与最新的科研成果和成功的工程实例,注重不同层次的实验训练等方面来丰富教学内容和形式,提高教学的效率和效果,从而满足当前环境工程领域对创新性人才的培养要求。

关键词: 环境工程微生物学;课程定位;教学内容;教学方法;实验设置

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谈数据库原理课程教学思路

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摘要: 数据库原理是高校计算机专业的核心专业课。文章结合笔者多年的教学经验和学生学习时存在的常见问题,介绍数据库原理教学中一些可行的授课思路,旨在引起学生的学习兴趣,增强学生的实践动手能力和应用创新能力。

关键词: 数据库;案例教学;成绩评价;实践教学

研究式教学方法在生物学专业综合实习中的应用

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摘要: 本文以北京林业大学生物学专业综合实习为例, 从实习的准备, 互动式实习全过程的选题、开展研究、总结汇报、成果交流及成绩评定等几方面介绍了研究式教学方法在整个实习过程中的应用。该方法的应用明显提高了综合实习的教学效果, 促进了学生科研能力、综合素质及创新意识的培养。

关键词: 生物学综合实习, 研究式教学方法, 创新能力

The Application of Research-teaching Methods in the Biological Comprehensive Practice for the Students in Biological Sciences

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深化人才培养模式改革 建设生物技术特色专业

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摘要: 深化人才培养模式和课程体系改革是林业院校生物技术专业提高自身竞争力的重要举措。在分析目前我国生物技术专业的发展现状及其在招生和就业方面面临的巨大挑战的基础上, 以北京林业大学生物技术专业人才培养模式改革为例, 提出建设生物技术特色专业的措施, 包括进一步明确、细化生物技术专业人才培养的特色; 精简生物技术专业的课程体系, 突出重点课程; 加强自然科学类基础课程与生物技术专业内容的衔接; 进一步优化生物技术专业的课程布局; 加强生物技术专业工程类课程的“工”科内容; 加强生物技术专业学生科研素质的培养, 规范学术道德。

关键词: 高等教育; 人才培养模式; 生物技术专业; 课程体系

LETTERS

Edited by Jennifer Sills

Applying antibiotics lessons to antivirals

READING THE PERSPECTIVE "Combating emerging viral threats" by E. Bekerman and S. Elnav (17 April, p. 282), I was struck by the call for broad-spectrum antiviral drugs, given the recognition of the problems caused by broad-spectrum antibacterial drugs (1) and the recent clarion calls for precision medicine (2). "One drug, one bug" antibiotics, along with appropriate point-of-intervention diagnostics, would mitigate the spread of drug resistance. The same is likely to be true for antivirals.

Furthermore, "one drug, multiple bugs" (broad-spectrum) antibiotics damage the highly diverse populations of bacteria

agents, each targeting only one bug. Such drugs could be developed, produced, and approved expeditiously and cost-effectively, as the world has managed to achieve effectively for annual influenza vaccines in most years.

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Response

The main arguments against broad-spectrum therapies presented by Martin are based on the pitfalls of this approach with antibiotics. However, the spread of

barriers to resistance offer a more feasible approach to limiting antiviral resistance than do precisely targeted antivirals.

The prior antibiotic efforts have saved millions of lives to date. They are likely a major contributor to the markedly extended life span in developed countries over the past century. Thus, while the overuse and misuse of antibiotics warrant scrutiny, the emergence of resistance is not an indication that this strategy failed.

Understanding of the virome and its role (both beneficial and detrimental) in human disease is in its infancy (2). We agree with Martin that broad-spectrum antiviral therapies may affect the human virome. Nevertheless, this potential concern needs to be offset by the tremendous cost and difficulty of developing drugs targeting individual viruses. The biggest success story in the past decade has been the development of targeted antivirals against hepatitis C virus (HCV). However, it took many billions of dollars and more than a decade to achieve this, and drug access has now become a major challenge (3). HCV is a single virus. The list of emerging and reemerging viruses that represent major threats to global health keeps increasing. More than 11,000 individuals died from the recent Ebola outbreak, and a greater number of patients die from dengue and other emerging viral infections every year. Therefore, as we wrote in our Perspective, we advocate combining specific development approaches with broad-spectrum approaches to enable global health protection and national security readiness more rapidly.

We too recognize the value of precision medicine (4). Nevertheless, the need for novel antivirals is broad and urgent. We should therefore not let precision medicine distract from lower-cost and effective population-wide interventions (5).

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China legitimizes ivory, again

IN THE PAST, the Chinese ivory industry was licensed to purchase a certain quota of ivory on the grounds of "the inheritance of



in and on our body. These microbiota are becoming increasingly appreciated as critical for health. Damage to the gut microbiota, particularly during early development, has lasting negative consequences for maturation and function of the immune and central nervous systems (3). The gut microbiota similarly harbor viral components important for health (4). Broad-spectrum antivirals are likely to damage these viral components of our gut microbiota.

Today's slow and expensive drug development process pressures industry to seek one drug for multiple bugs. However, efforts to manage viral infections, as for bacterial infections, should not focus on broad-spectrum agents but on technology platforms that allow the discovery, development, manufacturing, and regulatory approval of multiple precision antiviral

resistance in bacteria to which Martin refers is not directly applicable to viral resistance. Bacteria can spread antibiotic resistance either vertically by passing the antibiotic resistance genes to new generations or horizontally by sharing or exchanging antibiotic resistance genes through gene transfer mechanisms between even distantly related species (1). In contrast, the evolution of drug resistance within viruses is governed by their intrinsically error-prone replication. Hence, the likelihood that a virus develops resistance to a broad-spectrum agent is comparable to that of developing resistance to a therapeutic targeting a single virus. We therefore disagree with the statement that precision medicine for antivirals would mitigate the spread of drug resistance. Broad-spectrum host-targeted approaches with higher genetic

LETTERS

edited by Jennifer Sills

Airline Policies: Sickening Results?

THE IMPACT OF MODERN AIR TRAVEL ON MAGNIFYING the spread of communicable diseases to epidemic levels has been well recognized ["Coming to an airport near you," A. R. McLean, Perspectives, 13 December 2013, p. 1330; "The hidden geometry of complex, network-driven contagion phenomena," D. Brockmann and D. Helbing, Research Article, 13 December 2013, p. 1337; (1–3)]. Although some infections may be in their incubation phase and not obvious at time of travel, many are identifiable before the affected individuals board the plane.

Presumably, responsible individuals with a communicable disease (such as influenza) would cancel public "appearances," so as to avoid contributing to the spread of the disease they had contracted. However, these individuals face economic damage as a result, because airlines refuse to refund or fully credit such responsible behavior. By doing so, the airlines seem to be discouraging infected individuals from altering their travel plans.

By refusing to provide refunds to people with communicable diseases, are airlines responsible in part for the spread of influenza and other diseases? While the question of liability may be complex, the current policies clearly have public health implications.

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Recently, the Chinese government confiscated and destroyed 6 tons of ivory in an attempt to address this issue ("By the numbers," News of the Week, 10 January, p. 124). This inspiring step in the right direction sends a clear message that the government has zero tolerance for illegal ivory trade. To move forward, the relevant Chinese government departments should strictly track the legality of ivory resources and ivory products, amend as quickly as possible the supervision loopholes that exist in the illegal ivory trade under the shield of "legal ivory," and control the abnormal consumption of ivory and ivory products. These actions may be crucial to rescuing African elephants.

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China's Ivory Market:
The Elephant in the Room

LEVELS OF ILLEGAL IVORY HUNTING REACHED a peak in 2012, and in 2013 elephants were massacred at an unprecedented rate (1). One of the largest buyers hiding behind the massacre is China, and the Chinese market is the most important factor leading to the explosion of the illegal ivory trade.

In 2007, despite the great pressure of world opinion, the Chinese ivory industry persuaded the Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES) to grant it permission to purchase certain quotas of ivory, justifying the need by claiming to support "the

traditional heritage of ivory sculpture" (2). However, instead of slowing the decrease in the elephant population, the CITES decision, with its goal to keep "equilibrium between protection and utilization," has become a permanent umbrella for the illegal ivory trade, and ivory gained illegally can be laundered easily on the so-called "legal market" by smuggling it into China (3). In China, many or most legal enterprises dealing in ivory processing and sales are involved in illegal ivory trade, and there is a bulky ivory consumer market behind this black market chaos. Due to the influence of traditional ideology and the widespread love of flaunting wealth, the abnormal consumption of ivory products in China remains obstinately common.

Maritime Biosecurity Adrift

INTERNATIONAL SHIPPING HAS LONG BEEN recognized to pose a substantial environmental threat through the inadvertent transport of invasive alien species in ballast water (water collected and released to stabilize vessels at sea and maintain safe operating conditions throughout a voyage) (1, 2). After more than a decade of deliberation, the International Maritime Organization (IMO) adopted the Ballast Water Management Convention (BWMC) in 2004, whose goal is to legally require nations to prevent, minimize, and ultimately eliminate the transfer of harmful aquatic organisms and pathogens through the management of ballast water and sediments (3).

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LETTERS

Edited by Jennifer Sills

Fauna in decline:
Plight of the pangolin

IN THEIR REVIEW "Defaunation in the Anthropocene" (special section on Vanishing Fauna, 25 July, p. 401), R. Dirzo *et al.* discuss the human impacts on species decline and extinction. The pangolin is a good example of these anthropogenic effects. On 12 May, about 4 tons of smuggled frozen pangolins were seized in Zhuhai, China, making the country's largest smuggling case of a national protected animal in the past several years (1). The pangolin turns out to be "the most traded" wild animal, due to the large demand for its scale and flesh (2).

According to the *Chinese Medicinal Pharmacopoeia*, roasted pangolin scale can be used for detoxification, draining pus, attenuating palsy, and stimulating lactation (3). Since the 1990s, the price of pangolin scale has been continuously climbing, rising from £8.50 to £360 per kilogram (4). In even greater demand is the pangolin meat, despite the risk of infection associated with eating it. The excessive consumption has been catastrophic for the species, as the pangolin typically produces only one offspring per year.

In China, pangolins are facing the risk of extinction due to human consumption, which will have devastating effects on pangolins in other areas of the world. Similar to its cracking down on the smuggling of ivory and rhinoceros horn, the Chinese government should strengthen enforcement against illegal pangolin transactions and ban the wild animal markets. Further publicity and education are also called for to put an end to the chase for "wild-life delicacies." Finally, developing herbal alternatives to pangolin scales would benefit the population. These actions may be crucial to prevent the extinction of the pangolin in China.

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Fauna in decline:
First do no harm

IN THEIR REVIEW "Reversing defaunation: Restoring species in a changing world" (special section on Vanishing Fauna, 25 July, p. 406), P. J. Seddon *et al.* warn that loss of animal species can disrupt ecological communities, cause cascading effects, and alter ecosystem functions. Introduced nonnative animals can have similar consequences.

is impossible (9). Even carefully planned introductions for conservation purposes can have devastating consequences (10, 11).

These considerations are largely ignored by Seddon *et al.* in their discussion of assisted colonization and ecological replacements—deliberate introductions of species beyond their native range. Although Seddon *et al.* reassuringly cite new approaches (quantitative risk analysis, active adaptive management, and structured decision-making) for managing what could go wrong, none of the cited references offer reliable methods for predicting impacts of nonnative animal releases. Despite making considerable progress in understanding impact (5), invasion science has not developed a predictive capacity sufficient to engage in frequent introductions without harming biodiversity and ecosystems (7). Thus, risks of unintended effects cannot be evaluated and weighed against expected benefits.

At best, assisted colonization is analogous to other human interventions (such as geoengineering) that are prone to unpredictable consequences and do not address root causes of the problems they are supposed to mitigate (7, 12). Ironically, in an earlier article on using nonnative species for conservation purposes, Seddon *et al.* (13) rightly conclude that "the concern is not the failure to establish the intended ecological interactions, but rather the risk of creating new and unwanted interactions." Perhaps what is needed is a Hippocratic oath ("Do no harm") applicable to conservation biologists.

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Confiscated pangolin scales.

Burgeoning evidence implicates nonnative species as driving biodiversity loss (1–5) and a host of other ecological disruptions (6). Whereas some can have positive effects on ecosystem services, others have disproportionately large negative effects. Risk assessment of these outcomes is undermined by context-dependence and time lags (4, 5). An introduced species that has negligible effects in some areas, or whose population is threatened in its native range, can have strong impacts when translocated elsewhere (8, 7). Such species may appear innocuous for decades—well beyond the attention span of monitoring programs—before suddenly becoming problematic (8). Moreover, their impacts may be subtle, but nonetheless great, and remain unrecognized until damage is incurred and containment

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Reaping the benefits of no-tillage farming

As president of the Howard G. Buffett Foundation, I am disappointed with the suggestion by Ken Giller, our partner in the nitrogen-fixation research programme N2 Africa, that the teaching of conservation agriculture in sub-Saharan Africa is "wholly misplaced" (*Nature* 483, 525–527; 2012).

Millions of growers, large and small, are reaping the benefits of no-tillage farming. It is one of the most cost-effective ways to protect and improve soil — a farmer's most precious asset. It builds soil fertility by increasing biological activity, reducing the need for fertilizers and minimizing their effects on the environment. It also reduces soil erosion, improves water quality, increases crop yields, helps to sequester carbon and reduces labour.

No-tillage farmers are growing crops on roughly 111 million hectares worldwide, including 70% of farmland in Brazil and Argentina. At Brazil's agricultural-research organization Embrapa, no-tillage farming is helping to unlock the agricultural potential of the vast Cerrado savannah, fuelling economic growth.

There are challenges in teaching new practices to smallholder farmers, and much work is needed to adapt no-tillage farming to Africa's diverse agroecological and socioeconomic environments. But with the proper research, training and capacity, it will be one of many tools African farmers need to increase productivity sustainably.

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Protect the DNA of museum specimens

We support Henry Nicholls' plea to unite museum exhibitions with behind-the-scenes research

(*Nature* 484, 36; 2012). But to avoid jeopardizing the scientific worth of collections, caution is needed if that research is done in molecular-biology laboratories under the same roof.

Museums store important, often irreplaceable, biological specimens. To protect the authenticity of their DNA, contamination must be prevented. Extraneous DNA amplified in a museum lab by the polymerase chain reaction can easily be transferred to collection storage areas unless strict safeguards are in place.

Protocols similar to those used for studying ancient DNA should be applied to the development and operation of molecular-biology labs within museums. For example, the labs should be in a separate building, with a one-way flow of people and consumables from the collection area to the lab. **Lara Shepherd, Leon Perrie** Museum of New Zealand Te Papa Tongarewa, Wellington, New Zealand.
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China's bear farms prompt public outcry

Some 10,000 bears are farmed in China to procure their bile for traditional Chinese medicine. This cruel practice has stimulated a wave of condemnation across the country.

Bile is repeatedly collected from live bears through a surgically introduced opening into the bile duct, a procedure that is painful and distressing to the animals (see www.animalsasia.org). Some pharmaceutical companies use a variation of this technique that they say does not hurt the bears.

Even though the ursodeoxycholic acid found in bear bile has been available in synthetic form for decades, many wealthy patients prefer the natural product. Despite the disputed health benefits of bear bile, this has been an

incentive for companies to promote bear farming.

The animal-welfare organization Animals Asia Foundation, headquartered in Hong Kong, has been a pioneer in challenging the bear-farming industry. It was recently accused of undermining traditional medical practices by the Chinese Association of Traditional Chinese Medicine. After 10 years of fighting alone, the foundation's work now has strong public backing. Many delegates at the National People's Congress last month declared that the industry should not be tolerated in a modern civilized society (see go.nature.com/vg96sd; in Chinese).

China needs to promote substitutes for bear bile through further campaigning and public education. Legislation should be introduced for an animal welfare bill, which might eventually lead to a ban on bear farming.

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Validate gene findings before telling donors

You report on recommendations that US biobanks should make participants in genome studies aware of incidental findings about their own DNA that might be medically relevant (*Nature* 483, 373 and 387; 2012). But assigning participants access rights to research that is not validated could be putting the cart before the horse.

Incidental findings about an individual's gene variants need to be verified analytically before being returned to the DNA donor (S. M. Wolf *et al.* *Genet. Med.* 14, 361–384; 2012). Even if a variant is accurately defined, further evidence of both clinical validity and utility are needed if its discovery is to be meaningful.

It would be irresponsible to

follow the recommendation of Wolf *et al.* to communicate to the research subject the finding of one genotype variant when there may be hundreds of others related to the same phenotype, or when the phenotype varies with ethnic or environmental differences.

Investigations would be needed into whether evidence-based prevention or treatment is available for the particular gene finding, as well as into the reliability of genetic counselling based on complex, often ambiguous, risk information.

DNA donors should be informed that incidental findings must first be confirmed and translated into clinical application before information is communicated to them. We cannot side-step the process of proving clinical utility.

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Enhance visibility of India's academics

Policy-makers must take bold measures to improve the standing of Indian science (*Nature* 484, 159–160; 2012), but it is important that the country's scientists own up to their responsibility for the current state of affairs.

Take India's science academies. Because they wield little apparent influence on science, policy or society, they are largely invisible to scientists and to the public. Their relevance seems to be limited to making annual awards to a few scientists who publish their work in journals with high impact factors. It is time for these academies to wake up to the challenge and become scientifically and socially important.

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指导本科生第一作者在 SCI 源杂志等国内外重要期刊发表文章情况 (27 篇)

The Expression of Ferroptosis-Related Genes in Hepatocellular Carcinoma and Their Relationships With Prognosis

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Background: Ferroptosis, a form of cell death discovered in recent years, is expected to provide new targets for the diagnosis and treatment of hepatocellular carcinoma (HCC) through further research.

Methods: Based on data from The Cancer Genome Atlas (TCGA), we screened HCC-associated genes from 259 candidate genes in the FerriDb database. The screened genes were subjected to differential expression analysis, survival analysis, correlation analysis with clinical data, and univariate and multivariate Cox regression analysis. The results were validated with the Gene Expression Profiling Interactive Analysis 2 (GEPIA2) database and the Human Protein Atlas (HPA) database, and signaling pathways were analyzed with the Gene Set Enrichment Analysis (GSEA) enrichment analysis. Human normal hepatocytes and different liver cancer cell lines were used to verify the expression levels of genes, using quantitative reverse transcription PCR (RT-qPCR).

Results: Eight ferroptosis-related genes were finally selected, including *ACSL3*, *ASNS*, *CHMP5*, *MYB*, *PCK2*, *PGD*, *SLC38A1*, and *YTIAP1*. The expression of eight genes except *PCK2* was significantly correlated with a lower survival rate of HCC, and the expression of *PCK2* showed a correlation with a higher survival rate of HCC. The expression of all eight genes was also correlated with clinical traits. GSEA enrichment analysis obtained many pathways such as apoptosis, endocytosis, pathways in cancer, Wnt signaling pathway, primary bile acid biosynthesis, and fatty acid metabolism pathway.

Conclusion: The *ACSL3*, *ASNS*, *CHMP5*, *MYB*, *PCK2*, *PGD*, *SLC38A1*, and *YTIAP1* genes may become markers and new targets for early diagnosis and prognostic assessment of HCC.

Keywords: hepatocellular carcinoma, ferroptosis, prognostic markers, TCGA, FerriDb

Introduction

Global Cancer Statistics 2024 shows that primary liver cancer is the 12th most common cancer in the world in 2024, with the sixth highest mortality rate, and it is an extremely malignant tumor.¹ Among them, hepatocellular carcinoma (HCC) accounts for 75%–85% of primary liver cancers. The screening and diagnosis of HCC are mainly carried out through several methods nowadays, including screening of high-risk groups, imaging tests, hematological molecular markers, puncture biopsy, and pathological diagnosis, depending on the different conditions of patients. The field of HCC treatment is characterized by multidisciplinary participation and coexistence of multiple treatment methods, and general treatment methods include hepatectomy, liver transplantation, ablation therapy, precision radiotherapy, and systemic antitumor therapy. Choosing reasonable treatments for HCC patients with different stages can maximize the therapeutic efficacy.² Therefore, multidisciplinary and multicenter joint efforts are needed to achieve breakthrough progress in liver cancer treatment, and more high-quality studies should be carried out to improve the level of liver cancer diagnosis and

Exploring Autophagy-Related Gene Expression in Hepatocellular Carcinoma via TCGA, GEPIA2, and HPA Databases: Implications for Prognosis

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Objective: This study aimed to identify autophagy-related genes (ARGs) with prognostic significance in hepatocellular carcinoma (HCC) using bioinformatics and survival analysis.

Materials and Methods: ARGs were sourced from multiple references, including the Human Autophagy Database (HADb), relevant literatures, the Gene Set Enrichment Analysis (GSEA), and a final list was confirmed after eliminating duplicate entries. Differential expression analysis between normal and tumor tissues relied on data from The Cancer Genome Atlas (TCGA). Subsequently, the univariate and multivariate Cox regression analysis, along with the Kaplan-Meier survival analysis, were conducted to identify survival-associated genes. These findings were cross-validated using the Gene Expression Profiling Interactive Analysis 2 (GEPIA2) database and the Human Protein Atlas (HPA) database. Furthermore, expression levels of randomly selected ARGs were validated in HCC and normal cell lines using Real-time quantitative PCR (RT-qPCR), confirming bioinformatics findings.

Results: 41 ARGs were pinpointed. The bioinformatics analysis revealed elevated expression levels of these genes in HCC tissues compared to normal tissues. Notably, mRNA expression levels of ARGs were markedly higher in the tumor tissue samples than in the normal liver tissue samples. This observation was corroborated by data from the GEPIA2 and HPA databases, except for *ATG4B* and *CAPN10*. Results from the HPA database aligned with those from the TCGA analysis. GSEA uncovered potential signaling pathways associated with ARGs, including pathways relevant to cancer and autophagy. RT-qPCR analysis further confirmed significant upregulation of mRNA expression levels of randomly selected *BAG3*, *EIF2AK2*, *KIF5B*, and *RAB24* in HCC cell lines, consistent with the bioinformatics analysis findings.

Conclusion: This study showed that the 41 obtained ARGs, such as *ATG16L1*, *ATG4B*, *BAG3*, *KIF5B*, *MAPK1*, *RAB24*, and *SOGA1*, these findings suggest that ARGs may serve as prognostic biomarkers for HCC, warranting further validation in clinical cohorts and functional studies.

Keywords: hepatocellular carcinoma, bioinformatics, autophagy, prognostic markers, TCGA

Introduction

Globally, cancer ranks as a primary cause of mortality and poses a formidable obstacle to enhancing life expectancy.¹ Among liver cancers, hepatocellular carcinoma (HCC) stands out as the most prevalent form.² Notably, in 2020, primary liver cancer emerged as the sixth most frequently diagnosed cancer and the third leading contributor to cancer-related fatalities worldwide,³ within these statistics, HCC accounts for 85% to 90% of cases, often presenting late-stage diagnoses, depriving patients of curative interventions, and resulting in bleak prognoses.⁴ The primary risk factors

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GCRNet: Global Context and Coordinate Attention-Based Double-Branch Residual Network for High Spatial Resolution Hyperspectral Image Classification

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Abstract

Deep learning has been extensively researched in hyperspectral image classification. Compared with traditional methods, it has significantly improved accuracy and efficiency. However, further research is needed on how to extract and fuse the useful information in hyperspectral images more effectively with deep learning models. In addition, the classification effectiveness of the model under small sample conditions still needs to be improved. The models need to extract more discriminative features and reduce the misclassification of similar classes. This paper proposes a Global Context and Coordinate Attention Residual Network (GCRNet). In our model, a dual-branch structure based on two attention mechanisms is used for separate feature extraction. To evaluate the effectiveness of our model under limited data conditions and to address the challenge of data annotation burden, we trained GCRNet using only 1%, 2%, 2%, and 2% of the available samples from the Wuhan high spatial and spectral resolution dataset and the Salinas Valley dataset, respectively. Despite the small sample sizes, our proposed GCRNet achieved high accuracies of 99.56%, 99.11%, 99.38%, and 99.78% on these datasets, outperforming several existing methods. These results demonstrate GCRNet's ability to extract discriminative features and model global contexts effectively, even with limited training data, thus potentially reducing the need for extensive data labeling in practical applications.

Keywords Attention module · Global context · Hyperspectral image classification · Long-rang dependence · Residual network

Introduction

Hyperspectral images (HSIs) simultaneously record both the spatial and spectral information of features, achieving the integration of spatial and spectral data. In recent years, HSI technology has played a crucial role in and contributed

to significant advancements in practical applications, such as precision agriculture (Teke et al., 2013) and target tracking (Liu et al., 2022a). However, accurately and efficiently classifying HSI data remains challenging, particularly for high spatial resolution images, due to the scarcity of labeled samples and the high spatial heterogeneity of classes with

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Histological and histochemical characterization of the musk gland in forest musk deer (*Moschus berezovskii*): a preliminary study

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ABSTRACT

Musk is a biologically valuable secretion from the musk gland of male musk deer, with significant economic and medicinal importance. Due to severe decline and depletion of wild musk deer population, captive breeding of musk deer has become the primary approach for sustainable musk production. So far, the histological structure and secretion mechanism of the musk gland remain incompletely understood. In this study, we employed histological and immunohistochemical (IHC) techniques, along with three-dimensional (3D) tissue reconstruction, to systematically analyze the cellular composition and secretory functions of the musk gland in forest musk deer (*Moschus berezovskii*). Our results revealed that the musk gland was primarily composed of acinar structures containing two distinct glandular cell (GC) types based on the histological observation. IHC results showed type I glandular cells (GCIs) predominantly expressed GALNT7 while type II glandular cells (GCII) mainly expressed BMP6. The 3D reconstruction demonstrated structural heterogeneity along the gland's longitudinal axis, with the proportion of the acinar area varying between 40% and 65%. This is the first time that a detailed 3D view of musk gland in forest musk deer has been shown, which provides essential histological insights into musk gland function in this species. These preliminary observations may provide useful groundwork for future investigations into the regulatory mechanisms of musk secretion.

Key words: forest musk deer; musk gland; immunohistochemistry; tissue structure; three-dimensional reconstruction.

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Contributions: QW, data collection and analysis, manuscript original drafting; CH, sample collection; DZ, resources, project administration, methodology; YL, visualization, resources, investigation; YG, sample collection, resources, manuscript reviewing; DH, resources, project administration; HZ, supervision, manuscript reviewing and editing. All authors read and approved the final version of the manuscript and agreed to be accountable for all aspects of the work.

Conflict of interest: all authors declare no conflict of interest, and all authors confirm accuracy.

Ethical approval: this study design and animal experiments were conducted following the guidelines of the Animal Care and regulations of Beijing Forestry University, China (No. EAWC_BJFU_2025001).

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DBCF-Net: Enhanced Interactive Remote Sensing Image Segmentation With a Dual-Branch Network and Collaborative Feedback Integration

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Abstract—Semantic segmentation is crucial for the precise analysis of remote sensing (RS) images. However, it heavily relies on high-quality data annotation, which is often expensive and labor-intensive to obtain. Interactive image segmentation methods have been introduced to make the annotation of RS data more efficient through user interaction. However, current methods encounter challenges extracting edge features, utilizing user interaction information, and understanding complex scenes. To tackle these issues, we propose a dual-branch network structure named dual-branch network and collaborative feedback integration (DBCF-Net). DBCF-Net consists of a global feature extraction branch and an edge information enhancement branch, which effectively integrate global features and edge information. Moreover, we incorporate the collaborative feedback integration mechanism into our framework to effectively utilize user interaction in high-level feature maps. A hybrid training strategy is implemented, involving training on multiple datasets and refinement on specific datasets, enhancing the model's generalization ability. Experiments demonstrate that DBCF-Net achieves competitive performance in interactive RS image segmentation. On the WHU dataset, our method outperforms the RITM model by 10.40% and 38.97% on the NoC@85 and NoC@90 metrics, respectively, indicating a significant improvement. The proposed framework provides a promising solution to alleviate the workload of manual annotations.

Index Terms—Collaborative feedback integration, dual-branch network, edge information enhancement, interactive segmentation, remote sensing (RS) image.

I. INTRODUCTION

THE advancement of Earth observation technology has facilitated substantial advancements in both the quantity and quality of remote sensing (RS) images, thereby significantly broadening the application potential of RS technology. The accuracy of semantic parsing and interpretation of RS images is fundamentally dependent on the performance of image semantic segmentation algorithms. While related supervised algorithms have advanced in recent years, their effectiveness remains constrained by the quality and quantity of data annotations.

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Data is available on-line at <https://github.com/PengyuHuo/DBCF-Net>.

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RS image annotation presents unique challenges due to the complexity of scenes, diverse object scales, and intricate spatial relationships. Pixel-level annotation of RS images is particularly resource-intensive and time-consuming. While various approaches including semisupervised [1], unsupervised [2], [3], few-shot learning [4], self-supervised learning [5], and weakly supervised [6] methods have been proposed, these approaches frequently fail to achieve satisfactory accuracy levels.

Interactive segmentation is a semisupervised segmentation method that incorporates user interactions into the segmentation process. Interactive image segmentation has emerged as a promising solution in the RS field, offering a balance between automation and human expertise. Through the integration of user guidance, these methods can achieve high-quality segmentation while significantly reducing annotation effort. The key advantage lies in their ability to leverage human knowledge through simple interactions, making them particularly suitable for complex RS imagery where fully automated approaches demonstrate limited effectiveness. In the task of interactive segmentation of RS images, users commonly mark foreground or background objects through various interaction methods like bounding box [7], [8], [9], [10], scribble [11], [12], [13], extreme point [14], [15], [16], or click [17], [18], [19], [20], [21], [22] to achieve segmentation of target objects in a given image. The primary advantage of interactive segmentation methods is that users can achieve better segmentation results with fewer interactions compared to fully automatic ones. These approaches effectively address the challenges faced by the latter in handling images with unclear boundaries, occluded objects, and complex lighting conditions by integrating user feedback. Contextual information is highly beneficial for RS image segmentation [23]. By performing simple interactive operations such as marking key points or drawing boundaries, the algorithm can obtain essential contextual information from the user input, thereby guiding it to recognize and segment target objects more accurately. Additionally, these methods demonstrate the ability to adapt to previously unseen classes, showcasing robust domain adaptability and real-time interaction capabilities, significantly reducing the workload of data annotation. As a result, interactive segmentation methods have found wide application in various fields such as image segmentation [24], [25], [26], [27], [28], RS image analysis [4], [29], [30], [31], [32], [33], and geological exploration [34]. Recent advances in interactive segmentation have primarily focused on two aspects: improving interaction

CuPCA: a web server for pan-cancer association analysis of large-scale cuproptosis-related genes

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Abstract

Copper-induced cell death is a novel mechanism of cell death, which is defined as cuproptosis. The increasing level of copper can produce toxicity in cells and may cause the occurrence of cell death. Several previous studies have proved that cuproptosis has a tight association with various cancers. Thus, the discovery of relationships between cuproptosis-related genes (CRGs) and human cancers is of great importance. Pan-cancer analysis can efficiently help researchers find out the relationship between multiple cancers and target genes precisely and make various prognostic analyses on cancers and cancer patients. Pan-cancer web servers can provide researchers with direct results of pan-cancer prognostic analyses, which can greatly improve the efficiency of their work. However, to date, no web server provides pan-cancer analysis about CRGs. Therefore, we introduce the cuproptosis pan-cancer analysis database (CuPCA), the first database for various analysis results of CRGs through 33 cancer types. CuPCA is a user-friendly resource for cancer researchers to gain various prognostic analyses between cuproptosis and cancers. It provides single CRG pan-cancer analysis, multi-CRGs pan-cancer analysis, multi-CRIncRNA pan-cancer analysis, and mRNA–circRNA–lncRNA conjoint analysis. These analysis results can not only indicate the relationship between cancers and cuproptosis at both gene level and protein level, but also predict the conditions of different cancer patients, which include their clinical condition, survival condition, and their immunological condition. CuPCA procures the delivery of analyzed data to end users, which improves the efficiency of wide research as well as releases the value of data resources.

Database URL: <http://cupca.cn/>

Introduction

Copper is a crucial trace element necessary for cardiovascular, neural, and immune system functions [1]. It plays a significant supportive role in various life processes by maintaining homeostasis [2]. Copper-dependent cell death occurs when copper directly binds to lipoylated components of the tricarboxylic acid (TCA) cycle [3, 4]. This can lead to various types of cell death, such as apoptosis and autophagy, primarily through mechanisms like antiangiogenesis, proteasome inhibition, and accumulation of reactive oxygen species [5]. This unique type of copper-induced regulated cell death is called cuproptosis [6]. Cuproptosis is related to cancers since unbalanced Cu homeostasis can affect tumor growth and may cause irreversible damage to cancer cells. Thus, cuproptosis can be used for developing effective cancer therapies, and the expression of CRGs is of great importance in cancer therapy research. Pan-cancer studies have identified many genes that are frequently somatically altered across multiple tumor types,

suggesting that pathway-targeted therapies can be deployed across diverse cancers [7, 8].

Pan-cancer analysis can help researchers discover the relationship between multiple cancers and target genes precisely and efficiently. Some databases have provided gene data for tumor and normal samples through various cancer types, such as The Cancer Genome Atlas (TCGA, <https://portal.gdc.cancer.gov/>) and the exoRBase database (<http://www.exorbase.org/>). The data from these databases are downloaded and become the resource that we need, and there are various analyses that we can carry out through them, such as differential expression analysis, clinical analysis, correlation analysis, patient survival analysis, immune function analysis, and conjoint analysis. With the use of pan-cancer analysis, web servers can provide direct and convenient information to cancer researchers, which may help improve their experimental progress. For example, the Ferritin Database [9] (FerrDb) is a database for markers and regulators of

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The effects of low ambient temperature on steroidogenesis and mitochondrial functions in the testes of wild ground squirrels (*Spermophilus dauricus*)

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ABSTRACT

Seasonal reproduction is a widely used breeding strategy in wildlife, especially vertebrates inhabiting temperate regions. Generally, ambient temperature is considered a significant factor influencing the reproductive status of animals. In the present study, wild ground squirrels (*Spermophilus dauricus*), typical seasonal breeders, were used as an animal model to investigate the mechanism behind the impact of low ambient temperature on testicular function. To simulate the winter environment of wild ground squirrels, we lowered the temperature gradient in the rearing environment to 4 °C. At sampling, the body surface temperature of the squirrels reared under normal ambient temperature (22 °C, NAT group) and the low ambient temperature (4 °C, LAT group) were 31.5 °C and 22.8 °C, respectively. Subsequently, we conducted immunohistochemical assays, qPCR, and enzyme-linked immunosorbent assays (ELISA) to examine the variations in testicular functions, as well as the dynamics and functions of mitochondria, in the squirrels of NAT and LAT groups. As a result, the levels of positive immunostaining for PCNA, P21, and P27 were significantly lower in the testes of LAT group, while the levels of immunostaining for Cleaved Caspase-3 and TUNEL were significantly higher. In addition, the low-temperature treatment reduced the expression level of steroidogenesis-related genes, including LHR, FSHR, GATA-4, P450scc, and P450arom, and decreased the testosterone concentration. Moreover, markers of mitochondrial fission and fusion, DRP1 and MFN2, respectively, were increased in the testes of LAT group. Additionally, the mRNA level of SOD1 was notably higher in the testes of LAT group. In conclusion, the low ambient temperature inhibited spermatogenesis, steroidogenesis, as well as mitochondrial dynamics and functions in the testes of wild ground squirrels.

1. Introduction

Wild mammals inhabiting the temperate zone develop a variety of strategies to adapt to the harsh environment during winter, and one successful reproductive strategy they employ is seasonal breeding. This strategy ensures the survival and optimal growth of offspring in habitats with sufficient food resources and suitable conditions (Jimenez et al., 2015). Temperature and photoperiod are significant environmental factors that exert a profound influence on seasonal reproduction. The environmental temperature plays a critical role in regulating the energy balance of individuals, which, in turn, affects their reproductive behavior and physiology (Bronson, 2009). Many wild animals, such as orange-crowned warblers (*Vermivora celata*), terai tree frogs (*Polypedates*

teraiensis), common voles (*Microtus arvalis*), and many other small mammals including ground squirrels and bats, have evolved a range of adaptive behaviors in response to winter temperatures (Borah et al., 2019; Geiser, 2013; Horton et al., 2010; van Rosmalen et al., 2021). These behaviors include crouching, lethargy, and hibernation. Moreover, the reproductive organs and functions of wild animals also change significantly with temperature changes. However, the mechanism underlying the effect of low ambient temperature on the reproductive system is still unclear.

Mammalian testes are the paired organ of the male reproductive system, which is composed of seminiferous tubules and connective tissue (Leeson and Cookson, 1974). The testis essentially performs two functions: spermatogenesis and steroidogenesis (Cyr, 2016). The

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Article

Analysis of the Fungal Community Composition in Endemic Orchids with Terrestrial Habitat in Subtropical Regions

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Abstract: *Habenaria* and *Liparis* are well-known orchid genera that grow in terrestrial habitats in the tropics, subtropics or temperate zones. Three species have been found in subtropical regions of China, inhabiting terrestrial to epiphytic habitats. This study focuses on three species, *H. dentata* (distributed in Asia), *H. yachangensis*, and *L. gigantea*. For *H. yachangensis* and *L. gigantea*, there is no information about the mycorrhizal community in these species. This study aims to conduct the fungal community screening of Chinese ground orchids from subtropical regions. We performed a comparative analysis of the fungal community among *H. dentata*, *H. yachangensis*, and *L. gigantea*, determining their ITS regions using NGS paired-end sequences. The results clarified the diversity and the predominance of fungal genera. *Ascomycota* was abundant compared to *Basidiomycota* or other fungi groups in all communities, with a high dominance in all populations, especially for *L. gigantea*. At different root spatial locations, the fungal community diversity and richness were higher in the soil than in the rhizosphere or inner root. However, the results suggest that *L. gigantea* has a different fungal community compared to *Habenaria* species. In this order, the subtropical terrestrial orchids have a different fungal network compared to the northern terrestrial orchids. Also, there is a high probability of co-existence and co-evolution of endophytic fungi in these terrestrial orchids, indicating the potential role of host plants in selecting an endophytic fungal community. Furthermore, our results highlight the need to elucidate the microbe interactions of these unique orchids for long-term purposes, such as isolating indigenous fungi for suitable inoculants for further orchid propagation, restoration, and conservation.

Keywords: ITS; *Liparis gigantea*; *Habenaria yachangensis*; *H. dentata*; mycorrhiza

m⁶A 修饰调控细胞自噬参与雄性生殖疾病研究进展

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摘 要: N⁶-甲基腺苷(N⁶-methyladenosine, m⁶A)修饰是在腺苷核苷酸 N6 位置上发生的甲基化, 在多种 RNA 代谢过程如 mRNA 剪接、翻译、运输、降解中发挥关键作用, 进而对各种生命过程产生广泛影响。细胞自噬是真核细胞在自噬相关基因的调控下通过溶酶体对自身细胞质蛋白质和受损细胞器进行降解的过程。本文总结了 m⁶A 修饰调控细胞自噬在雄性生殖疾病发生发展过程中的研究进展, 旨在为今后 m⁶A 修饰调节自噬水平在雄性生殖中的调控机理研究提供参考资料, 为雄性生殖疾病的治疗策略提供新方向。

关键词: N⁶-甲基腺苷(m⁶A)修饰; RNA 修饰; 细胞自噬; 雄性生殖疾病; 男性不育

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Research Progress of m⁶A Modification Regulating Autophagy in Male Reproductive Diseases

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Abstract: N⁶-Methyladenosine (m⁶A) modification is methylation of adenosine nucleotides at the N6 position in RNA molecules. It plays a pivotal role in various pathways of RNA metabolism such as mRNA splicing, translation, transportation, and degradation, widely affecting life processes. Autophagy is a natural process in which eukaryotic cells use lysosomes to degrade cytoplasmic proteins and damaged organelles under the regulation of autophagy-related genes. Herein, the research progress of m⁶A modification in regulating autophagy in the occurrence and development of male reproductive diseases was summarized. It aimed to provide reference materials for studying the regulatory mechanisms of male reproduction through autophagy level regulation by m⁶A modification, and offer novel therapeutic strategies for treatment of male reproductive diseases.

Key words: N⁶-methyladenosine (m⁶A) modification; RNA modification; autophagy; male reproductive disease; male infertility

(Life Science Research, 2024, 28(1): 041-047)

N⁶-甲基腺苷(N⁶-methyladenosine, m⁶A)修饰是真核生物 mRNA 中含量最丰富的化学修饰^[1-3], 通过影响 RNA 代谢过程, 其在调控细胞增殖、代谢和肿瘤的生物学起源中发挥着重要作用。近年来, 甲基化修饰也被发现同睾丸发育、精子发生与发育等过程密切相关。细胞自噬(autophagy)是真核生物通过降解自身衰老及损伤的细胞器和大分子物质, 实现降解产物再利用和细胞器更新的过

程。研究发现, 在雄性生殖系统内, 细胞自噬是一种重要的生理机制, 涉及许多雄性生殖疾病的关键病理生理过程^[4]。本文综述了 m⁶A 修饰以及细胞自噬在雄性生殖疾病领域的研究进展, 并基于此阐述了 m⁶A 修饰通过调节细胞自噬水平参与雄性生殖的调控机制, 旨在为进一步探讨 m⁶A 修饰调控细胞自噬与雄性生殖的关系, 以及揭示雄性生殖疾病的分子调控机制提供参考依据。

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微生物菌种航天育种研究进展

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摘要 微生物是重要的生物资源,能给人类的生产生活带来重大的社会效益和经济效益。微生物菌种航天育种是指利用太空独特的环境对微生物进行诱变育种,以获得性状优良的菌株并将其应用于生产实际。近年来,微生物菌种航天育种已成为空间育种研究的热点,但迫切需要开发更多的技术和方法,以推动其在各领域的应用和发展。本文综述了微生物菌种航天育种的背景和机理,并分析了其在农业、食品加工、医药等领域的应用现状。通过列举和探讨宇宙空间独特环境条件对微生物生理生化特征产生的诱变效应,解析了航天育种在微生物资源开发与利用中的重要作用。随着航天技术的进步和育种研究的深入,微生物菌种航天育种有望为农业生产、食品安全和医药健康等领域带来更多创新与突破。本文在已有研究基础上展望了微生物菌种航天育种的发展方向,为微生物菌种的诱变育种研究及其应用提供了重要参考。

关键词 航天育种; 微生物; 诱变机理; 农作物菌株; 抗生素; 肠道功能菌

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Research Progress of Microbial Strain Space Breeding

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Abstract Microorganisms are important biological resources, offering significant social and economic benefits for human activities. Space breeding of microbial strains utilizes the unique space environment to conduct space mutagenic breeding of microorganisms, enabling the acquisition of strains with excellent traits that can be applied in practical production. In recent years, space breeding of microbial strains has become a hot topic in space breeding research, and there is an urgent need to develop more technologies and methods to promote its application and development in various fields. Herein, the background and mechanisms of microbial strain space breeding were reviewed, and its application in areas such as agriculture, food processing, and the pharmaceutical industry were analyzed. By discussing multiple mutagenic effects of the unique environmental conditions in cosmic space on the physiological and biochemical characteristics of microorganisms, the important role of space breeding in the development and utilization of microbial resources were elucidated. With the advancement of space technology and the deepening of breeding research, space breeding of microbial strains is expected to bring more innovations and breakthroughs in agricultural production, food safety, and medical health. This article outlines the future development directions of microbial strain space breeding on the basis of present research, providing valuable insights for mutagenic breeding of microbial strains.

Key words space breeding; microorganism; mutation mechanism; agricultural microbial strain; antibiotic; gut functional bacteria

(Life Science Research, 2025, 29(1): 069-076)

微生物菌种航天育种技术是一种基于微生物等太空环境影响下发生变异的新型诱变育种方法^[1],其过程是先通过卫星、飞船等返回式航天器将微

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陈一凡, 谢可欣, 樊雪琦, 等. 杨树溃疡病拮抗菌防治机制的研究进展[J]. 中国农业气象, 2024, 45(2): 170-177

杨树溃疡病拮抗菌防治机制研究进展*

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摘要: 随着杨树栽植面积不断扩大, 杨树溃疡病发生趋重, 对树木造成严重损害。杨树溃疡病主要防治手段为化学药剂, 但环境污染和病原菌耐药性等问题越发严重, 需开发无污染且防治有效的技术或策略。以植物根际微生态组学为研究手段, 可获得提升植物抗病能力的有益微生物。这些拮抗菌能够抑制溃疡病原菌的生长且无环境污染, 具有很好的生物防治潜力。鉴于此, 本综述主要探讨拮抗菌对防治杨树溃疡病的作用方式, 包括通过养分水分竞争和分泌抑菌物质抑制病原菌生长, 提高植物抗病性抵御病原菌侵染, 以及提高宿主自身的活性氧耐受性等机制。未来利用多组学手段, 将微生物培养与宏基因组学、代谢组学充分结合, 进一步探究拮抗菌的协同作用机制, 将有助于开发高效、稳定、环保的微生物菌剂; 同时, 寻找合适的纳米材料作为载体, 构建能最大限度发挥拮抗菌功能的菌剂体系, 也是未来生物控制剂研发的重要方向之一。

关键词: 拮抗菌; 杨树溃疡病; 生物防治; 作用机制

Research Progress on the Mechanisms of Controlling Poplar Canker by Antagonistic Microbes

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Abstract: Poplar is a major afforestation species which is widely planted worldwide. With the continuous expansion of poplar plant areas, the occurrence of poplar canker disease increased rapidly, causing serious damage to the trees. Currently, the major controlling method for poplar canker is chemical agents, but side effects such as environmental pollution and pathogen resistance are becoming more and more serious. There is an urgent need for developing effective non-polluting means to control the canker disease. By using microbiomes as a research tool, beneficial microorganisms that enhance plant disease resistance can be obtained. These antagonistic bacteria can inhibit the growth of canker pathogens without environmental pollution, and have good biological-control potential. This review mainly explores the role and mechanisms of antagonistic bacteria in the control of poplar canker, including inhibiting the growth of pathogenic bacteria through nutrient and water competition, secreting bacteriostatic substances, improving plant disease resistance to resist pathogen infection, and improving the host's own reactive oxygen species tolerance, in order to provide a theoretical basis for the development of efficient and

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Article

Seasonal Variation in Gut Microbiota of the Wild Daurian Ground Squirrel (*Spermophilus dauricus*): Metagenomic Insights into Seasonal Breeding

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Simple Summary: Wild Daurian ground squirrels (*Spermophilus dauricus*) breed only a few months out of the year, a behavior known as seasonal breeding. Despite the gut microbiota being an essential “organ” of animals, little is understood about how they relate to seasonal breeding. In the present investigation, metagenomic sequencing techniques were employed to examine the diversity of gut microbiota in wild Daurian ground squirrels across different breeding seasons. The findings indicate notable variations in the gut microbiota’s structure and function among wild Daurian ground squirrels during different seasons. This study may provide an in-depth discussion of how seasonal reproduction affects gut microbes and aid in analyzing how changes in gut microbes act on the host. This study could provide new insights into the seasonal reproductive behavior of animals as well as a new theoretical basis for the study of gut microbiology.



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Abstract: The *Spermophilus dauricus*, the wild Daurian ground squirrel, is known to exhibit seasonal breeding behavior. Although the importance of gut microbiota in animal digestion, metabolism, and immunity is well-established, the correlation between gut microbiota and seasonal breeding in this species remains inadequately explored. In the present study, using metagenomic sequencing technology, the compositions and functions of the gut microbiota of wild Daurian ground squirrels in different breeding seasons were explored. The dominant gut microbial phyla were Firmicutes and Bacteroidetes. The Firmicutes were predominant in the breeding season, whereas Bacteroidetes were predominant in the non-breeding season. At the genus level, *Lactobacillus* accumulated during the breeding season, whereas *Odoribacter* and *Alistipes* increased during the non-breeding season. GO (Gene Ontology) and KEGG (Kyoto Encyclopedia of Genes and Genome) annotations indicated that genes in gut samples were highly associated with metabolic functions. The differential expression gene analysis showed that genes related to the phosphotransferase system, cysteine, and methionine metabolism were highly expressed during the breeding season, whereas the non-breeding season upregulated genes were enriched in starch and sucrose metabolism and bacterial chemotaxis pathways. In conclusion, this study could provide a reference for investigating gut microbiota in seasonal breeding animals and offer new insight into gut microbial function.

Keywords: gut microbiota; wild Daurian ground squirrels; metagenome sequencing; seasonal breeding

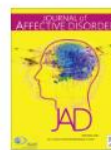
1. Introduction

The gut microbiota is defined as all microorganisms in the gastrointestinal tract of animals [1]. It comprises bacteria, viruses, fungi, and other microorganisms, with bacteria being the most abundant [2]. The gut microbiota is essential for human health, affecting



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Assessment of genetic variants in D2 dopamine receptor (*DRD2*) gene as risk factors for post-traumatic stress disorder (PTSD) and major depressive disorder (MDD): A systematic review and meta-analysis

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ABSTRACT

Background: Many studies have performed assessments of genetic variants in the D2 dopamine receptor (*DRD2*) gene as risk factors for post-traumatic stress disorder (PTSD) and major depressive disorder (MDD). However, the results are inconsistent. This meta-analysis aimed to systematically summarize published data to evaluate the reliable association between the *DRD2* genetic variants and the risk of PTSD and MDD.

Methods: A systematic literature search was conducted using the Web of Science, PubMed, Google Scholar, Excerpta Medica Database (EMBASE), Springer, ScienceDirect, Wiley Online Library, Cochrane Central Register of Controlled Trials, Chinese Biomedical Literature Database (CBM), WANFANG Data, CQVIP, and Chinese National Knowledge Infrastructure (CNKI) databases before January 1st, 2022.

Results: A total of 27 genetic variants in the *DRD2* gene were retrieved, and 7 of them met the inclusion criteria for meta-analysis. Our meta-analysis results indicated that the rs1800497 (TaqIA) polymorphism was significantly associated with the increased risk of PTSD (Dominant model (A1A1 + A1A2 vs. A2A2): OR = 1.49, 95 % CI, 1.08–2.04, $Z = 2.46$, $P = 0.014$). Subgroup analysis for ethnicity suggested that a significantly increased risk of PTSD was observed in Asians (Dominant model (A1A1 + A1A2 vs. A2A2): OR = 1.39, 95 % CI, 1.08–1.79, $Z = 2.60$, $P = 0.009$) and Caucasians (Dominant model (A1A1 + A1A2 vs. A2A2): OR = 1.87, 95 % CI 1.02–3.41, $Z = 2.04$, $P = 0.042$). Meanwhile, we detected significant association strengths between the rs1799978 and rs2075652 polymorphisms in the *DRD2* gene and MDD (for rs1799978, Homozygote comparison (GG vs. AA): OR = 0.60, 95 % CI = 0.37–0.97, $Z = 2.08$, $P = 0.038$; for rs2075652, Homozygote comparison (AA vs. GG): OR = 1.82, 95 % CI = 1.32–2.50, $Z = 3.67$, $P < 0.001$). Our cumulative meta-analyses indicated a continuous trend toward association strength with PTSD and MDD.

Conclusions: This meta-analysis indicated that genetic variants in the *DRD2* gene might potentially contribute to genetic susceptibility for PTSD and MDD. The utilization of *DRD2* genetic variants as risk factors for PTSD and MDD requires further validation by large well-designed case-control studies.

1. Background

Exposure to traumatic events or chronic stress is related to a series of psychiatric consequences, such as post-traumatic stress disorder (PTSD) and major depressive disorder (MDD). Various traumatic incidents such as war, combat, urban violence, and natural disasters (i.e. floods and earthquakes) could cause PTSD (Li et al., 2016; Hoxha et al., 2019). Previous studies have indicated that PTSD and MDD are highly comorbid (Licznarski et al., 2015). It is reported that approximately 50 % of

newly diagnosed individuals with PTSD also meet the criteria of MDD (Licznarski et al., 2015; Shalev et al., 1998; Morrison et al., 2019). Genetic variants as risk factors for higher PTSD and MDD symptoms have been well detected (Dunn et al., 2015; Skelton et al., 2012; Lowe et al., 2015). The impairment or interruption of the dopaminergic system has been associated with various pathological conditions, such as PTSD, MDD, Parkinsonism, schizophrenia, and drug addiction (He et al., 2019; Duan et al., 2015; Badgaiyan, 2010; Gurvich and Rossell, 2014). The D2 dopamine receptor (*DRD2*) gene is an important gene for the

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Article

Seasonal Changes in the Structure and Function of Gut Microbiota in the Muskrat (*Ondatra zibethicus*)

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Abstract: The gut microbiota plays a crucial role in the nutrition, metabolism, and immune function of the host animal. The muskrat (*Ondatra zibethicus*) is a typical seasonal breeding animal. The present study performed a metagenomic analysis of cecum contents from muskrats in the breeding and non-breeding seasons. The results indicated that the breeding muskrats and non-breeding muskrats differed in gut microbiota structure and function. During the breeding season, the relative abundance of phylum Bacteroidetes, genus *Prevotella*, and genus *Alistipes* increased, while the relative abundance of phylum Firmicutes and phylum Actinobacteria decreased. The muskrat gut microbiota was enriched in the metabolism-related pathways, especially amino acid and vitamin metabolism, and genetically related metabolites in the breeding season. We presumed that the muskrat gut microbiota might seasonally change to secure reproductive activity and satisfy the metabolic demands of different seasons. This study could explore potential mechanisms by which gut microbiota affects reproduction. Moreover, this study may provide a new theoretical basis for the management of muskrat captive breeding.

Keywords: gut microbiota; metabolism; muskrat; seasonal breeding; metagenome



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1. Introduction

The gut microbiota refers to the diverse microorganisms present in the digestive system of animals, which plays a vital role in animal metabolism, immunity, and reproduction [1–3]. Sometimes it is called a “forgotten organ” [4]. For the past few years, depending on the rapid development of bioinformatics, especially the rise of metagenomics, the functions of gut microbiota are being gradually understood [5,6]. The most important function of the intestinal microbiota is the nutritional function, providing energy to the host. Up to 35% of the digestive and metabolic enzymes in mammals are secreted by gut microbiota [7]. The gut microbiota is not static. It is diverse and unstable and is highly susceptible to external environmental influences, such as food [8,9], age [10], disease [11], and living areas [12,13]. The gut microbiota of the same species can vary greatly at different times and in different environments, which can help the host to adapt to its surroundings by influencing host energy metabolism or other aspects.

Recently, numerous studies have revealed that animal reproduction is closely linked to gut microbiota. *Clostridium scindens* American Type Culture Collection 35,704 can convert glucocorticoids to androgens via side-chain cleavage [14]. The gut microbiota can also be involved in gut metabolism and deglucuronidation of dihydrotestosterone (DHT) and testosterone (T) and results in higher DHT levels in the colon of young healthy mice than in germ-free mice [15]. Accordingly, studies for the composition and function of the gut microbiota might be essential for further research on animal reproduction.

Seasonal breeding is a phenomenon in which some animals mate only at certain times of the year. Seasonal breeding activity may be influenced mainly by photoperiodism [16]. Photoperiodic changes are sensed by the pineal gland in the brain. It secretes



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The expression of cuproptosis-related genes in hepatocellular carcinoma and their relationships with prognosis

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Background: The mechanism of cuproptosis has recently been reported in lipoylated proteins of the tricarboxylic acid (TCA) cycle. Besides, the role of copper was previously recognized in cancer progression. We evaluated the prognostic value of cuproptosis-related gene expression in hepatocellular carcinoma (HCC).

Methods: Remarkable genes were selected both in differential expression analysis and Kaplan-Meier survival analysis from ninety-six cuproptosis-related genes using The Cancer Genome Atlas (TCGA) database. The relationships between clinical characteristics and gene expression were performed with Wilcoxon signed-rank test, Kruskal-Wallis test, and logistic regression. Clinicopathologic factors correlated with overall survival in HCCs conducting univariate and multivariate Cox regression analysis. Gene Expression Profiling Interactive Analysis 2 (GEPIA2) and Human Protein Atlas (HPA) databases were utilized to verify the results. Furthermore, Gene Set Enrichment Analysis (GSEA) identified the potential key pathways that dominate cuproptosis in HCC.

Results: Elevated *ATP7A*, *SLC25A3*, *SCO2*, *COA6*, *TMEM199*, *ATP6AP1*, *LIPT1*, *DLAT*, *PDHA1*, *MTF1*, *ACP1*, *FDX2*, *NUBP2*, *CIAPIN1*, *ISCA2* and *NDOR1* expression, as well as declined *AOC1*, *FDX1*, *MT-CO1*, and *ACO1* expression were significantly emerged in HCC tumor tissues and were significantly associated with HCCs poor survival. The expressions of screened cuproptosis-related genes were prominently related to clinical features. GSEA analysis reported many key signaling pathways (such as natural killer cell mediated cytotoxicity, TCA cycle, glutathione metabolism, ATP-binding cassette (ABC) transporters, Notch signaling pathway, ErbB signaling pathway, and metabolism of xenobiotics by cytochrome p450) were



The association between several autophagy-related genes and their prognostic values in hepatocellular carcinoma: a study on the foundation of TCGA, GEPIA and HPA databases

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Abstract

Background The purpose of this study was to investigate the relationship between the expression of autophagy-related genes and prognosis in hepatocellular carcinoma (HCC).

Methods and Results We selected three autophagy-related genes (*ATG3*, *ATG7*, and *ATG9A*) from gene expression data of liver cancer patients in The Cancer Genome Atlas (TCGA) database by Kaplan-Meier survival analysis, univariate and multivariate Cox regression analysis, and Gene Set Enrichment Analysis (GSEA). Human Protein Atlas (HPA) and Gene Expression Profiling Interactive Analysis (GEPIA) databases were applied to testify the credibility of our results. The expression levels of *ATG3*, *ATG7*, and *ATG9A* were verified by real-time quantitative PCR (RT-qPCR) in normal liver cells (L02) and three HCC cell lines (HepG2, Hep3b, and Li-7). Data analysis results from TCGA showed high *ATG3*, *ATG7*, *ATG9A* expression in HCC tumor tissues. Kaplan-Meier survival analysis showed that the survival rate of the high expression group of *ATG3*, *ATG7*, and *ATG9A* was all significantly lower than the low expression group. GSEA analysis showed that many signaling pathways (such as the regulation of autophagy, glycine serine and threonine metabolism, pathways in cancer, mitogen-activated protein kinase (MAPK) signaling pathway, mammalian target of rapamycin (mTOR) signaling pathway, as well as P53 signaling pathway) were differentially enriched in HCCs with *ATG3*, *ATG7*, and *ATG9A* expression. GEPIA and RT-qPCR also identified that the mRNA expression level of *ATG3*, *ATG7*, and *ATG9A* in normal liver cells were significantly lower than in HCC cells. High protein expression of *ATG3*, *ATG7*, and *ATG9A* was displayed in HCCs from the HPA database.

Conclusions The *ATG3*, *ATG7*, *ATG9A* might be utilized as prognostic biomarkers for liver cancer.

Keywords *ATG3* · *ATG7* · *ATG9A* · Hepatocellular carcinoma · Prognosis · TCGA

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Seasonal expression of extracellular signal regulated kinases in the colon of wild ground squirrels (*Spermophilus dauricus*)

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Abstract

Background The purpose of the experiment was to explore the localization and seasonal expression of extracellular signal regulated kinase (ERK) in the colonic tissue of wild ground squirrels (*Spermophilus dauricus*).

Methods and results Hematoxylin–eosin staining, immunohistochemistry, real-time quantitative PCR and Western blotting were used in this experiment. The histological results showed that the diameter of the colon lumen enlarged and the number of glandular cells increased in the non-breeding season. It was found in the immunochemical results that both ERK1/2 and pERK1/2 were expressed in the cytoplasm of goblet cells and intestinal epithelial cells, while pERK1/2 was also expressed in the nucleus of them. The immune localization of both was more obvious in the non-breeding season, especially in intestinal epithelial cells. Real-time quantitative PCR and Western blotting showed that ERK1/2 and pERK1/2 were seasonally highly expressed in the non-breeding season.

Conclusions The expression of ERK1/2 and pERK1/2 was seasonal changes and had significant increases in the non-breeding season. This study revealed that ERK1/2 had potential roles in the colon to the adaptation of seasonal changes in wild ground squirrels.

Keywords Extracellular signal regulated kinase · Colon · Wild ground squirrel · Seasonal adaptation

Background

Extracellular signal regulated kinases (ERKs) are important members of the Mitogen activated protein kinases (MAPKs) family. ERK1 and ERK2 are the first reported MAPKs [1]. They share 84% in common and share many common functions [1], so usually, they are called ERK1/2. At the level of mRNA, ERK1/2 is often referred to as MAPK1/3.

ERK1/2 can regulate cell cycle progression, proliferation, cytokinesis, transcription, differentiation, cell death, migration, etc. [2]. In addition to these functions, ERK1/2 is also key enzyme in the development of the immune system,

nervous system, memory formation, and heart development [3–5].

ERK stimulating factors bind to receptors to activate the Ras pathway and then interact with downstream kinase Raf. Activated Raf binds and phosphorylates MAPKK. Activated MAPKK phosphorylates threonine and tyrosine in the conserved structure of Thr-Glu-Tyr (TEY) in the activation ring of ERK1/2 and the bind to downstream substrates [6].

The target sites of ERKs vary in location and function and include cytoplasmic, nuclear, and membrane proteins that encode transcription factors, RNA-binding proteins, or signaling proteins. After receiving external stimulation, ERK, which is widely distributed in the cell, is phosphorylated to pERK and moves toward the target. This is generally considered to be the activation of the ERK pathway. Phosphatase dephosphorylates and inactivates extracellular signal regulated kinases, thereby closing this pathway [7].

ERKs play important roles in nerve cell protection. Activation of ERKs is a pathway to induce the growth of nerve axons [8]. In tumor and cancer, aspirin can promote the enhancement of TNF-related apoptosis-inducing

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基于深度学习的 野生动物监测与识别研究进展

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摘要

简要阐述了深度学习及常用网络模型, 归纳了野生动物监测的发展进程与技术, 从图像、视频、音频 3 个角度总结了近年来深度学习在物种识别及观测中的研究进展, 对深度学习在野生动物保护与利用工作中存在的问题进行了分析与探讨, 并对其未来发展趋势做出展望。

Research Progress of the Wildlife Monitoring and Identification Based on Deep Learning

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Abstract: This paper briefly described deep learning and common network models, and summarized the process and technology of wildlife monitoring development. In this paper, the research progress of deep learning in species identification and observation in recent years has been summarized from the perspectives of image, video and audio. Then, the problems existing in deep learning in wildlife conservation and utilization were analyzed and discussed. The future development trend of deep learning has been prospected.

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基于混合卷积网络的高分辨率高光谱图像分类研究

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摘要 传统卷积神经网络模型未能充分利用高分辨率高光谱图像中丰富的空间-光谱信息,存在计算成本大、小样本数据分类精度低的问题。提出一种轻量化多尺度金字塔混合池化混合卷积模型。以混合卷积网络为基础,所提模型采用改进的金字塔池化模块增强对空间-光谱特征的提取能力,使用较少的卷积层和深度可分离卷积,并用全局平均池化层代替部分全连接层以实现卷积层到全连接层的过渡,显著降低了参数量。采用三个高分辨率高光谱数据集对所提方法进行测试,同时与经典高光谱图像分类方法进行对比实验,结果表明所提方法在分辨率高、地物种类多、边界复杂的情况下仍然能取得最佳的分类结果。在 WHU-Hi-LongKou、WHU-Hi-HanChuan、WHU-Hi-HongHu 数据集上仅使用 1%、2%、2% 训练样本的情况下,所提方法的总体精度分别达 99.12%、98.43%、98.84%,优于传统卷积网络,证明了所提模型计算成本小,在小样本问题上准确率高,能很好地适用于高分辨率高光谱数据集。

关键词 遥感; 高光谱图像分类; 混合卷积网络; 混合池化; 特征融合; 高分辨率

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The seasonal profile of proliferation and apoptosis in the prostate gland of the wild ground squirrel (*Spermophilus dauricus*)

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ABSTRACT

The seasonal cycle of growth and regression in the prostate gland of wild ground squirrel provide a unique research model to understand the morphological changes of prostate glands. Our previous studies showed that the local production of dihydrotestosterone could affect the morphology and function of the prostate gland in either an autocrine or paracrine manner. In the present study, we attempted to gain more insight into this process by investigating the expression of key factors implicated in cell proliferation, apoptosis, and the cell cycle, including mechanistic target of rapamycin (mTOR), cyclin-D2, p21, p27 and retinoblastoma 1 (pRB). Morphological and histological observations confirmed that the prostate increased significantly in both size and weight during the breeding season. Positive immunostaining for proliferating cell nuclear antigen (PCNA) was mainly localized to the prostate epithelial cells during the breeding season, which is significantly higher in the prostate gland during the breeding season ($2470 \pm 81/\text{mm}^2$) than that in the nonbreeding season ($324 \pm 54/\text{mm}^2$). However, there was no significant difference in the prostate gland when compared between the breeding and nonbreeding seasons, with regards to TUNEL staining. Moreover, cell cycle regulators were mainly localized to the epithelial cells, including mTOR, cyclin-D2, p21, p27 and pRB. The immunostaining of mTOR and cyclin D2 were stronger during the breeding season, whereas the immunostaining of p27 and pRB were stronger during the nonbreeding season. The mRNA expression levels of mTOR, cyclin D2, and PCNA, were higher during the breeding season while those of p27 and p21 were higher during the nonbreeding season. Collectively, this study profiled the distinct expression pattern of key cell cycle regulators throughout the breeding and nonbreeding seasons. Collectively, these factors may play important roles in regulating the seasonal growth and regression of the prostatic epithelium in the wild ground squirrel.

1. Introduction

The prostate is a male accessory gland featuring two major cell types: epithelial and stromal cells. Secretory cavities are surrounded by a single layer of epithelial cells while stromal cells are dispersed between the different layers of epithelial cells (Lee et al., 2011; Aaron et al., 2016; Ittmann, 2018). The principal role of the prostate gland is to secrete proteins and ions, including kallikrein-related peptidases and zinc ions (Zn^{2+}); these secretions help to form the seminal plasma by mixing with other fluids from the testis, epididymis, and other accessory glands (Hayward and Cunha, 2000; Verze et al., 2016). These molecules are crucial for male fertility because they exert influence on sperm function and ejaculation (Hayward and Cunha, 2000; Verze et al., 2016). In addition, abnormalities in cell function can lead to hyperplasia and

tumorigenesis in the prostate. These abnormalities can also induce lower urinary tract symptoms (LUTS) in humans (e.g. difficulty when emptying the bladder) by causing dysfunction in the circular smooth muscle surrounding the urethra that passes through the prostate gland (Barry et al., 2017; Grayhack, 1992; Mobley et al., 2015; Sheng et al., 2019).

Under the stimulation of suitable signals, a network of intracellular molecules is activated to drive the cell cycle and initiate cell proliferation. Mechanistic target of rapamycin (mTOR) integrates upstream signals, such as hormones and growth factors, and plays a central role in controlling cell growth, proliferation, and survival (Lapante and Sabatini, 2012; Saxton and Sabatini, 2017). With an appropriate stimulus, activated mTOR forms a protein complex with other proteins and eventually induces cell cycle progression (Cuyas et al., 2014). The cyclic assembly and activation of cyclin-cyclin-dependent kinase (CDK)

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Seasonal expression of 5 α -reductases and androgen receptor in the prostate gland of the wild ground squirrel (*Spermophilus dauricus*)

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ABSTRACT

The prostate gland is a male accessory reproductive gland that requires androgenic steroids for maintaining its vitality and function. The aim of the study was to investigate the localization and expressions of the androgen receptor (AR), SRD5A1 and SRD5A2 in the prostate glands of wild male ground squirrels during different reproductive periods by immunohistochemistry and real-time PCR. Gross mass of the prostate gland was higher in the breeding season than that of the non-breeding season. Histological observation showed that exocrine lumens in the prostate gland were enlarged in the breeding season and shrank in the non-breeding season. Immunohistochemical results demonstrated that AR was presented in both epithelial and stromal cells' nuclei during both the breeding and non-breeding seasons. Intriguingly, the positive staining of SRD5A1 and SRD5A2 was only found in the stromal cells. The mRNA expression of the three genes including *Ar*, *Srd5a1* and *Srd5a2* in the prostate gland was higher in the breeding season than those of the nonbreeding season. In addition, the circulating concentration of testosterone (T) and the concentration of dihydrotestosterone (DHT) in the prostate gland were also markedly higher in the breeding season than those of the nonbreeding season. These results suggest that expression levels of AR, SRD5A1 and SRD5A2, as well as DHT synthesis, might be correlated with seasonal changes in morphology and function of the prostate gland, indicating that DHT may serve as a pivotal regulator to affect the morphology and function of prostate gland via an autocrine/paracrine pathway in wild male ground squirrels.

1. Introduction

The prostate gland is a male accessory reproductive gland in mammals, whose morphology and structure varies widely in different species (Powers and Marker, 2013). In rodents, the prostate gland consists of distinct lobes, while it is a compact solitary structure in humans and dogs (Oliveira et al., 2016; Powers and Marker, 2013). Histologically, the prostate gland is composed of epithelial and stromal elements, with the tall columnar secretory epithelial cells lining the glandular ducts and the stromal cells surrounding them (Aaron et al., 2016; Lee et al., 2011; Singh et al., 2014). The prostate gland has various physiological functions, and its primary function is to produce the slightly alkaline fluid, which contributes to the components of seminal plasma. The prostate fluid provides the nutrition and protection for the sperm and therefore stimulates the vitality of sperm and promotes the formation of fertilized eggs (Hoover and Naz, 2012; Sanada and Yoshida, 1985). Besides the exocrine function, the prostate gland is also involved in the local metabolism of testosterone (T) (Wilson, 2011;

Zhou et al., 2013). In addition, the prostate gland can control urination or expel semen during ejaculation through muscular contractions surrounding with the urethra (Buttayan et al., 1999; Kumar and Majumder, 1995). The development of prostate is regulated by androgens, which are responsible for the appropriate embryological formation and post-pubertal growth of prostate gland, and the regulation of the vitality and functions of prostate gland during the adult period. (Buttayan et al., 1999; Fujii, 1977; Lewis and Mills, 2004; Williams-Ashman and Reddi, 1991).

Testosterone (T) and dihydrotestosterone (DHT) were two major types of androgens, while DHT has significantly higher potential to activate the androgen signaling than T (Cunha et al., 1987; Singh et al., 2014; Wilson, 2011). The circulating T could be taken intracellularly and transformed into DHT by locally expressed 5 α -reductase (Bjelfman et al., 1997; Buttayan et al., 1999; Enderle-Schmitt et al., 1986). There are two main types of 5 α -reductase isoenzymes exhibiting 5- α reducing capabilities, designated as SRD5A1 and SRD5A2, with different localizations in mammalian tissues. SRD5A1 is expressed

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Research paper

Seasonal expression of P450c17 and 5 α -reductase-2 in the scented gland of male muskrats (*Ondatra zibethicus*)

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ABSTRACT

Cytochrome P450 17A1 (P450c17) is the key enzyme required for the production of androgenic sex steroids by converting progesterone to androgens. 5 α -reductases are enzymes that convert testosterone (T) to dihydrotestosterone (DHT), which has a greater affinity for androgen receptors (AR) and stronger action than T. Our previous studies revealed that the scented glands of male muskrats expressed AR during the breeding and nonbreeding seasons. To further seek evidence of the activities of androgens in scented glands, the expression patterns of P450c17 and 5 α -reductase 2 were investigated in the scented glands of male muskrats during the breeding and nonbreeding seasons. The weight and size of scented glands in the breeding season were significantly higher than those of the nonbreeding season. Immunohistochemical data showed that P450c17 and 5 α -reductase 2 were presented in the glandular cells and epithelial cells of scented glands in both the seasons. The protein and mRNA expression of P450c17 and 5 α -reductase 2 were significantly higher in the scented gland during the breeding season than those during the nonbreeding season. In addition, the levels of DHT and T in the scented gland were remarkably higher during the breeding season. Taken together, these results suggested that the scented glands of male muskrats were capable of locally synthesizing T and DHT, and T and DHT might play an important role in the scented glandular function via an autocrine or paracrine manner.

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1. Introduction

Cytochrome P450 17A1 (P450c17) is a monooxygenase as a member of the cytochrome P450 superfamily localizing in the endoplasmic reticulum or mitochondria. P450c17 plays a critical role in sex steroid hormone synthesis by converting progesterone to androgens (Flück et al., 2003; Miller and Auchus, 2011). Besides traditional steroidogenic organs like adrenal glands and gonads, P450c17 was also found in other tissues, including brains, skins and adipose tissues, implying that they were potentially sources of local sex steroid hormone (Dharia et al., 2004; Puche et al., 2002; Schonemann et al., 2012; Slominski et al., 2013). There are three isoforms of 5 α -reductases: the type 1 and 2 isoforms possess the capacity to convert testosterone (T) to dihydrotestosterone

(DHT) in the cell nucleus or cytoplasm, while the type 3 participates in N-linked protein glycosylation, with little functional abilities to reduce steroid substrates (Cantagrel et al., 2010; Nacusi and Tindall, 2011). Moreover, 5 α -reductase 1 has the low affinity for steroid substrates and a high expression in the liver, which was generally considered as a catabolic agent to convert T into DHT for further degradation. In contrast, 5 α -reductase 2 was taken as an anabolic entity because of a high substrate affinity and a predominant expression in male reproductive tissues and accessory sex glands, playing an obviously crucial role in normal male sexual development, and its abnormal expression caused abnormal male external genitalia development, small prostate, benign prostatic hyperplasia and prostate cancer (Mendonça et al., 2016; Thigpen et al., 1993; Windahl et al., 2011; Zhu and Imperato-McGinley, 2009). And the type 3 isoform was related with intellectual dysfunction and cerebellar and ocular defects (Cantagrel et al., 2010). Therefore, instead of type 1 and 3 isoforms, 5 α -reductase 2 mainly takes part in androgen synthesis and promotion and maintenance of development and morphology of male androgen target organs and tissues.

Abbreviations: AR, androgen receptor; B, the breeding season; CSD, core secretory duct; DHT, dihydrotestosterone; EC, epithelial cells; GC, glandular cells; IC, interstitial cells; NB, the nonbreeding season; P450c17, Cytochrome P450 17A1; T, testosterone.

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Predictive value of *XPG* rs2296147T>C polymorphism on clinical outcomes of cancer patients

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ABSTRACT

The Xeroderma pigmentosum complementation group G (*XPG*) rs2296147T>C polymorphism is suspected to associate with the clinical outcomes of cancer patients. However, the results are inconsistent. This meta-analysis aimed to evaluate the reliable predictive value of *XPG* rs2296147T>C polymorphism on clinical outcomes of cancer patients. A total of 11 eligible studies were enrolled in this meta-analysis. Our results indicated that the cancer patients with TT and CT genotypes were significantly associated with better response rates when compared with the CC genotype (TT versus (vs.) CC: odds ratio (OR) = 2.05, 95% confidence intervals (CIs), 1.32-3.20, $P = 0.002$; TT+CT vs. CC: OR = 1.57, 95% CI, 1.14-2.17, $P = 0.005$). The TT genotype and/or T allele might be associated with higher survival time for cancer patients than the CC genotype and/or C allele. The cumulative meta-analyses showed an apparent beneficial objective response of TT genotype on cancer patients. In conclusion, this meta-analysis suggests that the *XPG* rs2296147T>C polymorphism is associated with the clinical outcomes of cancer patients. The *XPG* rs2296147T>C polymorphism might be a predictive factor of prognosis in cancer patients and contribute to individual treatment in the future.

INTRODUCTION

Nowadays, cancer has emerged as one of the most serious public health problems worldwide [1-3]. Despite intensive efforts have been made to improve the efficacy of cancer diagnosis and therapy, the overall survival (OS) time of cancer patients is still short [1-3]. It is very necessary to identify more reliable biomarkers for early diagnosis, accurate prognosis prediction, and efficacy for cancer patients [2]. Emerging evidence has demonstrated that genetic factors are considered to influence the cancer development, treatment effectiveness, survival time of cancer patients, therefore affect the prognosis of patients [3, 4]. It has been speculated that DNA damage was significantly associated with the DNA repair capacity [5-7]. The genetic variants in DNA repair genes alter the activity of DNA repair, thus influence the effectiveness of therapy, prognosis and survival of patients [1, 3, 4, 6]. The DNA repair genes have been identified in different DNA repair pathways [5-7]. The nucleotide excision repair (NER) pathway is the most

versatile repair mechanism responsible for repairing bulky DNA damage [5]. The xeroderma pigmentosum complementation group G (*XPG*), also known as excision repair cross-complementation group 5 (*ERCC5*), is one of the critical DNA repair enzymes of NER pathway. *XPG* gene is located on chromosome 13q32-q33, and encodes a protein of 1186 amino acids, which containing 15 exons and 14 introns. Previous studies indicate that the *XPG* rs2296147T>C polymorphism is suspected to have relationship with the clinical outcomes of cancer patients, such as colorectal cancer (CRC) [8-11], epithelial ovarian cancer (EOC) [12, 13], head and neck cancer (HNC) [14], non-small cell lung cancer (NSCLC) [15-19], gastric cancer (GC) [20] and osteosarcoma (OC) [21, 22]. Published data from these studies have shown inconsistent results. However, a systematic review and meta-analysis is still lacking. Thus, the aim of this meta-analysis was designed to summarize the currently available published findings and comprehensively assess the reliable predictive value of *XPG* rs2296147T>C polymorphism on clinical outcomes of cancer patients.

Immunoreactivity of *c-kit* Receptor Protein during the Prehibernation Period in the Oviduct of the Chinese Brown Frog, *Rana chensinensis*

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ABSTRACT. The objective of this study was to investigate immunoreactivity of the *c-kit* receptor in the oviduct of *Rana chensinensis* during the prehibernation period. Histological examination of oviducts was performed during the prehibernation period. The sections of oviduct were immunostained by the avidin-biotin-peroxidase complex method using rabbit polyclonal antisera raised against the rat *c-kit* receptor and PCNA. Total proteins were extracted from oviductal tissues and used for Western blotting analysis. Immunohistochemistry revealed the presence of the *c-kit* receptor and PCNA in the oviduct tissues during the prehibernation period. Also, positive signals for the *c-kit* receptor and PCNA by Western blotting were observed in oviduct tissues during the prehibernation period. These results suggested that the *c-kit* receptor might play a regulatory role in oviductal hypertrophy in the brown frog, *Rana chensinensis*.

KEY WORDS: *c-kit* receptor, oviduct, *Rana chensinensis*.

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The *c-kit* proto-oncogene encodes a transmembrane receptor and is associated with maturation of several cell types, including germ cells. The gene is widely expressed as a single 5-kb transcript localized to human chromosome 4 and to mouse chromosome 5 [5, 12, 19, 39]. The *c-kit* receptor whose ligand is a stem cell factor (SCF) belongs to the family of receptors for platelet-derived growth factor and colony-stimulating factor. It plays an important role in the signal transduction pathway that regulates cellular growth on repair [37]. The *c-kit* receptor is the gene product of the murine white spotting (W) locus [1, 26] mutation, which leads to defects in hematopoiesis, melanogenesis and gametogenesis [12]. The expression of *c-kit* receptor has been detected in various normal, fetal and adult tissues, including the gonads, brain, adrenal gland, skin, breast and bone marrow, and in several human malignancies like seminomas, including lung and brain cancers and glioblastomas [14, 16, 32]. The *c-kit* proto-oncogene encodes the receptor tyrosine kinase kit, which has also been shown to be important for normal mast cell survival, proliferation, differentiation and migration [6, 7, 27, 35, 40]. Evidence has accumulated that the *c-kit* receptor plays a critical role in the development of the mammalian ovary, oogenesis, folliculogenesis, blastocyst implantation and uterine growth and repair [8, 13, 22, 33]. Recently, the *c-kit* receptor has received increasing attention for its role in the reproductive function of lower vertebrates [18, 29, 41].

The Chinese brown frog (*Rana chensinensis*) is a special amphibian in northeastern China, as it has been used widely in traditional Oriental medicine [42]. The reproductive period for *R. chensinensis* is dependent on latitude and altitude and usually occurs from February to June following hibernation. However, one specific physiological phenomenon that occurs in *R. chensinensis* is that the oviduct abnormally expands prior to hibernation and not during the breeding period. Moreover, desiccated oviduct of the female *R. chensinensis*, Oviductus Ranae, is a valuable Chinese crude drug and is recorded in the Pharmacopoeia of the People's Republic of China (2005 edition) [36]. In the application of Oriental medicine, oviduct of *Rana chensinensis* is used to replenish the kidney essence, to nourish the yin and to moisten the lung [38]. The aim of present study was to investigate immunoreactivity of the *c-kit* receptor in the oviduct of *R. chensinensis* during the prehibernation period and to elucidate the relationship between the *c-kit* receptor and oviductal hypertrophy in *R. chensinensis*.

In October, 2010, ten adult female Chinese brown frogs (*Rana chensinensis*) were obtained during the prehibernation period from Jilin Baekdu Mountain Chinese Brown Frog Breeding Farm, Jilin Province (125°40'E–127°56'E, 42°31'N–44°40'N), China (Fig. 1). All the animals were treated in accordance with the National Animal Welfare Legislation. All experimental procedures were carried out in accordance with the guidelines established by the Beijing Forestry University. Both the left and right oviducts were collected from the frogs. One oviduct from the left side was immediately fixed for 12 hr in 4% paraformaldehyde (Sigma) in 0.05 M PBS, pH 7.4, for histological and immunohistochemical observations; another oviduct from the right side was immediately stored at -80°C for Western blot-

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Immunohistochemical evidence: testicular and scented glandular androgen synthesis in muskrats (*Ondatra zibethicus*) during the breeding season

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Abstract

In order to elucidate the relationship between androgens and the function of the muskrat (*Ondatra zibethicus*) scented glands during the breeding season, we investigated immunolocalization of steroidogenic enzymes P450scc, 3 β HSD and P450c17 in the muskrat testes and scented glands. Nine adult muskrats were obtained in March (n=3), May (n=3) and July (n=3) 2010. Steroidogenic enzymes were immunolocalized using polyclonal antisera raised against bovine adrenal P450scc, human placental 3 β HSD and porcine testicular P450c17. Histologically, all types of spermatogenic cells including mature-phase spermatozoa in seminiferous tubules were observed in all testes. Glandular cells, interstitial cells, epithelial cells and excretory tubules were identified in scented glands during the breeding season. P450scc, 3 β HSD and P450c17 were only identified in Leydig cells during the breeding season; P450scc and P450c17 were observed in glandular cells of scented glands, however, 3 β HSD was not found in scented glands during the breeding season. These novel findings provide the first evidence showing that scented glands of the muskrats are capable of locally synthesizing androgens and androgens acting via an endocrine, autocrine or paracrine manner may play an important role in scented gland function during the breeding season.

Introduction

Sex steroid hormones regulate diverse reproductive physiological processes of target tissues and are secreted mainly by the ovary,

testis, placenta and adrenal cortex. Two major families of enzymes are responsible for steroid biosynthesis. The first are the hydroxylase enzymes, encoded by genes belonging to the cytochrome P450 superfamily. The second family, the steroid dehydrogenase enzymes, belongs to one of two distinct groups, the short-chain alcohol dehydrogenase/reductase family or the aldo-keto reductase superfamily.¹ Cholesterol side-chain cleavage cytochrome P450 (P450scc), located on the matrix side of inner mitochondrial membranes, catalyzes the conversion of substrate cholesterol to pregnenolone, a common precursor of all steroid hormones.² Utilization of this universal steroid substrate is dictated by two enzymes. Thus, the absolute and relative levels of 3 β -hydroxysteroid dehydrogenase (3 β HSD) and 17 α -hydroxylase cytochrome P450 (P450c17) direct subsequent steroidogenesis, therefore, these two enzymes occupy a pivotal position in the pathways leading to androgen and progesterone synthesis.³

In mammalian testes, P450scc converts cholesterol to pregnenolone and is located in the inner mitochondrial membrane of the Leydig cell, the other biosynthetic enzymes 3 β HSD and P450c17 are situated in the endoplasmic reticulum. Androgens are synthesized in the endoplasmic reticulum of Leydig cells and 3 β HSD is the key enzyme in the regulation of the production of testosterone.^{4,5} By contrast, there is the assertion that P450c17 is the predominant regulator of testosterone production.⁶⁻¹¹ Thus, studies on the regulation of androgen synthesis in Leydig cells remain controversial. The functional significance of gonadal derived sex steroid hormones has been extensively studied; however, it is only recently that the importance of local extragonadal derived sex steroid hormones in cell physiology and pathophysiology is beginning to be appreciated in tissues such as brain, adipose tissue, breast, skin, bone and adrenal gland.¹²⁻¹⁴ Local metabolic pathways for testosterone and estrogen have recently been reported in the skeletal muscle cell, implying that skeletal muscle is potentially an important extragonadal source of sex steroid hormone.^{15,16}

The muskrat (*Ondatra zibethicus*) is a medium-sized, semiaquatic rodent living throughout Canada and the United States and in some parts of northern Mexico. The muskrat gets its name from the two scented glands near its tail that give off a musky odor.¹⁷ The muskrat is a seasonal breeder with sexually active period of approximately 8 months from March to October. During the breeding period, the male muskrat is sexually active and produces mature spermatozoa. Additionally, their scented glands secrete perfume substances that are used as expensive traditional Chinese medi-

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Key words: androgen, immunohistochemistry, muskrat, scented gland, testes

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Contributions: QW, experiments concerning and design; QL, JW, HZ, experiments performing; LL, XM, data analysis; SL, QW, HC, MX, contribution to reagents/materials/analysis tools; QL, QW, manuscript drafting; GW, RT, manuscript revision. All authors approved the final version.

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cines.¹⁸ In our previous studies, androgen receptor (AR), P450arom, estrogen receptor alpha (ER α) and estrogen receptor beta (ER β) were present in scented gland tissue of muskrats during the breeding season, which suggested the scented glands were the target organ for androgens, estrogens locally produced by P450arom could enhance scented gland function through autocrine/paracrine mechanism.¹⁹ To date, it is unclear if androgens acting on the scented glands are locally produced by steroidogenic enzymes. To help clarify this, we hypothesized that steroidogenic enzymes, especially P450scc, 3 β HSD and

Immunolocalization of Androgen Receptor, Aromatase Cytochrome P450, Estrogen Receptor Alpha and Estrogen Receptor Beta Proteins during the Breeding Season in Scent Glands of Muskrats (*Ondatra zibethicus*)

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Aromatase cytochrome P450 (P450arom) is an enzyme that catalyzes the conversion of androgen to estrogen. Expression of P450arom in extra-gonadal sites and locally-synthesized estrogen play an important role in physiological conditions. The purpose of this study was to investigate the cellular immunolocalization of androgen receptor (AR), P450arom, estrogen receptor alpha (ER α) and estrogen receptor beta (ER β) in muskrat scent glands during the breeding season. Histological observation and immunohistochemistry of AR, P450arom, ER α and ER β were performed in the muskrat scent glands. In addition, total proteins were extracted from scent glandular tissues in the breeding season and were used for Western blotting analysis for AR, P450arom, ER α and ER β . Histologically, glandular cells, interstitial cells, epithelial cells of the excretory duct and the excretory tubules were identified in the muskrat scent glands during the breeding season. AR was only observed in glandular cells of scent glands; P450arom was expressed in glandular cells and epithelial cells of the excretory duct; ER α was found in glandular cells, interstitial cells and epithelial cells of the excretory duct, whereas ER β was present in glandular cells and epithelial cells of the excretory duct. Also, the positive signals of AR, P450arom, ER α and ER β by Western blotting were all observed in scent glandular tissues. These results suggested that the scent gland is the target organ of androgens and estrogens, and that estrogens may play an important autocrine or paracrine role in glandular function of the muskrats.

Key words: androgen receptor, aromatase cytochrome P450, estrogen receptor, muskrat, gland

INTRODUCTION

It is well known that many of androgen's effects on male function are in fact estrogen effects. Testosterone is converted in target cells to estradiol by the enzyme aromatase. Aromatase is a member of the cytochrome P450 superfamily that catalyzes the conversion of androgens (C19), namely testosterone and androstenedione, into estrogens (C18), estradiol and estrone, respectively. The enzyme is active in various tissues in both females and males, thus estrogens are produced not only in gonads, but also in extra-gonadal organs such as brain, adipose tissue, breast, skin, and bone (Czajka-Oraniec and Simpson, 2010). Estrogen actions are mediated by two distinct estrogen receptors, estrogen receptor alpha (ER α) and estrogen receptor beta (ER β), both of which regulate the expression of a variety of different genes (Kuiper et al., 1996; Wong et al., 1996). In many tis-

sues, such as ovary, placenta, brain, and testis, the key genes of estrogen signaling and biosynthesis, *ESR1* (ER α), *ESR2* (ER β) and *Cyp19*, which encode the enzyme aromatase cytochrome P450, are co-expressed, suggesting that estrogen acts locally as an autocrine or paracrine factor (Leung et al., 1998; Tsuruo et al., 1995; O'Donnell et al., 2001; Ivanova and Beyer, 2000). Disruption of these genes demonstrated that estrogen signaling is not only important for the development and differentiation of the reproduction systems in females, but also in males (Lubahn et al., 1993; Krege et al., 1998; Fisher et al., 1998; Honda et al., 1998; Robertson et al., 2001). At present, the view that at least in rodents, the function of male gonads is essentially regulated by estrogens that are locally produced by all testicular somatic and germ cell types is now widely accepted (Nitta et al., 1993; Carreau, 2001). Evidence from several studies indicates that aromatase, ER α and ER β are encoded by separate genes but are co-expressed with androgen receptors in the male reproductive tract (Simpson et al., 1993; Brewster et al., 1997). Moreover, ERs and other steroid receptors have the ability to mediate biological effects

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Immunolocalization of Inhibin/Activin Subunit Proteins During the Breeding Season in Testes and Scented Glands of Muskrats (*Ondatra zibethicus*)

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ABSTRACT. The objective of this study was to investigate the cellular immunolocalization of inhibin α and inhibin/activin (β_A and β_B) subunits in the muskrat testes and scented glands during the breeding season. Inhibin α and inhibin/activin (β_A and β_B) subunits were expressed in Sertoli cells and Leydig cells of testes and glandular cells of scented glands, respectively. Also, positive signals of inhibin α and inhibin/activin (β_A and β_B) subunits by Western blotting were both observed in testicular and scented glandular tissues. These results suggested that the testes and scented glands of the muskrats had the ability to synthesize inhibins and activins and that activins and inhibins might play an important role in testicular and scented glandular function in muskrats.

KEY WORDS: activin, inhibin, muskrat, scented gland, testes.

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Inhibins and activins are growth and differentiation factors that have been localized in both the reproductive and nonreproductive organs. They exert their effects through both endocrine and local (autocrine/paracrine) mechanisms [18]. Inhibins and activins are structurally related dimeric gonadal proteins with the ability to regulate follicle-stimulating hormone (FSH) secretion from the pituitary glands [26, 27]. They are dimeric glycoproteins formed by two of three different subunits (α , β_A and β_B). Inhibins consist of either of the β -subunits dimerized with a common α -subunit (α - β_A and α - β_B ; inhibin A and inhibin B, respectively). Activins are dimers of β -subunits (β_A - β_A , β_A - β_B and β_B - β_B ; activin A, activin AB and activin B, respectively). In mammalian species, apart from their action on FSH secretion, inhibins and activins have been shown to exert paracrine/autocrine effects within the gonads [3, 12, 23, 31, 32] and other tissues [22] and have been proposed to have an important autocrine/paracrine function during cells growth [35]. The testis is not the only source of inhibins and activins in the male reproductive tract, and there are several reports of inhibin/activin subunit mRNA and protein expression in the prostate, seminal vesicles and epididymis [20]. Recent reports indicated that these proteins were shown subsequently to affect a range of tissues and systems beyond their role in reproduction [1, 11, 19].

The muskrat (*Ondatra zibethicus*) is a medium sized, semiaquatic rodent that lives throughout Canada and the United States and in some parts of northern Mexico. It gets its name from the two scented glands near its tail that give off a musky odor [29]. The muskrat is a seasonal breeder with a sexually active period of about 8 months from March

to October. During the breeding period, the male muskrat is willing to mate and produces mature spermatozoa, and at the same time, the scented glands secrete perfume substances that are used as expensive traditional Chinese medicines [4]. In this study, we investigated the expression of inhibin/activin subunits during the breeding season in testes and scented glands of the muskrat. The aim of the present study was to elucidate inhibins and activins as endocrine or paracrine/autocrine factors that play a physiological role in testicular and scented glandular function in muskrats.

Nine adult muskrats were obtained in March ($n=3$), May ($n=3$) and July ($n=3$) 2010 from Xichuan Wangnong Muskrats Breeding Farm, Beijing, China (Fig. 1). One male and one female muskrat were kept in each enclosure. All the animals were treated in accordance with the National Animal Welfare Legislation. All experimental procedures were carried out in accordance with the guidelines established by the Beijing Forestry University. Each pair of testicular and scented glandular tissues was obtained from each muskrat. The testis and scented gland from one side were immediately fixed for 12 hr in Bouin's solution or 4% paraformaldehyde (Sigma Chemical Co., St. Louis, MO, U.S.A.) in 0.05 M PBS, pH 7.4, for histological and immunohistochemical observations; the testis and scented gland from the other side were immediately stored at -80°C until they were used for Western blotting detection.

The testicular and scented glandular specimens were dehydrated in an ethanol series and embedded in paraffin wax. Serial sections ($4\ \mu\text{m}$) were mounted on slides coated with poly-L-lysine (Sigma, St. Louis, MO, U.S.A.). Some sections were stained with hematoxylin-eosin (HE) for observations of general histology.

The serial sections of testes and scented glands were incubated with 10% normal goat serum to reduce background staining caused by the second antibody. The sec-

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RESEARCH

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Genome-wide identification and characterization of the ubiquitin-specific protease (USP) gene family in cattle: primary analysis of muscle-specific USP genes and their influence on myogenesis

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Abstract

Background The ubiquitin-proteasome system(UPS) is a critical biological pathway that regulates protein function and plays a pivotal role in muscle formation. Nevertheless, the current comprehension of the ubiquitin-specific protease (USP) family, an important component of the UPS, in relation to bovine myoblast development remains relatively limited. This study aims to characterize the bovine USPs and conduct a preliminary analysis of their function, to provide valuable insights for enhancing beef yield and quality.

Results A comprehensive genome-wide analysis was conducted to explore the genetic characteristics of the USP family, which is categorized into 13 unique categories. The genetic homology of the USP family between cattle and other related species was discovered through collinearity analysis. Notably, cattle muscle tissue exhibits high expression levels of *USP2*, *USP13*, *USP19*, *USP25*, *USP28*, *USP38*, *USP47*, and *USP53*. Furthermore, the expression patterns of these genes during myogenic cell differentiation can be categorized into 4 distinct types. By designing small interfering RNA(siRNA) to interfere with the expression of *USP2*, *USP28*, *USP38*, and *USP47* in the myogenic cell, the silencing of these genes reduced the proliferation capacity of the myogenic cell. Meanwhile, the silencing of *USP2*, *USP28*, and *USP38* facilitated myogenic cell differentiation, while *USP47* exerted an opposing effect.

Conclusions In this study, a total of 53 members of USPs were successfully identified in *Bos taurus*. SiRNA interference experiments revealed that *USP2*, *USP28*, *USP38*, and *USP47* are implicated in the regulation of myogenic cell

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Review Article

Decoding the Genetic Code: Scientific Exploration of the Telomere-totelomere (T2T) Genome

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RESEARCH

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Plant growth promotion and biocontrol properties of a synthetic community in the control of apple disease

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Abstract

Background Apple Replant Disease (ARD) is common in major apple-growing regions worldwide, but the role of rhizosphere microbiota in conferring ARD resistance and promoting plant growth remains unclear.

Results In this study, a synthetic microbial community (SynCom) was developed to enhance apple plant growth and combat apple pathogens. Eight unique bacteria selected via microbial culture were used to construct the antagonistic synthetic community, which was then inoculated into apple seedlings in greenhouse experiments. Changes in the rhizomicroflora and the growth of aboveground plants were monitored. The eight strains, belonging to the genera *Bacillus* and *Streptomyces*, have the ability to antagonize pathogens such as *Fusarium oxysporum*, *Rhizoctonia solani*, *Botryosphaeria dothidea*, and *Phytophthora pinicola*. Additionally, these eight strains can stably colonize in apple rhizosphere and some of them can produce siderophores, ACC deaminase, and IAA. Greenhouse experiments with *Malus hupehensis* Rehd indicated that SynCom promotes plant growth (5.23%) and increases the nutrient content of the soil, including soil organic matter (9.25%) and available K (1.99%), P (7.89%), and N (0.19%), and increases bacterial richness and the relative abundance of potentially beneficial bacteria. SynCom also increased the stability of the rhizosphere microbial community, the assembly of which was dominated by deterministic processes ($|β\text{NTI}| > 2$).

Conclusions Our results provide insights into the contribution of the microbiome to pathogen inhibition and host growth. The formulation and manipulation of similar SynComs may be a beneficial strategy for promoting plant growth and controlling soil-borne disease.

Keywords Plant growth promoting rhizobacteria (PGPR), Beneficial microbes, Biological control, Synthetic community (SynCom), Apple disease

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Article

Vomeroneural Receptors Associated with Circulating Estrogen Processing Chemosensory Cues in Semi-Aquatic Mammals

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Abstract: In numerous animals, one essential chemosensory organ that detects chemical signals is the vomeronasal organ (VNO), which is involved in species-specific behaviors, including social and sexual behaviors. The purpose of this study is to investigate the mechanism underlying the processing of chemosensory cues in semi-aquatic mammals using muskrats as the animal model. Muskrat (*Ondatra zibethicus*) has a sensitive VNO system that activates seasonal breeding behaviors through receiving specific substances, including pheromones and hormones. Vomeronasal organ receptor type 1 (V1R) and type 2 (V2R) and estrogen receptor α and β (ER α and ER β) were found in sensory epithelial cells, non-sensory epithelial cells and lamina propria cells of the female muskrats' VNO. V2R and ER α mRNA levels in the VNO during the breeding period declined sharply, in comparison to those during the non-breeding period, while V1R and ER β mRNA levels were detected reversely. Additionally, transcriptomic study in the VNO identified that differently expressed genes might be related to estrogen signal and metabolic pathways. These findings suggested that the seasonal structural and functional changes in the VNO of female muskrats with different reproductive status and estrogen was regulated through binding to ER α and ER β in the female muskrats' VNO.

Keywords: chemosensory processing; estrogen; semi-aquatic mammals; vomeronasal organ; vomeronasal receptors



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1. Introduction

Information exchange can transmit information between different animals, which is essential for animal social behavior and physiology involving sexual recognition, individual survival and mating [1–3]. Chemical communication is an essential way of information exchange between individuals, which is usually less influenced by external environmental factors [4,5]. In mammals, the olfactory and vomeronasal systems can receive a chemosensory signal that mediates their particular pattern of behaviors [6]. The main olfactory system is known to be closely related to the limbic system and has a crucial role in emotions and behavior. The vomeronasal system (VNS), considered an accessory olfactory system, which is associated with specific behaviors and hormonal responses to pheromone stimuli, is related to reproductive behavior, for instance, sexual attraction, maternal behavior or aggression [7–9]. The occurrence and development of the vomeronasal system varies greatly among mammals, depending on the environment in which they live [10]. Most rodents and land mammals have a VNS, but marine mammals and birds' VNS disappeared [11]. It would appear that the vomeronasal system is of less use for airborne vertebrates and marine mammals [12]. In most mammals, the vomeronasal organ (VNO) comprises three parts: ducts, tissue and cartilage [13,14]. The vomeronasal duct (VND) is a bilateral mucus-filled superior duct at the bottom of the nasal septum and is typically crescent shaped with a thick sensory epithelium (SE) in the middle and ciliated non-sensory epithelium (NSE) on the sides [15]. The VND is surrounded by cartilage and



The beneficial and pathogenic flora, environmental drivers, and community assembly mechanism of perennial poplar plantation

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Abstract

Background and Aims Soil microorganisms play a crucial role in promoting growth and development, nutrient absorption, and disease resistance in poplar plantations. Long-term planting decays soil nutrient contents and changes the microfloral structure, and pathogenic microorganisms accumulate. It is of great significance to clarify the distribution and synergistic relationships between beneficial and pathogenic microorganisms in plantation soil for solving the long-term planting obstacles of poplar plantation.

Methods High-throughput sequencing, culture, pure bacterial identification, functional verification, and bioinformatics methods were used to explore the population and functional characteristics of the soil microorganisms in the perennial poplar forest, identify the main pathogenic and beneficial microorganisms in the soil, and investigate the synergistic relationships among the microorganisms in the system.

Results An evaluation of soil from a perennial poplar plantation revealed the presence of many beneficial microbes, such as *Bacillus*, *Sphingomonas*, *Variovorax*, and *Streptomyces*, as well as pathogenic microorganisms, including *Fusarium* and *Alternaria*. Most of these microorganisms were enriched in the rhizosphere soil. The study found that phosphorus was the driving factor affecting soil microorganisms, with available phosphorus ($K=0.189$) and pH value ($K=0.113$) significantly affecting fungal phylogeny. Bacterial community assembly processes were

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Zhanbiao Li, Zhen Song and Rongye Qiao contributed equally to this work.

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ORIGINAL ARTICLE



Seasonal change of circulating leptin associated with testicular activities of the wild ground squirrels (*Citellus dauricus*)

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Abstract

The purpose of this study was to explore the variations in the circulating leptin concentrations of the wild ground squirrels in relation to seasonal changes in testicular activities. Hematoxylin-eosin staining showed all types of elongated spermatids and spermatogenic cells existed in the testis in April, while the primary spermatocytes and spermatogonia were most advanced stages of germ cells in June. In addition, the primary spermatocytes, secondary spermatocytes, and spermatogonia were most advanced stages of germ cells in September. The highest circulating leptin concentration was consistent with the maximum body weight results from accumulation of adipose tissue in September. The mRNA expression level of leptin receptor (Ob-R) and STAT3 was lowest in June, raised in September, and remained increased in April. Ob-R and STAT3 were stronger staining in the Leydig cells in July. Moreover, the concentrations of testosterone (T) showed the maximum values in April, the minimum values in June, and significant increases in September. Furthermore, it is worth noting that the levels of T increased with the mRNA levels of Ob-R, STAT3, Star, and testicular steroidogenic enzymes (3 β -HSD, P450c17, and P450scc). Moreover, RNA-seq analyses of testis during the different periods showed that a total of 4209 genes were differentially expressed genes (DEGs); further analysis revealed that DEGs related with the Jak/STAT pathways and reproduction were altered. Taken together, the results suggested that the leptin regulated testicular function through the Jak/STAT pathways and testicular steroidogenic factor expressions.

Key words: leptin, Ob-R, STAT3, steroidogenic enzyme, testis, wild ground squirrel

INTRODUCTION

In animals, endogenous leptin plays an important role in the regulation and control of energy metabolism, body

weight, and food intake (Triantafyllou *et al.* 2016; Zhang & Chua 2017). Leptin can be synthesized and secreted by adipose tissue. Thus, accumulations of adipose tissue are considered to be related to the corresponding increases in the synthesis and secretion of leptin by adipocytes in mammals, thereby resulting in increased concentrations of leptin in the serum (O'Rahilly 2014; Seoane-Collazo *et al.* 2020). It has been observed that upon binding to a membrane receptor, leptin acts on the hypothalamic arcuate nucleus neurons and peripheral tissues, as well as organs (Gorska *et al.* 2010; Li *et al.* 2016). Therefore, when

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N6-methyladenosine RNA demethylase *ALKBH5* is testis-specifically downregulated in hybrid male sterile dzo and is a target gene of *bta-miR-200a*

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ABSTRACT

N6-methyladenosine (m⁶A) is the most common RNA methylation modification in mammals, which is controlled in the male germline to ensure coordinated gene expression in the entire process of spermatogenesis. Dzo is the male offspring of a cross between the domestic cattle (*Bos taurus*) and yak (*Bos grunniens*), and is sterile. This study aimed to investigate whether m⁶A-associated genes are linked with dzo male sterility. The mRNA expression pattern of m⁶A-associated genes and spermatogenesis-related genes modified by m⁶A was characterized in cattle, yak, and dzo. Compared with fertile cattle and yak, m⁶A erasing (*ALKBH5* and *FTO*), writing (*METTL14*, *WTAP*, and *ZC3H13*), and reading (*YTHDC2*, *YTHDF1*, and *YTHDF2*) were testis-specifically downregulated in infertile dzo. The expression of m⁶A target genes in spermatogonial self-renewal and proliferation (*BCL6B*, *FOXO1*, *TAF4B*, and *FGFR1*) and differentiation genes (*DNMT3B* and *SOHLH2*) were deregulated in dzo testis. Immunofluorescent staining showed that intense ALKBH5 immunoreactivity was present in spermatogonia, primary spermatocytes, and round spermatids of cattle and yak testis. However, the number of ALKBH5 immunoreactive-positive cells were significantly reduced in dzo testis, especially in primary spermatocytes and round spermatids. Whole genome bisulfite-seq data showed that the promoter regions of *FTO* and *YTHDC2* genes were hypermethylated in dzo testis. Moreover, *bta-miR-200a* was significantly downregulated in dzo testis, and it targeted the m⁶A-associated genes such as *ALKBH5*, *FTO*, *WTAP*, and *YTHDF2*. In conclusion, mRNA of *ALKBH5* was testis-specifically downregulated in dzo, which may be because fewer specific spermatogenic cells express this gene. The role of m⁶A-associated genes in dzo male sterility and the interaction of DNA methylation and miRNA with m⁶A-associated protein expression need to be further explored.

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1. Introduction

The Tibetan word dzo refers to the male offspring of a cross-breed between the domestic cattle (*Bos taurus*) and yak (*Bos grunniens*), while dzomo refers to the female offspring. The cross-breeding between cattle and yak exhibits significant hybrid

advantages in milk yield and meat production. Such benefits of crossbreeding make it an important strategy. This strategy has been widely exploited in areas surrounding the Qinghai-Tibet plateau, with a long history. Dzos are sterile while dzomos are fertile, which prevents the fixation of excellent gene combinations in their F1 generations. The infertility of dzo may be due to the arrest of meiosis at the pachytene stage [1,2]. Previous studies revealed that DNA hypermethylation is enriched in P-element induced wimpy testis (*PIWI*)-interacting RNA (*piRNA*) pathway genes and that the disruption of *piRNA* production contributed to unsuccessful germ cell development that may drive dzo male sterility [3]. The gene expression of histone lysine methylases and demethylases was deregulated in dzo testis [4,5]. Patterns of histone modifications

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Article

Mass Spectrometry Imaging of Lipids in the Scent Glands of Muskrat (*Ondatra zibethicus*) in Different Reproductive Statuses

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Abstract: As a typical seasonal breeding animal, male muskrats have a pair of scent glands that can emit musky odor substances to attract females during the breeding period. The present study aimed to visualize the differences in the distribution of lipids in the scent glands of muskrats during their different reproductive statuses by imaging mass spectrometry and quantitative real-time PCR (qRT-PCR). The results revealed remarkable differences in the expression and spatial distribution of lipids detected in the scent glands of muskrats during the different reproductive statuses. In addition, the expression levels of lipid molecules PC (32:0) and LysoPC (16:0) were found to be significantly higher in the breeding season than in the non-breeding season. Moreover, the mRNA expression levels of lipid synthesis enzyme *Pemt* and *Pla2g4b* were higher in the breeding season than in the non-breeding season, and there were positive correlations between the expression intensities of lipid molecules and the expression levels of *Pemt* and *Pla2g4b*. The present study investigates the changes and distribution of the endogenous lipid in the scent glands of muskrats and elucidates that the seasonal changes in the lipid metabolism may affect the functions of the scent glands in muskrats.

Keywords: lipid metabolism; MALDI-MSI; seasonal changes; scent gland; muskrat

1. Introduction

Lipids are a class of compounds that are readily soluble in organic solvents and are non-homogeneous in chemical composition and structure. Lipids are essential organic compounds that fulfill a fundamental role as the structural components of cell membranes. Additionally, lipids play a role as energy stores, sources of signaling molecules and signal transducers [1–3]. Several studies have reported that the main lipids present in the biological membranes of mammalian cells consist of several lipid categories, including triacylglycerols, sphingolipids, fatty acids, glycerolipids and sterols [4,5]. The structures of lipids are complex and varied among species, suggesting that different lipids play enormous and vital roles in various critical biological functions [6–8]. Recent publications have reported that lipids regulate various cellular and physiological processes, including energy conversion, transport, information recognition and transmission, cell development, differentiation and apoptosis [3,7]. Lipids are also involved in hormonal signaling pathways that exert essential effects on the seasonal fluctuations in vertebrates [9,10]. The study of lipids has developed into a research field of increasing importance, which is expanding rapidly due to the identification of new lipids and their multiple biological functions.



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Mechanisms of nitrogen transformation driven by functional microbes during thermophilic fermentation in an *ex situ* fermentation system

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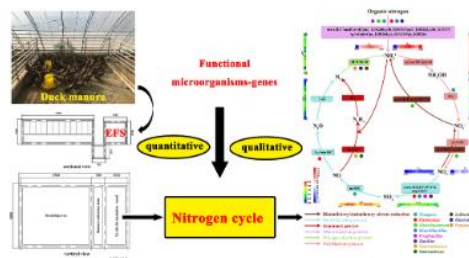
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HIGHLIGHTS

- Temperature strongly affected the succession of bacteria.
- Fermentation accelerated nitrogen conversion and mineralization was fast.
- The *nosZ* gene could excellently characterize denitrification in the EFS.
- Some microbes may drive several nitrogen conversion processes with various key genes.

GRAPHICAL ABSTRACT



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ABSTRACT

In this study, we explored the pathways and mechanisms of nitrogen (N) transformation driven by functional microbes carrying key genes in an *ex situ* fermentation system (EFS). Temperature and N content were found to be the most important factors driving variation in bacterial and fungal communities, respectively; *Bacillus* became the most abundant bacteria and *Batrachochytrium* became the most abundant fungi. Co-occurrence network analysis showed that some bacteria including *Halomonas*, *Truepera*, and *Gemmatimonas* species carry genes that promote mineralization, nitrification, dissimilatory/assimilatory nitrate reduction, denitrification, anammox reactions, and N fixation. The maximum rate of total mineralization reached $136.60 \mu\text{g N g}^{-1} \text{d}^{-1}$. Functional microbes promoted various N conversion processes at different rates in the EFS, with levels increasing by at least $0.23 \mu\text{g N g}^{-1} \text{d}^{-1}$. These results provide a theoretical basis for feasible optimization measures to address N loss during fermentation.

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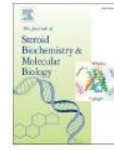
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Estrogen signaling regulates seasonal changes of the prostate in wild ground squirrels (*Spermophilus dauricus*)

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ABSTRACT

Previous studies found that testosterone was converted to dihydrotestosterone under the catalysis of 5 α -reductase in the prostate of the wild ground squirrels. As a result, this study explored further whether testosterone could be converted to estrogen to affect the prostate gland function in wild ground squirrels. Histological observation showed that the area of epithelial cells and the prostatic secretory lumen were enlarged significantly during the breeding period. Transcriptome analysis revealed that the differentially expressed genes in the prostate were concentrated in the estrogen signaling pathway. Immunohistochemical analysis showed that the immunoreactivities of P450arom were detected in the stromal cells during the breeding and non-breeding periods, indicating the possible conversion of androgen into estrogen locally. Moreover, the immunolocalizations of ER α and ER β were detected mainly in the epithelial or stromal cells. Additionally, qPCR analysis displayed that the mRNA expression level of P450arom in the prostate was significantly higher during the breeding period than that in the non-breeding period. Consistently, the concentration of 17 β -estradiol (E₂) was higher in the prostate during the breeding period than the non-breeding period, which is positively correlated with the seasonal changes of prostatic weight. In conclusion, the present results indicated that estrogen produced by P450arom presented in stromal cells might regulate the growth and function of the prostate gland via the locally expressed estrogen receptors in wild ground squirrels. The results of this study were momentous for further uncovering the mechanism of the seasonal regulated by signal pathways in the prostate of wild ground squirrels.

1. Introduction

The prostate is an important accessory reproductive organ in male mammals, located at the lower side of the bladder and surrounding the upper orifice of the urethra [1]. In addition to exocrine function in prostatic fluid production, the prostate is also involved in urination and ejaculation [2–4]. Therefore, the prostate's abnormal growth and cell proliferation would lead to prostatic hyperplasia. Furthermore, the enlargement of the prostate results in the development of lower urinary tract symptoms, such as a sense of incomplete emptying of the bladder and weakness of the urinary stream [5]. Therefore, it is necessary to uncover the mechanism underlying prostate growth.

The wild ground squirrel (*Spermophilus dauricus*) is a type of wild rodent distributed in the steppe or semi-desert area of north China, which has a short active reproductive period from April to May [6–10]. As a typical seasonal breeding animal, the prostate of wild ground

squirrel exerts the seasonal growth and regression from the breeding period to the non-breeding period [11–14]. For instance, the average volume and weight of the prostates increased during the breeding period, while decreasing during the non-breeding period [12,14]. The seasonal changes of the prostate enable the wild ground squirrel to be an ideal animal model for studying the mechanisms of prostate growth and regression. Our previous study showed that the circulating testosterone could be converted to dihydrotestosterone by the locally expressed 5 α -reductases and affect the prostate function in the prostate of wild ground squirrel [14]. However, androgens could also be catalyzed into estrogens in several tissues, such as muscle, brain, etc. Thus, it would be interesting to uncover whether the estrogen signaling pathway is also involved in the seasonal changes in prostate growth and regression of wild ground squirrels.

Estrogen is an endogenous steroid composed of 18 carbons, with a wide range of biological activities in reproductive organs. The synthesis

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Seasonal changes in the expression of PACAP, VPAC1, VPAC2, PAC1 and testicular activity in the testis of the muskrat (*Ondatra zibethicus*)

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ABSTRACT

Pituitary adenylate cyclase-activating polypeptide (PACAP) plays an important role in the steroidogenesis and spermatogenesis in the testis through its receptors PAC1, VPAC1 and VPAC2. In this study, we investigated the seasonal expressions of PACAP, PAC1, VPAC1, VPAC2, luteinizing hormone receptor (LHR), follicle stimulating hormone receptor (FSHR), steroidogenic acute regulatory protein (StAR), 3 β -hydroxysteroid dehydrogenase (3 β -HSD) and CYP17A1 in the testis of male muskrat during the breeding season and non-breeding season, respectively. Histologically, we observed the presence of Leydig cells, Sertoli cells and various types of germ cells in the testis during the breeding season, yet only Leydig cells, Sertoli cells, spermatogonia and primary spermatocyte during the non-breeding season. In addition, the immunohistochemical localizations of PACAP and VPAC1 were identified in the Leydig cells, spermatogonia and spermatozoa during the breeding season, while only in the Leydig cells and spermatogonia during the non-breeding season, and PAC1 and VPAC2 were localized in the Leydig cells in both seasons, among which LHR, StAR, 3 β -HSD and CYP17A1 were also expressed. Meanwhile, the protein and mRNA expression levels of PACAP, PAC1, VPAC1, VPAC2, LHR, FSHR, StAR, 3 β -HSD and CYP17A1 in the testis during the breeding season were significantly higher than those during the non-breeding season. These results suggested that PACAP is involved in the regulation of steroidogenesis and spermatogenesis via an endocrine, autocrine or paracrine manner in the testis of muskrat.

Key words: Pituitary adenylate cyclase-activating peptide (PACAP); PACAP receptors; steroidogenesis; testis; *Ondatra zibethicus*.

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Contributions: ZT, XY, QW, experiments performing, data analysis, manuscript drafting, manuscript revision; ZT, XY, YB, YG samples collection assistance, experiments performing; HZ, ZY, YH, QW study design and supervision, manuscript revision. All the authors have read and approved the final version of the manuscript and agreed to be accountable for all aspects of the work.

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Ethics approval: All animals were treated according to the Policy on the Care and Use of Animals by the Ethical Committee and Animal Welfare Committee and all procedures were approved by Beijing Forestry University, China (EAWC_BJFU_2022003).



Expression of glycogenic genes in the oviduct of Chinese brown frog (*Rana dybowskii*) during pre-brumation

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Rana dybowskii

ABSTRACT

The oviduct of Chinese brown frog (*Rana dybowskii*) displays seasonal morphological and functional changes, which expands specifically during pre-brumation. To uncover the molecular mechanism underlying this phenomenon, we firstly confirmed the increased weight and enlarged diameter of the oviduct in pre-brumation by morphological observation. Interestingly, the glycogen content in the oviduct increased significantly during pre-brumation, indicating *Rana dybowskii* stores energy in the oviduct before brumation. Transcriptome analysis further identified the differentially expressed genes in the synthesis and metabolism pathways of carbohydrates in the oviduct during pre-brumation. Based on that evidence, we focused on the mRNA and protein expression of glycogenic genes in the oviduct of *Rana dybowskii*. qPCR confirmed that the expression of glycolysis and glycogenesis-related genes were up-regulated while gluconeogenesis-related genes were down-regulated during pre-brumation. Western blot data showed that glucose transporter GLUT1 and glycogen synthesis-regulation proteins including GYS, and p-GSK-3 β were highly expressed in the oviduct during pre-brumation. Moreover, immunohistochemical data showed that GLUT1, GYS, p-GYS, GSK-3 β and p-GSK-3 β were expressed regionally in the oviduct of *Rana dybowskii*. The data suggests that glycogen synthesis may be involved in the oviductal expansion of *Rana dybowskii* during the pre-brumation.

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1. Introduction

Hibernation, or brumation (dormant state for amphibians and reptiles), is a survival strategy of many animals facing low temperatures and food limitations in cold winters [1–4]. Winter survival of various amphibians and reptiles that hibernate on land depends on freeze tolerance [4]. Amphibians exhibit a low-energy lifestyle and thus can tolerate environmental conditions that impose nutrient limitations [5]. During this time, their metabolism

is strongly suppressed, and the metabolic energy is mainly derived from glycogen and fat [6]. In Wood frog (*Rana sylvatica*), the ability to survive freezing was strongly influenced by the amount of glucose during freezing [7]. Previous studies have revealed the alteration of the proteins and enzymes related to the regulation of carbohydrate metabolism during hibernation/brumation, and that changes in carbohydrate metabolism during this process [8]. The molecular regulation of energy metabolism during brumation is known to exert a vital impact on their health [9].

Abbreviations: GLUT1, Glucose transporter; PFK-1, Phosphofructokinase-1; L-PK, Liver-type pyruvate kinase; GPI, Glucophosphoisomerase; PEPCK, Phosphoenolpyruvate carboxykinase; TCA cycle, Tricarboxylic acid cycle; GYS, Glycogen synthase; GSK-3, Glycogen synthase kinase 3; PGM1, Phosphoglucomutase 1; HE, Hematoxylin-Eosin; PAS, Periodic Acid-Schiff; cDNA, Complementary DNA; Q-PCR, Quantitative polymerase chain reaction; PMSF, Phenylmethanesulfonyl fluoride; BSA, Bovine Serum Albumin; HRP, Horseradish peroxidase; RIN, RNA integrity number; DEGs, Differentially Expressed Genes; KEGG, Kyoto Encyclopedia of Genes and Genomes; GC, Glandular cells; EC, Epithelial cells; TL, Tubule lumen; PFK1, 6-phosphofructokinase 1; FBp, Fructose 1,6-bisphosphatase.

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RESEARCH ARTICLE

Seasonal changes of mitochondrial autophagy and oxidative response in the testis of the wild ground squirrels (*Spermophilus dauricus*)

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Abstract

Mitochondria are the main organelles for mammalian energy metabolism and have been implicated in the regulation of germ cell maintenance and spermatogenesis. However, little is known about the changes in the mitochondria of the testis of seasonal breeders. Here, we characterized the seasonal changes in the mitochondria in the testis of the wild ground squirrels. Increased testicle weight, seminiferous tubule diameter, and sperm count were observed in the wild ground squirrels at the breeding season. RNA-seq analysis of the wild ground squirrel testes revealed that mitochondrial-related genes were expressed differentially between the breeding and nonbreeding seasons. Immunohistochemical staining showed that key mitophagy factors including PINK1, MFN2, and PARKIN were highly expressed in various cell types of testis during the breeding season. In addition, the abundance and enzymatic activities of mitochondrial-localized antioxidant enzymes superoxide dismutase 2 (SOD2) and Catalase were decreased in the testis during the breeding season, suggesting a tightly controlled redox balance at least partially facilitated by mitophagy during the seasonal breeding. Taken together, our study reveals that mitochondrial autophagy and oxidative stress may be implicated in the seasonal reproductive recrudescence of the wild ground squirrels, which deepens our understanding of the mitochondrial regulation of seasonal reproductivity in wildlife and provides new insights into the development of potential therapeutic interventions of male infertility.

autophagy; mitochondria; oxidative stress; testis; wild ground squirrel

INTRODUCTION

Wild animals possess unique reproductive strategies, including the peculiar seasonal trends in the reproductive characteristics. Seasonal changes have been widely reported in the testicular morphology and sperm maturity of male animals (1). Despite numerous studies showing that energy metabolism plays a pivotal role in seasonal reproduction, little is known about the changes in the mitochondria, the powerhouse of the cells, in the seasonal regulation of male reproductivity.

Testis is the male sex gland responsible for sperm development and production. It is covered by a fibrous capsule called tunica albuginea and is divided by partitions of fibrous tissue from tunica albuginea into 200 to 400 wedge-shaped sections, or lobes (2). Each section consists of the seminiferous tubules and Leydig cells, the latter of which are evenly distributed and irregularly shaped in the seminiferous tubules. As the most important supportive cell type, Leydig cells secrete a variety of sex hormones to promote male reproductive organ development and spermatogenesis, as well as to maintain secondary sexual characteristics (3).

Spermatogenesis occurs in the seminiferous tubule that is mainly composed of Sertoli cells and germ cells (4). Sertoli cells are irregularly conical and are attached to the base of the seminiferous tubules, enclosing germ cells at different developmental stages (5). Spermatogonia, primary spermatocytes, secondary spermatocytes, spermatids, and spermatozoa are sequentially distributed from the basal to the central area of the seminiferous tubules (6). For seasonal breeders, males undergo a switch between decreased testis size with lower testosterone production, spermatogenesis arrest, and inactive mating behavior during the nonbreeding season and increased testis size with higher testosterone production, spermatogenesis, and active mating behavior during the breeding season (1, 7, 8).

Mitochondria, as the primary energy source of eukaryotic cells, are required for spermatogenesis. Mitochondrial fitness is intricately coordinated by mitochondrial dynamics (fusion and fission) and mitophagy (9, 10). It has been found that multiple mitochondrial dynamics genes including optic atrophy 1 (*opa1*) and dynamin-related protein 1 (*drp1*) are essential for *Drosophila* germline stem cells (11, 12) and that mitochondrial fusion are required for spermatogonial differentiation and

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Seasonal expressions of ER α , ER β , EGF, EGFR, PI3K and Akt in the scent glands of the muskrats (*Ondatra zibethicus*)

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ABSTRACT

Epidermal growth factor (EGF) is an important autocrine and/or paracrine mediator of steroid hormones to stimulate growth and differentiation in mammals. The aim of this study is to investigate seasonal expressions of estrogen receptor α (ER α), estrogen receptor β (ER β), EGF, epidermal growth factor receptor (EGFR), phosphatidylinositol 3-kinase (PI3K) and protein kinase B (Akt) in the scent glands of the muskrats during the breeding and non-breeding seasons. Histologically, three types of cells including the glandular cells, interstitial cells and epithelial cells were identified in the scent glands in both seasons. Immunohistochemical results showed that ER α , ER β , EGF, EGFR, PI3K and Akt were presented in the different types of cells of the scent glands during the breeding and non-breeding seasons. Transcriptome data of the scent glandular tissues from muskrats in the breeding and non-breeding seasons showed that differential seasonal changes might be related to the estrogen-EGFR signaling pathway. The gene expression levels of ER α , ER β , EGF, EGFR, PI3K were increased, while the gene expression level of Akt were decreased in the breeding season than those in the non-breeding season. Besides, the concentrations of 17 β -estradiol (E $_2$) in the serum and the scent glandular tissues were remarkably higher in the breeding season than those of the non-breeding season. Taken together, our results suggested that EGFR signaling pathway may coordinate with ERs signaling to regulate the seasonal changes of the scent glandular functions.

1. Introduction

Interactions of growth factors and steroid hormones play an important role in cell proliferation, differentiation or a series of biological effects associated through their receptors or steroid receptors, initiate downstream multi-signaling pathways [1–3]. Accumulating evidence has found that steroid hormones play an essential role in regulating epidermal growth factor receptor (EGFR) activity or inducing autocrine growth factor secretion [4,5]. 17 β -Estradiol (E $_2$) is the most potent estrogen hormone in the circulation and is involved in a wide variety of vital physiological functions [6,7]. Estrogen receptor α (ER α) and estrogen receptor β (ER β), mediated the effects of E $_2$, showed tissues-specific distribution, for example, ER α predominates in the uterus but ER β plays a critical role in the prostate [7–9]. Epidermal growth factor (EGF) could act as an important mediator in E $_2$ -regulating physiological processes, due to the studies found that the EGF antibody

prevents E $_2$ -induced growth of tissue [10]. A series of evidence has demonstrated that the transient expression of steroid receptors that bind to steroid hormones in EGF signaling can lead to EGFR tyrosine phosphorylation triggered by EGF [11,12]. In breast cancer cells, estrogen rapidly acts to stimulate the transactivation of EGFR through the cross-talk/activation of the membrane EGFR and the membrane ER, as a receptor capable of activating G proteins, leading to activate downstream signaling pathways [12,13]. Besides, in human prostate cancer (LNCaP) cells, EGF can trigger rapid association of proto-oncogene tyrosine-protein kinase (SRC) with ER β to induce cell proliferation [11].

Recently, PI3K/Akt signaling pathway is considered as one of the most important kinase cascades in the downstream of ER-EGF signaling that induces a wide range of cellular functions such as survival, proliferation [3,14,15]. EGF is a growth factor that was first purified from mouse salivary glands, which play a vital role in cell growth and differentiation by binding to its receptor, EGFR [16]. EGFR is one of the

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Seasonal expressions of GPR41 and GPR43 in the colon of the wild ground squirrels (*Spermophilus dauricus*)

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ABSTRACT

G-protein-coupled receptor 41 (GPR41) and G-protein-coupled receptor 43 (GPR43) are important short-chain fatty acids (SCFAs) receptors. Previous studies indicated that GPR41 and GPR43 are involved in the secretion of gastrointestinal peptides, and glucose and lipid metabolism, and are closely related to obesity and type II diabetes, and other diseases. The purpose of the study was to explore the relationship of the GPR41 and GPR43 with seasonal breeding, and provide new prospects for further exploring the nutritional needs of breeding. We identified the localization and expression levels of GPR41 and GPR43 in the colon of the wild ground squirrels (*Spermophilus dauricus*) both in the breeding season and non-breeding season. The histological results revealed that the lumen diameter of the colon had obvious seasonal changes, and the diameter of the colonic lumen in the non-breeding season was larger than that in the breeding season. Immunohistochemical staining suggested that GPR41 and GPR43 are expressed in the simple layer columnar epithelium. In addition, compared with the breeding season, the mRNA and protein expression levels of GPR41 and GPR43 in the colon were higher during the non-breeding season. In general, these results indicated that GPR41 and GPR43 might play a certain role in regulating seasonal breeding.

Key words: GPR41; GPR43; colon; wild ground squirrel; seasonal breeding.

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Seasonal expressions of oxytocin and oxytocin receptor in the epididymides in the wild ground squirrels (*Citellus Dauricus* Brandt)



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ABSTRACT

The aim of this study was to detect the seasonal expressions of oxytocin (OT), oxytocin receptor (OTR), extracellular signal-regulated kinase1 and 2 (ERK1/2) and phospho-ERK1/2 (pERK1/2) in the epididymis of the wild ground squirrels (*Citellus Dauricus* Brandt) during the breeding season and non-breeding season. Histological results showed that size, weight, cell number and lumen diameter of epididymis underwent acute seasonal changes, which were all peaked in the breeding season. Immunohistochemical results suggested that strong staining of OT, OTR, ERK1/2, and pERK1/2 were observed in the epithelial layer in the whole epididymis, along with intense OT and OTR signal in smooth muscle cell (Smc) in caudal epididymis in the breeding season. The protein expression levels of OTR, ERK1/2, and pERK1/2 in the epididymis were higher in the breeding season than those of the non-breeding season. Besides, hormone assay revealed that there was no significant serum concentration of OT in these two periods, while epididymal concentration showed higher value in the breeding season. In summary, the identified localization and local concentration of OT in the epididymis in the wild ground squirrel suggested that epididymis may assume as a source of OT, and OT could act via OTR to activate ERK1/2 signaling to regulate seasonal epididymal functions.

1. Introduction

The mammalian epididymis is an essential reproductive organ for male fertility. A fully developed, functional epididymis is vital for male fertility (Xu et al., 2010). Previous studies have suggested that the epididymis can be roughly divided into three histologically parts including caput, corpus, and cauda (Cornwall, 2009; Turner, 2008). The epithelial cells (Ep) of epididymis have five major cell types: principal, basal, clear, apical, and halo cells (Arrighi, 2014; Browne et al., 2016). The epididymis is a hormone-dependent organ, steroid hormones including androgen and estrogen are main regulators for epididymis. Steroid hormones are known to regulate epididymal gene expressions, thus lead to the development of the epididymis, proliferation, and differentiation of Ep and the composition of seminal fluids.

Oxytocin (OT) is secreted from the hypothalamus, stored in the posterior pituitary, released into bloodstream, and then exerted physiological functions in the male reproductive system controlling ejaculatory process and sperm transport through stimulating contractility of seminiferous tubules (Harris and Nicholson, 1998), epididymis (Nicholson et al., 1999) and vas deferens (Prapaiwan et al., 2017;

Knight, 1974). To date, a number of studies have found the presence of oxytocin receptor (OTR) in the epididymis of several species (Thackare et al., 2006; Mewe et al., 2007), such as humans (Filippi et al., 2002a,b; Frayne and Nicholson, 1998), the marmoset monkey and macaque monkey (Einspanier and Ivell, 1997; Frayne and Nicholson, 1998), pig (Maggi et al., 1987), bovine (Mewe et al., 2007), sheep (Whittington et al., 2001), dog (Prapaiwan et al., 2017), rabbit (Filippi et al., 2002a; Filippi et al., 2002b), and muskrat (Liu et al., 2019). These published studies have indicated that OT has played endocrine and paracrine roles in male reproduction (Thackare et al., 2006). The function of OT supposes to be mediated through OTR activation (Einspanier and Ivell, 1997; Filippi et al., 2002a; Filippi et al., 2002b; Frayne and Nicholson, 1998; Maggi et al., 1987). The extracellular signal-regulated kinases (ERKs) play important roles in many cellular and physiological functions (Ramos, 2008; Xu et al., 2013), including the regulation of epididymal cellular processes (Xu et al., 2013). The components of mitogen-activated protein kinase (MAPK)/ERK signaling pathway are involved in the regulation of cell proliferation, survival, apoptosis, and differentiation in the epididymis (Ramos, 2008; Kim and Breton, 2016; Xu et al., 2010, 2011). Previous studies have provided evidence that the

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Seasonal expressions of luteinising hormone receptor, follicle-stimulating hormone receptor and prolactin receptor in the epididymis of the male wild ground squirrel (*Spermophilus dauricus*)

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Abstract. Luteinising hormone (LH), follicle-stimulating hormone (FSH) and prolactin (PRL) are pituitary-derived hormones and mediate their functions through LH receptor (LHR), FSH receptor (FSHR) and PRL receptor (PRLR) respectively. This study aimed to investigate the seasonal expression patterns of LHR, FSHR and PRLR in the epididymis of the male wild ground squirrel during the breeding and non-breeding seasons. Histologically, principal cells, basal cells, cilia and mature spermatozoa were found in the lumen of caput, corpus and cauda epididymidis in the breeding season, whereas in the non-breeding season, cilia and basal cells were rarely found and the epididymidal duct was devoid of spermatozoa. Immunohistochemical results showed that LHR, FSHR and PRLR were mainly present in the filamentous cytoplasm layer of epithelial cells of the caput, corpus and cauda epididymidis and FSHR and PRLR displayed stronger staining in the breeding season than in the non-breeding season. Furthermore, the mRNA and protein levels of *FSHR* and *PRLR* in all regions of epididymis as well as the levels of *LHR* in the caput and cauda epididymidis were higher during the breeding season. The protein levels of FSHR, LHR and PRLR were positively correlated with epididymal weight. Together, these results suggest that LHR, FSHR and PRLR may regulate epididymal functional changes in the male wild ground squirrel during its seasonal breeding cycle.

Additional keywords: adaption to environment, breeding cycle, pituitary-derived hormones, reproductive function.

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Introduction

The epididymis is a paired, highly coiled accessory reproductive organ that can be roughly divided into three histological parts including caput, corpus and cauda (Cornwall 2009). It connects the efferent ducts to the vas deferens and acts as a place where spermatozoa produced from the testis transit through and gradually become mature (Robaire and Viger 1995). There are numerous elements affecting sperm maturation in the epididymis, in which the diverse types of epithelial cells are thought to play major roles (Breton *et al.* 2016). Rodent epididymal epithelial cells are comprised of universally spread principal cells and basal cells, as well as region-specific clear cells, which exist in caput, corpus and cauda epididymidis (Arrighi 2014). Principal cells make up ~80% of the total epithelial cell population and are the major secretory cells for luminal proteins via merocrine or apocrine secretion (Belleannée *et al.* 2011, 2012).

Clear cells intersperse among principal cells and act as the main endocytic cells (Joseph *et al.* 2011) and basal cells are believed to assist in regulating the functions of principal and clear cells (Leung *et al.* 2004; Joseph *et al.* 2011). Epithelial cells together form a tight junction, called the blood–epididymis barrier, with adjacent epididymal epithelial cells, which functions as a means of selective transport of molecules between blood and lumen and separates immunogenic germ cells within the epididymal tubules from immune attack (Gregory and Cyr 2014).

Luteinising hormone (LH), follicle-stimulating hormone (FSH) and prolactin (PRL) are secreted from the pituitary and act exclusively through LH receptor (LHR), FSH receptor (FSHR) and PRL receptor (PRLR) respectively. Thus, LHR, FSHR and PRLR expression determines both the target and the extent of LH, FSH and PRL actions, ultimately directing hormone responses to target organs. Most studies about the



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Seasonal expressions of SF-1, StAR and P450scc in the scent glands of the muskrats (*Ondatra zibethicus*)

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ABSTRACT

The steroidogenesis occurs in specific cells and tissues in the mammals which begins with the transfer and intracellular processing of cholesterol converted to pregnenolone. This study investigated the gene and protein expression levels of steroidogenic factor 1 (SF-1), steroidogenic acute regulatory protein (StAR) and cytochrome P450 cholesterol side-chain cleavage enzyme (P450scc) in the scent glands of the muskrats during the breeding and non-breeding seasons. The immunohistochemical localizations of StAR and P450scc were identified in the glandular cells and epithelial cells while SF-1 was only expressed in glandular cells during the breeding and non-breeding seasons. The gene and protein expression levels of SF-1, StAR and P450scc in the scent glands were remarkably higher in the breeding season than those of the non-breeding season. The interaction of micro RNAs (miRNAs) and transcriptome results showed that miR-762 and miR-4454 might be the genes encoding (*Nr5a1*, *Star* and *Cyp11a1*) in key biological processes. Taken together, these results suggested that the scent glands of the muskrats potentially owned ability to synthesize steroid hormones *de novo*, and the steroid hormones might affect the scent glandular functions of the muskrats during the breeding and non-breeding seasons.

1. Introduction

The synthesis of steroid hormones has been extensively studied in endocrine tissues and many non-steroid tissues [1]. The common regulatory mechanism of the synthesis of steroid hormones in all steroidogenic tissues is the utilization of cholesterol as the substrate for steroid formation [2,3]. The steroid hormones represent an important group of compounds, which are synthesized mainly in the gonads and the adrenal glands, but are also synthesized in other tissues in the body [4,5]. The initial rate-limiting and regulated step in steroid biosynthesis and metabolism in the mammals is the transport of cholesterol, the substrate for all steroid hormones, from the outer to the inner mitochondrial membrane, where steroidogenic acute regulatory protein (StAR) plays a pivotal role in the transport [6,7]. StAR is a 37-kDa protein with an N-terminal mitochondrial targeting sequence that is cleaved off during mitochondrial import to yield 30-kDa intramitochondrial StAR [8]. StAR is composed of a single functional domain with an α/β helix-grip fold structure containing a nine-stranded anti-parallel β -sheet forming a long hydrophobic cleft that binds cholesterol and has a direct role in hormone-regulated steroid production [9]. StAR belongs to the

mammalian StAR subfamily StARD1 which has two members, StAR (StARD1) and MLN64 (StARD3). MLN64 is a related StAR domain protein, appears to play a role in the placenta which is lacked the StAR protein [10]. Therefore, instead of MLN64, StAR mainly plays major roles in intracellular cholesterol transport and maintenance of steroid hormones synthesis and promotion.

At the inner membrane, cholesterol is converted to form the first steroid, pregnenolone by the cytochrome P450 side-chain cleavage enzyme (P450scc), cleaves the cholesterol side chain to which is further converted by a series of enzymes to various steroid hormones in specific tissues, the crucial enzymatic step in the biosynthesis of all steroid hormones [11]. As we known, the transcription of P450scc and other steroidogenic enzymes requires the action of steroidogenic factor 1 (SF-1) (NR5A1) [12]. SF-1 is a member of the nuclear receptor family that is a key regulator of the endocrine axes and is essential for adrenal and gonad development [13]. As a key regulator of steroid hormone receptors, SF-1 is a 461 amino acid protein that originally found in the adrenal gland, gonads and other organs. SF-1 not only acts as an *in vivo* major regulator of some steroidogenic cells of the testis, ovary and fetal adrenal gland but also is involved in initiation of steroid synthesis and

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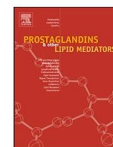
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Original Research Article

Seasonal expressions of COX-1, COX-2 and EP4 in the uteri of the wild Daurian ground squirrels (*Spermophilus dauricus*)

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ABSTRACT

Prostaglandins (PGs) play a pivotal role in uterine reproductive process including maternal recognition of pregnancy, cell proliferation, and myometrium contractions in mammals. In this study, we investigated the immunolocalizations and expression levels of Prostaglandin E2 synthases cyclo-oxygenase (COX)-1 and COX-2, as well as one of PGE2 receptor subtypes 4 (EP4) in the uteri of the wild Daurian ground squirrels (*Spermophilus dauricus*) during the breeding and non-breeding seasons. Histologically, the thickness of endometrium: myometrium ratio in the uteri of the breeding season was higher than that of the non-breeding season. The immunostainings of COX-1, COX-2 and EP4 were observed in stromal cells, glandular cells and myometrium cells in the breeding and non-breeding seasons. The protein and mRNA expression levels of COX-1, COX-2 and EP4 were higher in the uteri of the breeding season than those of in the non-breeding season. The mean mRNA levels of COX-1, COX-2 and EP4 were positively correlated with uterine weights. In addition, the PGE2 concentration of uterine tissues as well as plasma PGE2, 17 β -estradiol, progesterone, LH and FSH levels were also significantly higher in the breeding season compared to those of the non-breeding season. These results suggested that PGE2 might play an important autocrine or paracrine role in the regulation of seasonal changes in the uterine functions of the wild Daurian ground squirrels during the breeding and non-breeding seasons.



Seasonal expressions of androgen receptor, P450arom and estrogen receptors in the epididymis of the wild ground squirrel (*Citellus dauricus* Brandt)

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ABSTRACT

The aim of this study was to investigate the seasonal expressions of androgen receptor (AR), estrogen receptors alpha and beta (ER α and ER β) and aromatase cytochrome P450 (P450arom) in the epididymis of the wild ground squirrel. Histologically, the epididymis was with larger duct diameter and cell population during the breeding season. AR was presented in the peritubular smooth muscle cells and epithelial cells in the whole epididymis with stronger staining in the breeding period. P450arom was intensely localized in epithelial cells and spermatozoa during the breeding season, absent in the non-breeding season and moderately stained in pre-hibernation. During the breeding season, ER α was intensely expressed in epithelial cytoplasm and/or nucleus, whereas in the non-breeding season and pre-hibernation, weaker staining signal was found in nucleus of epithelial cells. ER β was absent in the entire annual cycle by immunohistochemical and Real-time PCR detection. The mRNA levels of AR, P450arom and ER α were higher in the epididymis of the breeding season when compared to those of the non-breeding season and pre-hibernation. Taken together, these results suggest that epididymis of the wild ground squirrel is a primary target for androgen and estrogen, and the expression of P450arom represents that epididymis may be a potential source of estrogen.

1. Introduction

The mammalian epididymis is essential for sperm maturation, including acquisition of motility and capacity to fertilize an oocyte (Dacheux and Dacheux, 2014). It happens during spermatozoa transit through the epididymal ducts, which can be roughly divided into caput, corpus and cauda regions based on structural and functional parameters (Cornwall, 2009). Because spermatozoa are almost sythetically inactive, the maturation processes involve the interaction of spermatozoa and micro-environment primarily created by epithelial cells of epididymal epithelium (Cornwall, 2009). The epididymal epithelial cells are comprised of 5 major cell types: principal, basal, clear, apical, and halo cells, of which principal cells make up the majority of the population (Arrighi, 2014). Epithelial cells play different roles in epididymal functions, cells within each region of the epididymis have a unique transcriptome and distinct functions (Cornwall, 2009). In addition, principal cells line the lumen of the epididymis forming a blood-epididymis barrier to control the exchange of molecules between blood

and epididymal lumens (Gregory and Cyr, 2014). Altogether, the epididymis provides a critical environment for sperm maturation, and due to the hormone-dependent feature, the epididymal function is mainly under maintenance of androgen and estrogen (Breton et al., 2016; Shayu et al., 2007).

The testicular Leydig cells are main source of epididymal androgen and estrogen. In mature adults, androgen is produced in testicular Leydig cells under stimulation of luteinizing hormone (Menon and Menon, 2012), and a portion of androgen is irreversible converted into estrogen by cytochrome P450 aromatase (P450arom) (Li et al., 2015). The transfer of testicular androgen and estrogen to epididymis was mainly proceeded by androgen binding protein and testicular luminal fluids respectively (Baltontin and Bustos-Obregon, 1989; Pearl et al., 2007). In the meantime, the epididymis was proved to be a source of estrogen by detectable P450arom localized in epididymis (Shayu and Rao, 2006). Androgen and estrogen exert their physiological roles via nuclear receptors. Unlike androgen which acts exclusively through androgen receptor (AR), estrogen function is mediated through

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Insights into functional microbial succession during nitrogen transformation in an ectopic fermentation system



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ABSTRACT

The ectopic fermentation system (EFS) is an advanced technology for treating farm wastewater, and it reduces ammonia nitrogen emission and nitrogen loss of fermentation products. This study observed the functional bacteria succession related to nitrogen metabolism in EFS by high throughput sequencing, and evaluated their associations with environmental factors. Results revealed that with the changes of temperature, pH, moisture content, and nitrogen content during fermentation, the species richness and diversity of ammonia oxidizing bacteria (AOB) with *amoA* increased, but those of denitrifying bacteria carrying *nirK* and *nosZ* decreased. During the fermentation process, the dominant bacterial populations of AOB and denitrifying bacteria changed significantly, and different bacterial populations showed different positive/negative correlations with the environmental factors. This study revealed the role of functional bacteria in ammonia removal and nitrogen conservation of EFS, and provided a theoretical basis for the improvement of microbial agents and EFS application.

1. Introduction

An ectopic fermentation system (EFS), composed of complex microbial communities including functional thermophilic microbes mixed with litter, was developed to overcome the problem of pollution from existing farm wastewater systems (Guo et al., 2013). The proposed EFS successfully settled farm wastewater and prevented straw burning in rural areas, and the post-fermentation material has substantial economic value as a bio-fertilizer. As an *ex situ* experimental setup, EFS functions dynamically based on the inoculation of complex microbial agents and successive supplementation of collected farm wastewater. Previous studies have explored the microbial agents suitable for EFS and the proper amounts of waste and litter to add, and identified the physical and biochemical indicators associated with optimisation and expansion of fermentation. Six thermophilic bacterial strains were identified and used in EFS, to process wastewater via aerobic fermentation (Guo et al., 2013). Further research revealed that EFS mainly containing maize straw, six thermophilic bacteria, and 20% cow dung supplementation provided an optimal model for continuous fermentation. In this system, environmental factors and the dominant bacterial

species synergistically yielded better fermentation performance, improved litter quality, and increased microbial abundance (Guo et al., 2015; Yang et al., 2018). In addition, changes in the viable bacteria groups were observed and demonstrated to play an important role in EFS (Yang et al., 2018).

In order to reduce the environmental pollution during high temperature fermentation, and retain more active ingredients in fermentation products, the thermophilic bacteria agent added into EFS contains ammonia–nitrogen removal bacteria. Previous studies have preliminarily proved that EFS has good effect of reducing ammonia–nitrogen emission and preventing nitrogen loss from fermentation products. In order to reveal the specific role of functional bacteria in nitrogen cycle and provide basis for further improvement of EFS, it is necessary to study the changes of bacteria and functional genes related to nitrogen metabolism in the fermentation process.

In general, nitrogen transformation during fermentation comprises nitrification and denitrification, and nitrogen losses are caused by the release of NH₃, N₂O, N₂ and NO_x (Zhang et al., 2017). NH₃ is often used as an important indicator of odour that can harm the ecological environment and human health, and N₂O contributes significantly to

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Seasonal expressions of luteinising hormone receptor, follicle-stimulating hormone receptor and prolactin receptor in the epididymis of the male wild ground squirrel (*Spermophilus dauricus*)

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Abstract. Luteinising hormone (LH), follicle-stimulating hormone (FSH) and prolactin (PRL) are pituitary-derived hormones and mediate their functions through LH receptor (LHR), FSH receptor (FSHR) and PRL receptor (PRLR) respectively. This study aimed to investigate the seasonal expression patterns of LHR, FSHR and PRLR in the epididymis of the male wild ground squirrel during the breeding and non-breeding seasons. Histologically, principal cells, basal cells, cilia and mature spermatozoa were found in the lumen of caput, corpus and cauda epididymidis in the breeding season, whereas in the non-breeding season, cilia and basal cells were rarely found and the epididymidal duct was devoid of spermatozoa. Immunohistochemical results showed that LHR, FSHR and PRLR were mainly present in the filamentous cytoplasm layer of epithelial cells of the caput, corpus and cauda epididymidis and FSHR and PRLR displayed stronger staining in the breeding season than in the non-breeding season. Furthermore, the mRNA and protein levels of *FSHR* and *PRLR* in all regions of epididymis as well as the levels of *LHR* in the caput and cauda epididymidis were higher during the breeding season. The protein levels of FSHR, LHR and PRLR were positively correlated with epididymal weight. Together, these results suggest that LHR, FSHR and PRLR may regulate epididymal functional changes in the male wild ground squirrel during its seasonal breeding cycle.

Additional keywords: adaption to environment, breeding cycle, pituitary-derived hormones, reproductive function.

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Introduction

The epididymis is a paired, highly coiled accessory reproductive organ that can be roughly divided into three histological parts including caput, corpus and cauda (Cornwall 2009). It connects the efferent ducts to the vas deferens and acts as a place where spermatozoa produced from the testis transit through and gradually become mature (Robaire and Viger 1995). There are numerous elements affecting sperm maturation in the epididymis, in which the diverse types of epithelial cells are thought to play major roles (Breton *et al.* 2016). Rodent epididymidal epithelial cells are comprised of universally spread principal cells and basal cells, as well as region-specific clear cells, which exist in caput, corpus and cauda epididymidis (Arrighi 2014). Principal cells make up ~80% of the total epithelial cell population and are the major secretory cells for luminal proteins via merocrine or apocrine secretion (Belleannée *et al.* 2011, 2012).

Clear cells intersperse among principal cells and act as the main endocytic cells (Joseph *et al.* 2011) and basal cells are believed to assist in regulating the functions of principal and clear cells (Leung *et al.* 2004; Joseph *et al.* 2011). Epithelial cells together form a tight junction, called the blood–epididymis barrier, with adjacent epididymidal epithelial cells, which functions as a means of selective transport of molecules between blood and lumen and separates immunogenic germ cells within the epididymidal tubules from immune attack (Gregory and Cyr 2014).

Luteinising hormone (LH), follicle-stimulating hormone (FSH) and prolactin (PRL) are secreted from the pituitary and act exclusively through LH receptor (LHR), FSH receptor (FSHR) and PRL receptor (PRLR) respectively. Thus, LHR, FSHR and PRLR expression determines both the target and the extent of LH, FSH and PRL actions, ultimately directing hormone responses to target organs. Most studies about the

Seasonal expressions of prolactin, prolactin receptor and STAT5 in the scented glands of the male muskrats (*Ondatra zibethicus*)

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Abstract

Prolactin (PRL) production in mammals has been demonstrated in extrapituitary gland, which can activate autocrine/paracrine signaling pathways to regulate physiological activity. In the current study, we characterized the gene expression profiles of PRL, prolactin receptor (PRLR) and signal transducers and activators of transcription 5 (STAT5) in the scented glandular tissues of the muskrats, to further elucidate the relationship between PRL and the scented glandular functions of the muskrats. The weight and volume of the scented glands in the breeding season were significantly higher than those of the non-breeding season. Immunohistochemical data showed that PRL, PRLR and STAT5/phospho-STAT5 (pSTAT5) were found in the glandular and epithelial cells of the scented glands in both seasons. Furthermore, we found that PRL, PRLR and STAT5 had higher immunoreactivities in the scented glands during the breeding season when compared to those of the non-breeding season. In parallel, the gene expressions of PRL, PRLR and STAT5 were significantly higher in the scented glands during the breeding season than those of the non-breeding season. The concentrations of PRL in scented glandular tissues and sera were measured by enzyme-linked immunosorbent assay (ELISA), and their levels were both notably higher in the breeding season than those of the non-breeding season. These findings suggested that the scented glands of the muskrats were capable of extrapituitary synthesis of PRL, which might attribute PRL a specific function to an endocrine or autocrine/paracrine mediator.

Introduction

In all vertebrates, prolactin (PRL) is a 23-kDa polypeptide hormone that is synthesized and stored by lactotroph cells in the anterior pituitary gland, and regulates multiple biological functions via endocrine signaling.^{1,3} The numerous different biological functions of PRL are mediated by the prolactin receptor (PRLR), which is a single membrane-bound protein that belongs to class I of the cytokine receptor superfamily.^{2,4} There are three major PRLR isoforms described in rats are the long, intermediate, and short isoforms.^{3,5} The short and long forms differ from each other in the length of their cytoplasmic domain resulting from alternative splicing of a single primary transcript. Generally, the most abundant PRLR is the long isoform, whereas other intermediate and short forms also exist in mammals. All three types of PRLR are devoid of any intrinsic enzymatic activity, the first intracellular event in PRLR signaling is Janus Kinase-2 (JAK2) activation.^{6,7} It is the most common that the phosphorylated transcription factors activated by JAK2 that belong to the family of signal transducers and activators of transcription (STAT), STAT1, STAT3 and STAT5 are the central transducer molecules of the signal transduction pathways initiated by PRLR activation. Of the STAT1, STAT3 and STAT5 proteins, STAT5 is identified as the most important transducer of the long and intermediate isoforms of the PRLR, whereas few amounts of phosphorylated STAT1 and STAT3 are detected.⁷ After activation by PRL, STAT5 recruits transcription factors of different signaling pathways leading to cell growth and differentiation.⁸

In a broad sense, when secreted into the circulation, PRL binds to the PRLR and activates JAK2-STAT5 signaling, which modulates a wide variety of physiological processes, including lactation, metabolism, immune responses and reproduction. PRL-null mice are unable to lactate due to a failure of lobuloalveolar differentiation of the mammary epithelium, similarly to PRLR-null and STAT5a-conventional knockout mice.⁹⁻¹¹ The expressions of PRLR have been discovered in many nonclassical endocrine organs, such as skins, testes, prostates and reproductive accessory tissues.¹²⁻¹⁶ The almost ubiquitous presence of PRLR in multiple extrapituitary sites of PRL production implicates that some of these actions reflect local autocrine and paracrine roles of extrapituitary PRL.¹⁷ Autocrine and paracrine actions of PRL within the reproductive system are not only known to complement the endocrine actions of pituitary PRL in reproductive functions but also provide causal mechanisms for the

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Key words: Muskrat; prolactin; prolactin receptor; scented glands; STAT5.

Contributions: WX, HL, QL, QG, participated in sample collection, performing the experiments, analyzing the data and drafting the manuscript; HZ, FG, QW, assisted with all experiments and helped revising the manuscript; YH, ZY, QW, designed, supervised the study, and revised manuscript. All authors read and approved the final version.

Conflict of interest: The authors declare that they have no competing interests.

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induction of reproductive behavior.¹⁸ Recent studies in mice have suggested that circulating PRL is also detected in males, and it is found at lower levels than in females.^{12,19} The presence and abundance of PRL in the prostate, has provided a novel perspective on roles of PRL in the normal development, growth and function of the male reproductive physiology.²⁰ Similarly, the finding of PRL and its receptor generally suggest that PRL positively modulates testicular functions in several ways.²¹ However, autocrine and paracrine mechanisms of PRL in male reproductive system remain unclear.

The muskrat (*Ondatra zibethicus*) is a kind of medium-sized, semi-aquatic rodent natively living in Canada, the United States and some parts of northern Mexico, later introduced in China.²² The muskrat has pre-

Seasonal expressions of androgen receptor, estrogen receptors and cytochrome P450 aromatase in the uteri of the wild Daurian ground squirrels (*Spermophilus dauricus*)

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Abstract

The reproductive tissues including the uterus undergo dramatic changes in seasonal breeders from the breeding to non-breeding seasons. Classically, sex steroid hormones play important roles in the uterine morphology and functions. To clarify the relationship between sex steroid hormones and seasonal changes in the uterine morphology and functions, the wild Daurian ground squirrels (*Spermophilus dauricus*) were used as seasonal breeder model. And the immunolocalizations and expression levels of androgen receptor (AR), estrogen receptors α and β (ER α and ER β) and cytochrome P450 aromatase (P450arom) were investigated in the uteri of the wild Daurian ground squirrels in the breeding (April) and the non-breeding (June) seasons via immunohistochemistry, Western blot and RT-PCR. Histologically, the uterine weight, the thickness of endometrium and the glandular density were significantly higher in the uteri of the breeding season than those of the non-breeding season. In both seasons, the immunostaining of AR was only presented in stromal cells of the uteri; the positive staining of ER α and ER β were localized in stromal cells and glandular cells; P450arom was merely immunolocalized in glandular cells. The protein and mRNA expression levels of ER α , ER β and P450arom were higher in the uteri of the breeding season than those of the non-breeding season; conversely, the expressions of AR were higher in the uteri of the non-breeding season comparing with those of the breeding season in both protein and mRNA levels. The AR:ER ratio in the uteri of the non-breeding season exceeded the

AR:ER ratio in the uteri of the breeding season in the wild Daurian ground squirrels. These results suggested that seasonal changes in the expression levels of AR, ERs and P450arom might be correlated with the uterine morphology and histology changes, and estrogen may play an important autocrine/paracrine role in regulating the uterine functions of the wild Daurian ground squirrels.

Introduction

The uterus is one of the major components in female reproductive system, which is composed of endometrium and myometrium.¹ The endometrium, which consists of the luminal epithelial cells, the glandular cells and the stromal cells,^{2,4} is the dominant functional unit of the uteri.¹ And the endometrium is a hormone-dependent multicellular tissue, whose compartments respond to hormonal cues in a coordinated spatial and temporal manner characterized by extensive cross-talk to regulate the development and homeostasis of the tissue.² During the estrous cycle and pregnancy, the uterus undergoes significant changes,^{3,5} such as cell proliferation and differentiation to prepare the suitable environment for the development of fertilized oocyte and embryo.^{1,2} Moreover, the annual changes in the uterine structure and functions are also observed in seasonal breeders including horses⁶ and stray bitches.⁷ The endometrium of seasonal breeders exhibits regeneration during the breeding season and degeneration during the non-breeding season.^{1,8}

The endometrium is known to be one of the major target tissues of sex steroid hormones.^{9,10} Sex steroid hormones including androgens and estrogens play key roles in the structural and functional changes of the endometrium in vertebrates.³ Androgens and estrogens exert their physiological functions via androgen receptor (AR),^{11,13} estrogen receptor α (ER α) and estrogen receptor β (ER β)^{10,14} respectively to mediate the signaling pathways.^{4,9} After binding with the receptors, the ligand-receptor¹² complex enters the nuclei to regulate the expressions of target genes and influences a wide range of biological activities, for instance, the cell proliferation in the endometrium.^{2,15} In addition, cytochrome P450 aromatase (P450arom) is the key limited enzyme in the procedure of estrogen synthesis,^{14,16} which functions to aromatize androgens to estrogens.^{4,11,17} P450arom is usually expressed in the gonadal tissue, for example, the granulosa cells in the ovary,¹⁸ however, it is also found in extra-gonadal

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Key words: Androgen receptor; estrogen receptor α ; estrogen receptor β ; P450arom; uteri; wild Daurian ground squirrel.

Contributions: YW, ZW, WY, participated in sample collection, performing the experiments, analyzing the data and drafting the manuscript; HZ, XS, assisted with all experiments and helped revising the manuscript; HZ, YH, ZY, QW, designed, supervised the study, and revised manuscript. All authors read and approved the final version.

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tissue, such as bones,¹⁹ brains,^{20,22} adipose tissues,²³ breasts,^{24,25} skins²⁶ and uteri.^{5,14,22} Extra-gonadal estrogens that are converted by P450arom from androgens exert important physiological functions in the local tissues, such as the role of local estrogen in brain sexual differentiation^{20,22} and the protective effects on bones.¹⁹

The wild Daurian ground squirrel (*Spermophilus dauricus*) is a typical seasonal breeder, which has a strict and extremely compressed breeding season from April to May and a long period of non-breeding season from June to the following March.^{8,20,21,27} In the wild Daurian ground squirrels, our previous studies have implicated that there were seasonal changes in the ovarian weight and follicular compositions and furthermore the circulating levels of estradiol-17 β were also changed seasonally.¹⁸ In a previous study of our group, there were statistical significant differences in the glandular nuclear numbers of endometrium between the breeding and non-breeding seasons.⁸ The regulations of endometrium growth and regression were orchestrated by the growth factors and sex



Toxicological effects of 3-methyl-4-nitrophenol on mouse ovarian and testicular cell proliferation, apoptosis and oocyte maturation

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ABSTRACT

The aim of the present study was to reveal the effects of 3-methyl-4-nitrophenol (PNMC) on mouse gonadal cell proliferation and apoptosis. Immature female and male mice were intramuscularly injected with 100 mg/kg PNMC or vehicle every five days. One-month later, ovarian rather than testicular weights were significantly decreased. The positive terminal deoxynucleotidyl transferase-mediated dUTP-digoxigenin nick end-labeling staining was enhanced in both testicular seminiferous epithelium and ovarian corpus luteum. Further study in ovaries showed that PNMC treatment increased the protein expressions of PCNA, p21 and p27, and decreased the expression of Cyclin D2. Whereas PNMC had no significantly influence on those protein expressions in testes. In addition, we demonstrated that 100 nM PNMC significantly suppressed mouse oocyte meiotic resumption and cumulus cell expansion *in vitro*. These findings suggest that the reproductive toxicities of PNMC involve affecting the processes of gonadal cell apoptosis and proliferation.

1. Introduction

Methyl-4-nitrophenol (PNMC), a nitrophenol derivative, is a major degraded product of the organophosphate insecticide fenitrothion, widely existing in food, soil and water [1,2]; it is also an important component of motor vehicles-generated diesel exhaust particles (DEPs), leading to serious air pollution throughout the world [3,4]. PNMC is absorbed mainly via inhalation, orally or skin, and is hardly degraded. Increasing number of studies have indicated the toxicological effects of PNMC on the function of the endocrine, reproductive and immune systems [5–7]. It has been reported that PNMC induced reproductive abnormalities in various animal models. In male birds and rodents, PNMC treatment lead to testicular atrophy with reduced sperm formation and plasma luteinizing hormone (LH) and testosterone concentrations [8,9]. Studies in female Japanese quails have demonstrated that PNMC could induce endocrine malfunction by influencing hypothalamo-pituitary-gonadal (HPG) axes at the central level and disrupt the corresponding reproductive processes [10,11]. Those male and female reproductive toxicities have been extensively studied, especially regarding to the anti-androgen and anti-estrogen effects, but few focus on the impairment of gonadal cell proliferation and apoptosis.

Cell proliferation and apoptosis are prerequisites for normal gonadal development. In female, granulosa cell proliferation is essential for follicle growth [12] and early corpus luteum formation [13]; meanwhile, apoptosis of granulosa cells lead to follicular atresia and corpus luteum regression [14,15]. In male, balance between self-renewal and apoptosis of germ cells is required to maintain normal testicular homeostasis [16]. Thus, fates of ovaries and testes are regulated by the relative “death” and “growth” factors.

During past two decades, several molecular families have been identified playing key roles in regulating cell cycle progression. Among them, D-type cyclins (Cyclin D1, D2 and D3) are widely expressed and differentially functioning in somatic and germ cells during folliculogenesis and spermatogenesis [17]. They promote G1/S transition by binding to cyclin-dependent kinases (CDKs) and increasing retinoblastoma protein phosphorylation to relieve inhibition of the transcription factor E2F [18,19]. Contrary to D-type cyclins, CDK inhibitors (CDKIs) inhibit G1/S cell cycle progression via binding to CDKs. There are two groups of CDKIs: INK4 (p15, p16, p18 and p19) and Kip/Cip (p21, p27 and p57) proteins. Among them, p27 and p21 are widely expressed CDKIs in various cell types [20]. It has been proved that loss of both genes would lead to large increase in testis weight in male mice

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Detection of Corn and Whole Wheat Adulteration in White Pepper Powder by Near Infrared Spectroscopy

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Abstract White pepper is a high-value commodity that is a target for adulteration, leading to loss of quality and encroachment on the rights and interests of consumers. Therefore, it is imperative to develop fast and reliable methods for detecting white pepper powder adulteration. The present paper investigated the feasibility of using near infrared (NIR) spectroscopy for quantifying adulteration (including whole wheat flour and corn flour) in white pepper powder. Partial least squares (PLS) calibration models were developed. Results showed that the standard error of calibration (SEC) and prediction (SEP) were 0.788% and 0.920%, respectively.

Keywords: white pepper powder adulteration, NIR spectroscopy, PLS calibration models, whole-wheat flour, corn flour

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Proliferation and apoptosis processes in the seasonal testicular development of the wild Daurian ground squirrel (*Citellus dauricus* Brandt, 1844)

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Abstract. The aim of the present study was to elucidate the regulatory role of cell proliferation and apoptosis in testicular development of wild Daurian ground squirrels during the breeding season (April), the non-breeding season (June) and before hibernation (September). Gross mass and hormonal analysis showed that the testis: body mass ratio and plasma testosterone concentration fluctuated seasonally, with a peak in April and lowest values in June. Similarly, spermatogenesis was fully developed in April but suppressed in June and September. Testicular decellularisation and vacuolisation was seen during the transition from the breeding to the non-breeding season. Furthermore, testicular levels of proliferating cell nuclear antigen, cyclin D2 and caspase-3 protein were significantly increased in June and September. Intriguingly, positive terminal deoxynucleotidyl transferase-mediated dUTP-digoxigenin nick end-labelling staining and nuclear translocation of caspase-3 in testicular germ cells appeared only during the prehibernation period, whereas accumulation of cyclin D2 in spermatocyte nuclei occurred in September. These findings demonstrate, for the first time, that both cell proliferation and apoptosis are stimulated during the prehibernation period, indicating that a hormonal-regulated balance of testicular germ cell proliferation and apoptosis may play a pivotal role in preparing for testicular recrudescence of wild Daurian ground squirrels.

Additional keywords: seasonal breeding.

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Introduction

Seasonal reproduction, a process by which sexual activity takes place during a specific time of year, is a common adaptive strategy among wild species to ensure the survival and growth of offspring at the optimal time. Due to circannual fluctuating environmental conditions and energetic restrictions, male seasonal breeders show synchronised cycles of testicular growth and involution throughout the breeding cycle (Young and Nelson 2001; Klonisch *et al.* 2006; Jiménez *et al.* 2015), which requires communication among endocrine, neurobiological and biological rhythms across multiple cell types (Dardente 2012; Boufermes *et al.* 2014; Sáenz de Miera *et al.* 2014; Li and Zhou 2015). Studies in both seasonal and non-seasonal breeders have revealed that spermatogenesis can be regulated by gonadotrophin and testosterone (Nandi *et al.* 1999; Janett *et al.* 2012; Ramaswamy and Weinbauer 2014); however, the precise mechanism regulating seasonal spermatogenesis is not completely understood and requires further investigation.

Spermatogenesis is a highly intricate process during which spermatozoa are produced from male primordial germ cells and involves cell proliferation, differentiation and apoptosis

(Pastor *et al.* 2011; O'Shaughnessy 2014). During testicular regression, diminished proliferation and increased apoptosis have been shown to be associated with aged and photoregressed mammalian seminiferous epithelium (O'Shaughnessy 2014). This triggered testicular apoptosis in the atrophic testes has been demonstrated in various seasonal breeding vertebrates, including the Syrian hamster (Seco-Rovira *et al.* 2015), white-footed mice (Young *et al.* 2000), the large hairy armadillo (Luaces *et al.* 2014) and the Japanese Jungle crow (Islam *et al.* 2012). Meanwhile, proliferative activity is usually detected in undifferentiated spermatogonia during the testicular regression phase (O'Shaughnessy 2014), which plays a central role in restoring spermatogonia lost during the period of testis inactivity (Dadhich *et al.* 2013). Thus, an appropriate balance between cell proliferation and apoptosis in the seminiferous epithelium may play an important regulatory role in male seasonal reproduction.

Proliferating cell nuclear antigen (PCNA), a 36-kDa auxiliary protein of DNA polymerases, is necessary for DNA synthesis (Dieckman and Washington 2013). Immunoeexpression of PCNA has been detected in spermatogonia, spermatocytes and

RESEARCH ARTICLE | Hormones, Reproduction and Development

Seasonal expression of P450arom and estrogen receptors in scented glands of muskrats (*Ondatra zibethicus*)

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Zhang H, Lu L, Zhu M, Zhang F, Sheng X, Yuan Z, Han Y, Watanabe G, Taya K, Weng Q. Seasonal expression of P450arom and estrogen receptors in scented glands of muskrats (*Ondatra zibethicus*). *Am J Physiol Regul Integr Comp Physiol* 312: R380–R387, 2017. First published December 30, 2016; doi:10.1152/ajpregu.00458.2016.—Male muskrats have one pair of scented glands that grow and involute annually. To investigate the annual changes in the scented gland, we measured the expressions of aromatase cytochrome P-450 (P450arom) and estrogen receptors (ERs) in the scented glands. P450arom was expressed in glandular cells and epithelial cells in the scented glands during the breeding season, and only in glandular cells during the nonbreeding season. ER α and ER β were also detected in different types of cells in the scented gland during the breeding and nonbreeding seasons. Both mRNA and protein levels of P450arom, ER α , and ER β were higher in the scented glandular tissues during the breeding season than those during the nonbreeding season. In addition, small RNA sequencing showed that the predicted targets of the significantly changed microRNAs might be the genes encoding P450arom and ERs. In conclusion, the seasonal changes in the expression of P450arom and ERs may be involved in the regulation of scented gland functions.

estrogen receptors; microRNA; muskrat; P450arom; scented gland

ESTROGENS ARE TYPICALLY identified as female hormones, but they also have many physiological functions in male organs. The origin of estrogens is the conversion of androgens mediated by aromatase cytochrome P-450 (P450arom) in males. P450arom is a member of the cytochrome P-450 superfamily that catalyzes the conversion of androgens, namely testosterone and androstenedione, into estrogens, estradiol, and estrone, respectively (32). In males, this enzyme is expressed in various tissues, including testis and some nongonadal organs, such as brain, adipose tissue, skin, and bone, indicative of the ability of producing estrogens in those organs (7, 11, 16, 35, 46). The classical estrogen signaling pathway is mediated by estrogens via its two receptors, estrogen receptor- α (ER α) and estrogen receptor- β (ER β) (20, 44). Binding with ER α and/or ER β , estrogens could play important roles in regulation of multiple cellular processes, including gene expression, apoptosis, cell proliferation, and differentiation in various tissues (4, 29, 36).

In male reproductive organs, including testis, epididymis, and reproductive tract, the coexpression of P-450 with ER α and ER β suggests that estrogens act locally as autocrine or paracrine factors (17, 21, 31, 40). Disruption of the genes encoding for these key factors showed that estrogen signaling is essential for the development and differentiation of the reproduction systems in males (10, 15, 19, 26, 34). In recent years, it has been widely accepted that the function of male gonads is essentially regulated by estrogens that are locally produced by all testicular somatic and germ cell types in rodents (3, 30, 47). Compared with the well-studied role of estrogens on male reproduction, the function of estrogens in nonreproductive tissues in males remains unclear.

Small RNAs are classified into 18–24 nt microRNAs (miRNAs), 21–22 nt short interfering RNAs, and 26–30 nt PIWI-associated RNAs based on their length and their association protein argonaute family proteins (13). Multiple types of small RNAs (sRNAs) have been reported to regulate cellular functions via suppressing target gene transcripts and many other aspects of RNA biogenesis. miRNAs constitute a dominating class of sRNAs in most somatic tissues, primarily functioning at a posttranscriptional level by inhibiting mRNA translation with or without transcript degradation (37). In recent years, the development of gene sequencing technology has enabled an easy way to investigate tremendous sRNAs and analyze their different expression profiles.

The muskrat (*Ondatra zibethicus*) is a medium-sized, semi-aquatic rodent that lives throughout Canada and the United States and in some parts of northern Mexico. The muskrat gets its name from the two scented glands near its tail that give off a musky odor. The muskrat is a seasonal breeder with sexually active period of ~8 mo from March to October. During the breeding period, the male muskrat actively mates and produces mature spermatozoa; simultaneously, the scented glands secrete perfume substances that are expensive Chinese herbal medicine. Our laboratory's previous research data have shown the seasonal changes in morphology, granular cells number, and function of scented glands (22, 25, 27). To understand the mechanism for the changes in the scented glands, we investigated seasonal changes in the expressions of P450arom, ER α , and ER β during the breeding and nonbreeding seasons in the scented glands of muskrats. Meanwhile, the different expression levels of sRNAs in the scented glands during different seasons were measured, and their targeting genes were predicted. Based on these results, the relationship between estro-

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RESEARCH ARTICLE | *Hormones, Reproduction and Development*

Seasonal expressions of follicle-stimulating hormone receptor and luteinizing hormone receptor in the scented gland of the male muskrat (*Ondatra zibethicus*)

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Zhang H, Zhang F, Zhu M, Wang J, Sheng X, Yuan Z, Han Y, Watanabe G, Taya K, Weng Q. Seasonal expressions of follicle-stimulating hormone receptor and luteinizing hormone receptor in the scented gland of the male muskrat (*Ondatra zibethicus*). *Am J Physiol Regul Integr Comp Physiol* 312: R569–R574, 2017. First published February 22, 2017; doi:10.1152/ajpregu.00506.2016.—Accumulating evidence has shown that follicle-stimulating hormone (FSH) and luteinizing hormone (LH) may influence the functions of nongonadal tissues in addition to their classic target gonads. Our previous studies revealed that the scented glands of male muskrats expressed prolactin receptor, steroidogenic enzymes, and inhibin/activin subunits. To further seek the evidence of the activities of pituitary gonadotropins in scented glands, we investigated the seasonal expression patterns of FSH receptor (FSHR) and LH/choriogonadotropin receptor (LHCGR). The weight and size of scented glands during the breeding season were significantly higher than those during the nonbreeding season. Immunohistochemical studies showed that FSHR was present in the serous cells of scented glands, whereas LHCGR was present in the interstitial cells. The protein and mRNA expression levels of FSHR and LHCGR were significantly higher in the scented glands during the breeding season than those during the nonbreeding season. Importantly, the levels of circulating FSH and LH were remarkably higher during the breeding season. Taken together, these results suggested that gonadotropins may affect the function of muskrat scented gland via the locally expressed receptors in a season-dependent manner.

follicle-stimulating hormone receptor; luteinizing hormone/choriogonadotropin receptor; muskrat; scented gland; seasonal change

FOLLICLE-STIMULATING HORMONE (FSH) and luteinizing hormone (LH) are gonadotropic hormones produced and released from anterior pituitary cells. Upon the stimulation of gonadotropin-releasing hormones, FSH and LH are produced and released into circulation and exert the physiological effects on the gonads through their receptors the FSH receptors (FSHR) and LH/choriogonadotropin receptors (LHCGR), respectively (33). Both FSHR and LHCGR belong to the G protein-coupled receptor family (35). The binding of respective ligand to FSHR or LHCGR leads to the activation of G protein and subsequent increase in the cyclic adenosine monophosphate (cAMP) sys-

tem as well as phosphorylation of protein kinases, resulting in the activation of steroidogenic gene transcription (28, 35). The notion that FSHR and LHCGR were present exclusively in gonadal cells lasted for many years. In general, FSHR and LHCGR are localized in Sertoli cells and Leydig cells of testis, respectively (19). In ovaries, FSHR is localized in granulosa cells, whereas LHCGR is localized in theca cells as well as interstitial cells (16). However, recently, the expressions of FSHR and LHCGR have also been detected in nongonadal tissues such as mammary gland (6, 10), kidney (2), uterus (1, 37), and blood vessel (34), indicating that FSH and LH have broader functions (38).

The muskrat (*Ondatra zibethicus*) is a medium-sized, semi-aquatic rodent. It is a seasonal breeder with a sexually active period of ~8 mo from March to October. To attract the females during the breeding season, the males secrete musk (perfume substances), a widely used but very expensive ingredient in traditional Chinese medicine, from their scented glands (11, 14, 18). Our previous studies showed that the prolactin receptor was expressed in the scented glands, indicating that the pituitary may be involved in the regulation of scented gland function (9). Moreover, steroidogenic enzymes, steroid hormone receptors, and inhibin/activin subunits were also detected, further suggesting that the scented gland is actively regulated by circulating hormones (22–24, 26). To test whether other classic pituitary hormones, including FSH and LH, are involved in the regulation of scented gland function, we examined the expressions of FSH receptor and LH receptor in the scented gland of the muskrat in breeding and nonbreeding seasons in the present study.

MATERIALS AND METHODS

Animals. Fifteen adult muskrats were obtained during the breeding season (April, $n = 5$; July, $n = 5$) and the nonbreeding season (January, $n = 5$) from XichuanWangnong Muskrats Breeding Farm, Beijing, China. The muskrats were kept with a pattern of one male and one female in one enclosure. All of these animals were treated in accordance with National Animal Welfare Legislation guidelines. All experimental procedures were approved by the Animal Ethics Committee at the Experimental Center of Beijing Forestry University in accordance with the guidelines. Each pair of scented glandular tissues was obtained from the male muskrat. One side of scented gland was immediately fixed for being kept overnight in Bouin's solution for

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RESEARCH ARTICLE | *Hormones, Reproduction and Development*

Expression of leptin receptor in the oviduct of Chinese brown frog
(*Rana dybowskii*)

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Xi L, Liu Y, Tang Z, Sheng X, Zhang H, Weng Q, Xu M. Expression of leptin receptor in the oviduct of Chinese brown frog (*Rana dybowskii*). *Am J Physiol Regul Integr Comp Physiol* 312: R912–R918, 2017. First published March 15, 2017; doi:10.1152/ajpregu.00020.2017.—The oviduct of Chinese brown frog (*Rana dybowskii*) expands specifically during prehibernation instead of in the breeding period. In this study, we investigated the expression of leptin receptor (Ob-Rb) in *Rana dybowskii* oviduct during the breeding period and prehibernation. Histologically, the oviduct of *Rana dybowskii* consists of glandular cells, tubule lumen, and epithelial cells. The oviductal weight and pipe diameter also revealed significant differences, which were higher in prehibernation than that of the breeding period. Ob-Rb was observed in stromal cells of oviductal tissue in both the breeding period and prehibernation. The mean protein and mRNA levels of the Ob-Rb were significantly higher in prehibernation as compared with the breeding period. In addition, oviductal content of leptin was also higher in prehibernation than that of the breeding period. These results suggested that oviduct of *Rana dybowskii* might be a target organ of leptin, and leptin may play an autocrine/paracrine role mediated by Ob-Rb in regulating the oviductal hypertrophy during prehibernation.

leptin; leptin receptor; regulation; oviduct; *Rana dybowskii*

THE OVIDUCT, the tubular organ connecting the periovarian space with the uterus, is regulated by many hormones and cytokines that modulate complex early reproductive events, including gamete transport, fertilization, and embryo development. By creating suitable conditions for the transport and maturation of gametes and generating appropriate environments for fertility and early embryo development, the oviduct plays a vital role in the success of early reproductive events (14, 19). In addition, the oviductal fluid is also essential for its reproductive functions (5, 20). It is composed of hundreds of macromolecules derived either by secretion from oviduct epithelium or serum transudate (6, 21).

Energy storage and expenditure are two factors affecting reproduction in wildlife. Adipose tissue, as the main energy storage tissue, participates in the regulation of energy homeostasis and secretes a large number of biologically active adipokines to regulate physiological functions (9). Leptin (Ob) is one of the best-characterized adipokines. In 1994, leptin was the first adipokine claimed to be the “missing link” between fat and reproduction (29). As one of the most important hormones,

leptin is a nonglycosylated polypeptide of 16 kDa, which is mainly produced and secreted into the bloodstream by white adipose tissues. Gene expression and production of leptin have been observed in a variety of tissues, including skeletal muscle (39), pituitary (15), mammary tissue (33), hypothalamus, and placenta (24). The leptin receptor (Ob-R) is a member of the class I cytokine receptor family. However, only two of them, long Ob-Rb and short Ob-Ra isoforms, are thought to play essential roles in mediating leptin signaling and transport and degradation of leptin. Leptin carries out its biological actions on target tissues through interaction with its receptor, especially by binding and activating the long form of Ob-Rb (34). The long Ob-Rb form is highly expressed in the hypothalamus and capable of initiating signal transduction (3).

Leptin plays an integral role in the normal physiology of the reproductive system with complex interactions at all levels of the hypothalamic-pituitary gonadal axis (stimulatory effects at the hypothalamus and pituitary and inhibitory actions at the gonads). Thus leptin serves as a putative signal that links metabolic status with the reproductive axis (29). Leptin and its receptor are expressed in ovary (42) and testis (27, 30). Identification of leptin in these organs pointed out its participation in the control of reproductive function in both sexes (7, 37).

The Chinese brown frog (*Rana dybowskii*) is distributed throughout China, Korea, Japan, and eastern Siberia (41). The oviduct of *Rana dybowskii* has been used widely in traditional Chinese medicine, which is recorded in the Pharmacopoeia of the People's Republic of China (due to its improvement on immune system and lung function). The breeding period for *Rana dybowskii* ranges from February to June, followed by hibernation from October to February (32). Different from the oviduct expansion during the breeding or estrous period in mammals, a unique physiological phenomenon of *Rana dybowskii* is that its oviduct expands specifically during prehibernation (13). Our previous studies showed that proliferating cell nuclear antigen (PCNA), peroxisome proliferator-activated receptor γ 2 (PPAR γ 2), leptin, P450arom, estrogen receptor α (ER α), prostaglandin-E2, and its receptor subtype 4 (EP4) had higher expression levels in the prehibernation oviduct (12, 22, 32, 40), which suggested that the intrinsic regulators might play a regulatory role in cell proliferation and differentiation of the oviduct (12). To extend our understanding of this process, in this study, we investigated the expression of Ob-Rb in the oviduct of *Rana dybowskii* during the breeding period and prehibernation to elucidate the physiological regulation of leptin in oviductal hypertrophy in *Rana dybowskii*.

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Seasonal changes of androgen receptor, estrogen receptors and aromatase expression in the hippocampus of the wild male ground squirrels (*Citellus dauricus* Brandt)

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ABSTRACT

The wild ground squirrel is a typical seasonal breeder whose annual life cycle can be roughly divided into the breeding season, the post-breeding season and hibernation. Our previous study has reported the seasonal changes in the expressions of androgen receptor (AR), estrogen receptors α and β (ER α and ER β), and aromatase cytochrome P450 (P450arom) in the hypothalamus of male wild ground squirrels. To further seek evidence of seasonal expression of steroid hormone receptors and steroid hormone synthases in other brain regions, we investigated the protein and mRNA expressions of AR, ER α , ER β and P450arom in the hippocampus of the male wild ground squirrels during these different reproductive periods. Histological observation showed that the number of pyramidal cells in Cornu Ammonis 1 (CA1) increased in the breeding season. Both protein and mRNA of AR, ER α , ER β and P450arom were present in CA1 and CA3 of all seasons. There was significant increment in the immunosignal intensity and mRNA level of AR and ER α during the pre-hibernation, whereas those of ER β and P450arom were higher during the post-breeding season. In addition, the profile of plasma testosterone concentration showed the nadir in the post-breeding season, a marked elevation in the pre-hibernation, and the summit in the breeding season. These findings suggested that the hippocampus may be a direct target of androgen and estrogen; androgen may play important regulatory roles through its receptor and/or the aromatized estrogen in the hippocampus of the wild male ground squirrels.

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1. Introduction

Photoperiodism is the ability of wild animals to measure environmental day length, and this ability permits organisms to ascertain the time of year and engage in seasonally appropriate adaptations (Walton et al., 2011). With the day length shifting, wild animals, such as wild ground squirrels (Li et al., 2015), bears (Tsubota et al., 1997) and raccoon dogs (Weng et al., 2012), mate and breed seasonally. In addition to the reproductive system, non-reproductive organs and tissues cope with the environmental changes as well. This includes the function of hippocampus, which

plays a central role in the process of cognition and memory (Bannerman et al., 2002). In avian, the hippocampus undergoes seasonal changes which is associated with food storing, reproductive behavior and annual migration (Sherry and MacDougall-Shackleton, 2015). Moreover, the sizes of brain and hippocampus in wild rodents also decreased under the exposure of short photoperiod (Workman et al., 2011).

Androgen and estrogen are major sex steroid hormones, and testosterone (T) and 17 β -estradiol (E₂) are the main forms of each. The effect of androgen is mainly mediated by androgen receptor (AR) to regulate target gene transcription (Palvimo, 2012). Similarly, the genomic action of estrogens is mediated by two distinct intracellular receptors, estrogen receptor alpha (ER α) (Green et al., 1986) and beta (ER β) (Kuiper et al., 1996). So far, numerous studies have demonstrated that the functions of hippocampus can be directly influenced by androgens and estrogens via AR (Moghadami et al., 2016; Patchev et al., 2004) and ERs

Abbreviations: AR, androgen receptor; CA, Cornu Ammonis; ER α , estrogen receptor α ; ER β , estrogen receptor β ; P450arom, aromatase cytochrome P450; B, the breeding season; PB, the post-breeding season; P, pre-hibernation.

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Seasonal expression of luteinizing hormone receptor and follicle stimulating hormone receptor in testes of the wild ground squirrels (*Citellus dauricus* Brandt)



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ABSTRACT

The objective of this study was to evaluate whether luteinizing hormone (LH), follicle stimulating hormone (FSH) and their receptors luteinizing hormone receptor (LHR) and follicle stimulating hormone receptor (FSHR) play roles in the seasonal spermatogenesis of the wild ground squirrels. To that end, we characterized the testicular immunolocalization of LHR and FSHR, their expression on both mRNA and protein levels, as well as serum concentrations of LH and FSH in male wild ground squirrels throughout the annual reproductive cycle. Histologically, all types of spermatogenic cells including mature spermatozoa were identified in the breeding season (April), while spermatogonia and primary spermatocytes were observed in the non-breeding season (June), and spermatogonia, primary spermatocytes and secondary spermatocytes were found in pre-hibernation (September). LHR was present in Leydig cells during the whole periods with more intense staining in the breeding season; Stronger immunostaining of FSHR was observed in Sertoli cells during the breeding season compared to the non-breeding season and pre-hibernation. Consistently, the mRNA and protein levels of LHR and FSHR were higher in testes of the breeding season, and then decreased to a relatively lower level in the non-breeding season and pre-hibernation. Meanwhile, serum LH and FSH concentrations were significantly higher in the breeding season than those in the non-breeding season and pre-hibernation. These results suggested that gonadotropins and its receptors, LHR and FSHR may be involved in the regulation of seasonal changes in testicular functions of the wild ground squirrels.

1. Introduction

The luteinizing hormone (LH) and follicle stimulating hormone (FSH) are essential communicating factors between the hypothalamus, pituitary and gonads, and play crucial roles in the regulation of reproductive functions in both females and males through LH receptor (LHR) and FSH receptor (FSHR) (Plant, 2008). In males, LH promotes testosterone (T) synthesis by acting on Leydig cells of the testis where LHR is present (Shiraishi and Matsuyama, 2017), which induces the expression of a cluster of steroidogenic enzymes, such as cytochrome P450 cholesterol side-chain cleavage enzyme (P450_{scc}), cytochrome P450 17-hydroxylase/17,20 lyase (P450_{c17}) and 3β-hydroxysteroid dehydrogenase (3β-HSD) (Lavoie and King, 2009; Payne and Hales, 2004). In addition to stimulating T synthesis, LH also exerts direct action on spermatogenesis. The findings from *Lhr* knockout mice showed that the round spermatids were dramatically decreased and the

elongated spermatids were completely absent, even though Sertoli cell and spermatogonia numbers were parallel to wild types (Lei et al., 2004). FSH stimulates Sertoli cell proliferation during fetal and early postnatal life, facilitates Sertoli cell differentiation during puberty and spermatogenesis during adulthood (Gromoll et al., 1996; O'Shaughnessy et al., 2012; Walker and Cheng, 2005). FSH also plays vital roles in supporting blood-testis barrier, which consists of tight junctions between Sertoli cells and provides the specific micro-environment for spermatogenesis (Stanton, 2016). In addition, FSH stimulates the production of cytokines and growth factors from Sertoli cells that activate Leydig cell function or germ cell development (Cheng and Mruk, 2010; Rebourcet et al., 2014). Hence, FSH is essential for both physical and biochemical support of germ cell development via its impact on Sertoli cells.

Animals inhabiting temperate latitudes adapt seasonal reproductive activities since they experience marked seasonal changes in the quality

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Expressions of IL-6, TNF- α and NF- κ B in the skin of Chinese brown frog (*Rana dybowskii*)

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Abstract

The cytokine interleukin-6 (IL-6) mediates a wide range of inflammatory and immune responses. Tumor Necrosis Factor α (TNF- α) has a myriad of pro-inflammatory effects on the skin. Nuclear factor κ B (NF- κ B) is a transcriptional factor that regulates a battery of genes that are critical to immune system. In this study, we investigated the localizations and expression levels of IL-6, TNF- α and NF- κ B in the skin of *Rana dybowskii* during the breeding period and pre-hibernation. Histologically, the skin of *Rana dybowskii* consisted of epidermis and dermis. Four kinds of cells were identified in the epidermis, while the dermis was composed of homogenous gel, mucous glands and granular glands. IL-6, TNF- α and NF- κ B were immunolocalized in the epithelial and glandular cells in both periods. Western blotting showed that IL-6, TNF- α and NF- κ B were significantly higher in the pre-hibernation compared to the breeding period. Real-Time PCR revealed that the relative mRNA levels of IL-6 and NF- κ B in the pre-hibernation increased significantly compared with the breeding period, while the TNF- α mRNA expression levels were not significantly different between these two periods. These results suggested that IL-6, TNF- α and NF- κ B might collectively be involved in the skin immune system of *Rana dybowskii* during the breeding period and pre-hibernation.

Introduction

Amphibian skin is naked and directly exposed to harsh environments and damaged by varieties of external factors, such as predators, microorganisms, parasites, and some physical injuries.^{1,2} As the first line of defending against external infection, the skin provides the most important barrier against environmental influences. Wound healing, regeneration and the development

of immune tolerance are main functions of the skin immune system.³ Moreover, the skin, as a biochemically and physiologically complex organ, has functions of defending against predators and microorganisms, which makes amphibians thrive in a wide range of habitats and ecological conditions.^{1,4} The secretions of cytokines by epidermal keratinocytes, particularly tumor necrosis factor alpha (TNF- α), interleukin-6 (IL-6) and interleukin-1 β (IL-1 β), play a key role in various immunological disorders and inflammation in the skin.^{5,6} However, most relative reports were about the roles of IL-6, TNF- α and NF- κ B in mammals skin, there were few reports about the physiological roles of IL-6 and TNF- α in amphibian skin, and until now there were no reports about the changes in the expressions of IL-6 and TNF- α in amphibian skin during different physiological states.

Cytokines are mediators with multiple functions, including the initiation or influence of numerous biological processes, such as, inflammation, sepsis and wound healing.^{7,8} The pro-inflammatory cytokines IL-6 and TNF- α play key roles within the cytokine network.⁹ As a multifunctional cytokine, IL-6 is involved in the regulation of growth of various malignant tumors and inflammation.¹⁰ IL-6 is produced by various types of cells, such as leukocytes, keratinocytes, endothelial cells, fibroblasts, and some tumor cells. What's more, IL-6 is frequently associated with the early stages of host defense and mediates a wide range of inflammatory and immune responses.^{11,12} IL-6 contributes to the growth and differentiation of numerous cell types, including those of dermal and epidermal origin¹³ and is closely linked to skin wound healing.¹⁴ IL-6 treatment also appears to modulate stratum corneum regeneration and skin barrier function¹⁵ to maintain skin homeostasis. TNF- α acts as a mediator of both natural and acquired immunity, which could regulate many cellular and biological processes such as immune function, proliferation, cell differentiation, apoptosis and energy metabolism.¹⁶ TNF- α plays an important role in host defense against viral, bacterial, fungal, and parasitic pathogens, in particular against intracellular bacterial infections, such as *Mycobacterium tuberculosis* and *Listeria monocytogenes*.¹⁷ In addition, TNF- α participates in re-epithelialization and neovascularization and has a beneficial effect on tissue repair of the skin.^{18,19}

Nuclear factor κ B (NF- κ B) is a transcriptional factor that regulates a battery of genes that are critical to innate and adaptive immunity, cell proliferation, inflammation, tumor development and inhibition of apop-

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Key words: IL-6; TNF- α ; NF- κ B; *Rana dybowskii*; skin.

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tosis.²⁰ NF- κ B is involved in the activation of immune cells by upregulating the expressions of many cytokines (such as IL-1 β , IL-6, IL-18 and TNF- α), which are essential for the immune response.²¹ In the skin, NF- κ B regulates the expressions of many genes that are involved in the initiation of the inflammatory response, including cytokines, adhesion molecules and chemokines, matrix metalloproteases, and nitric oxide synthase.²²

The Chinese brown frog (*Rana dybowskii*) is distributed throughout China, Korea, Japan, and eastern Siberia.²³ Depending on the latitude and altitude, the hibernation of *Rana dybowskii* is from October to February next year, which is followed by the breeding period from February to June.²⁴ The skin of *Rana dybowskii* has been used extensively in traditional Chinese medicine to heal burnt wounds because of the antimicrobial components, which may contribute to efficacy in wound healing.²⁵ Our previous study demonstrated the presence and seasonal expressions of IL-1 β and IL-1R in the *Rana dybowskii* skin,²⁶ which suggested that

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Seasonal Expression of Oxytocin and Oxytocin Receptor in the Scented Gland of Male Muskrat (*Ondatra zibethicus*)

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Oxytocin (OT) can modulate multiple physiological functions via binding to the widely distributed oxytocin receptor (OTR). In this study, we investigated the seasonal expressions of OT, OTR and extracellular signal regulated kinase (ERK1/2) signaling pathway components in the scented gland of muskrat during the breeding and non-breeding seasons. Histologically, glandular cells, interstitial cells and excretory tubules were identified in the breeding season scented glands, whereas epithelial cells were sparse in the non-breeding season. Immunohistochemical results showed that OTR was present in epithelial cells and interstitial cells while OT, pERK1/2, ERK1/2 and c-fos were expressed in epithelial cells and glandular cells. The protein and mRNA expressions of OTR, OT and c-fos were significantly higher in the scented gland in the breeding season than in the non-breeding season. Importantly, the levels of OT in scented glands and serum were measured by hormone assays, and their concentrations were both significantly higher in the breeding season than in the non-breeding season. Moreover, bioinformatics analysis showed that the predicted targets of the differentially expressed microRNAs might include the genes encoding OTR, ERK1/2 and c-fos. These findings suggested that OT may regulate the function of muskrat scented glands by the locally expressed receptors.

Oxytocin (OT) is a nonapeptide hormone produced primarily in the neurons of the hypothalamic paraventricular nucleus and supraoptic nucleus and released into systemic circulation by posterior pituitary¹. It is expressed as an inactive precursor, which goes through post-translational progressive hydrolysis facilitated by a series of enzymes before maturing into the active form². OT plays an important role in lactation, parturition, maternal behavior and sexual reproduction in both sexes^{3,4}. Meanwhile, OT is also synthesized in a variety of tissues besides the brain, including the corpus luteum⁵ and the placenta⁶ as well as testis⁷ and epididymis⁸.

The physiological functions of OT is mediated via binding to the widely distributed oxytocin receptor (OTR), which belongs to the rhodopsin-type (class I) G protein (G_{oq11})-coupled receptors (GPCRs) family⁹. In humans, the *OXTR* gene is present in the genome as a single copy at the gene locus 3p25¹⁰. OTR is involved in the regulation of multiple physiological activities in peripheral tissues, such as the female uterine contractions and mammary gland milk ejection, as well as the male penile erection and ejaculation^{10,11}. So far, studies about OTR function in peripheral organs have been mainly focusing on the reproductive system, with few reports on the non-reproductive organs, such as the scented gland.

Upon activation, OTR initiates different intracellular signaling pathways, many of which have not been studied in depth. Among them, the extracellular signal-regulated kinase 1/2 (ERK1/2) is one of the most important pathways^{12–14}. Activated ERK1/2 plays a critical role in delivering the extracellular stimuli from the surface receptor to the nucleus, which then triggers context-dependent biological effects, such as cell proliferation, differentiation, morphology maintenance, cytoskeleton construction and apoptosis^{15,16}. Phosphorylated ERK1/2 (pERK1/2) translocates from the cytoplasm to the nucleus, which in turn activates multiple transcription factors. For example, nuclear pERK1/2 mediates proliferative effects via mechanisms that trigger the induction

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Zeolite modification for adsorptive removal of nitrite from aqueous solutions

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ABSTRACT

Considering the occurrence of nitrite in drinking water sources, this paper investigated the modification of natural zeolite by acid, base, salt, organic surfactant, calcination and ultrasonication for eliminating nitrite from aqueous solutions. The structural and surface properties were analysed by X-ray diffraction (XRD), scanning electron microscopy-energy dispersive X-ray spectroscopy (SEM-EDS) and nitrogen adsorption-desorption isotherm, and were used to explain the nitrite adsorption capacities of the zeolites. The results show that except acid modification, the rest measures did not impose notable influences on the zeolite properties. Modification of zeolite by acids markedly increased the specific surface area and strongly protonated the material, which greatly favored the nitrite adsorption onto the resulting zeolite. The adsorption isotherms were in good agreement with Langmuir-Freundlich models, and indicated an endothermic process. At 25 °C, the nitrite adsorption capacity of the zeolite modified by 0.75 mol L⁻¹ of H₂SO₄ for 12 h (ACMZ) was 54.5 mg N g⁻¹, being over 7-fold higher than that by the raw zeolite. The adsorption of nitrite onto ACMZ followed pseudo-first order kinetics. These facts suggest that the uptake of nitrite by acid modified zeolite was a chemical adsorption in nature.

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Immunoreactivities of IL-1 β and IL-1R in oviduct of Chinese brown frog (*Rana dybowskii*) during pre-hibernation and the breeding period



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ABSTRACT

The Chinese brown frog (*Rana dybowskii*) has one special physiological phenomenon, which is that its oviduct goes through expansion prior to hibernation instead of during the breeding period. In this study, we investigated the localization and expression level of interleukin-1 (IL-1 β) and its functional membrane receptor type I (IL-1R1) proteins in the oviduct of *R. dybowskii* during pre-hibernation and the breeding period. There were significant differences in both oviductal weight and pipe diameter, with values markedly higher in pre-hibernation than in the breeding period. Histologically, epithelium cells, glandular cells and tubule lumen were identified in the oviduct during pre-hibernation and the breeding period, while sizes of both cell types are larger in the pre-hibernation than those of the breeding period. IL-1 β was immunolocalized in the cytoplasm of epithelial and glandular cells in both periods, whereas IL-1R1 was observed in the membrane of epithelial and glandular cells in the breeding period, whereas only in epithelial cells during pre-hibernation. Consistently, the protein levels of IL-1 β and IL-1R1 were higher in pre-hibernation as compared to the breeding period. These results suggested that IL-1 β may play an important autocrine or paracrine role in oviductal cell proliferation and differentiation of *R. dybowskii*.

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1. Introduction

The female reproductive tract exhibits alterations in structure and function during the course of development as well as seasonal reproduction. Oviduct goes through significant morphological, biochemical, and physiological modifications throughout the reproductive cycle (Weng et al., 2009). The oviduct and the fluid contained within provide a distinct microenvironment that influences sperm capacitation, final oocyte maturation, fertilization and early embryo development (Gabler et al., 2001). Oviductal fluid is indispensable to perform its reproductive functions in the oviduct (Lam et al., 2003). Chemical analyses have indicated that oviductal fluid is a complex mixture of constituents derived from the plasma plus some specific proteins formed by the oviductal epithelium (Leese, 1998; Buhi et al., 2000). A wide array of intercellular signals is required for cell-to-cell communication between the oviduct and the embryo and between various cellular components of the oviduct. Among the molecules involved in this communication are assorted cytokines (Robertson et al., 1994; Buhi et al., 2000), including interleukin-1 (IL-1).

Cytokines are soluble mediators of the innate immune response, an ancient immunological defense mechanism presents throughout vertebrates (Vilcek and Le, 1994). IL1 is a cytokine whose importance has been widely documented in vertebrate reproduction (Jantra et al., 2007). IL1 system consists of different components including two bioactive ligands (IL-1 α and IL-1 β) and two receptors: IL1 receptor type I (IL-1R1) and type II (IL-1R2) (Eisenberg et al., 1991; Martin and Falk, 1997; Sims et al., 1993). Only the binding to IL-1R1 results in signal transduction (Roger et al., 2003), whereas IL-1R2 acts as a competitor (Colotta et al., 1993; Dinarello, 2010). Of the IL1 system, IL-1 β and IL-1R1 were relatively more studied (Dinarello, 1997; Dinarello, 2013; Paulesu et al., 2008), and have been detected in the female reproductive tissues of animals ranging from elasmobranchs to mammals (Catani et al., 2003; Paulesu et al., 1995, 2004, 2005, 2010). Viviparity has the mode of retaining the embryo maternal reproductive tissues, while oviparity holds the mode of laying fertilized eggs in the external environment (Paulesu et al., 2008). Recent reports showed expression of IL-1 β and IL-1R1 in the female reproductive tissues of oviparous amphibian species, namely those with external fertilization (Jantra, 2007; 2011), suggesting that the presence of IL1 system in the female genital tract is primarily related to the defense against microorganisms, regardless of the specific reproductive mode (Jantra et al., 2007).

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RESEARCH ARTICLE

In vitro effect of 4-pentylphenol and 3-methyl-4-nitrophenol on murine splenic lymphocyte populations and cytokine/granzyme production

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ABSTRACT

Gasoline exhaust particles (GEP) and diesel exhaust particles (DEP) are considered to be some of the most important air pollutants. Among the many constituents in these pollutant particles, 4-pentylphenol (PP) and 3-methyl-4-nitrophenol (PNMC) are considered important phenolics in GEP and DEP, respectively. The aim of this study was to investigate the effect of *in vitro* exposure to commercially-supplied PP and PNMC on populations of, and production of interleukin (IL)-2, IL-4 and granzyme-B by mouse splenic lymphocytes. After *in vitro* exposure to PP or PNMC for 48 h, splenocyte viability was measured, cell phenotypes, e.g. B-cell (CD19), T-cells (CD3), T-cell subsets (CD4 and CD8), were quantified by flow cytometry and production of IL-2, IL-4 and granzyme-B was assessed via ELISA. The oxidative toxicity of PP and PNMC toward the splenocytes was also evaluated using measures of hydroxyl radical and malondialdehyde production and changes in glutathione peroxidase and superoxide dismutase activities. Results showed that *in vitro* exposure to PP and PNMC inhibited splenic cell parameters in a dose-related manner. Exposure to PP and PNMC decreased splenic T-lymphocyte populations and splenocyte production of cytokines and granzyme B, as well as induced oxidative stress in the splenocytes. The results also showed that the percentages of CD3⁺ T-cells overall and of CD4⁺ and CD8⁺ T-cells therein, among exposed splenocytes, were reduced; neither compound appeared to affect levels of CD19⁺ B-cells. Overall, the suppressive effects of PP were stronger than PNMC. The data here provide support for the proposal that PP/PNMC-induced toxicity in splenocytes may be due at least in part to oxidative damage and that PP and PNMC – as components of GEP and DEP – might significantly impact on splenic T-cell formation/release of cytokines/granzymes *in situ*.

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Introduction

Air pollution has become a major worldwide health issue in part due to increasing vehicle emissions containing gasoline exhaust particles (GEP) and/or diesel exhaust particles (DEP) (Nakamura et al. 2012; Alexis & Carlsten 2014; Claxton 2015). Accumulating evidence has indicated that GEP exposure increases the risk of pulmonary diseases (Sureshkumar et al. 2005) and induces reproductive toxicity (Guo et al. 2004). DEP contain thousands of compounds that can have hazardous effects on human health, causing a variety of diseases, including lung cancer.

4-pentylphenol (PP) derived from GEP matter (Murahashi et al. 2003) has been shown to significantly affect the endocrine and reproductive systems as well as the redox status of Atlantic cod (Satoh et al. 2005; Meier et al. 2007). *In vivo* exposure to polycyclic aromatic hydrocarbons, an important class of GEP,

caused inhibitory effects on T-cell proliferation (Karakaya et al. 2004). However, there have been no reports on immune effects from PP itself so far. Many studies have also implicated DEP in the disruption of the endocrine, reproductive and immune systems (Singh et al. 2005; Hemmingsen et al. 2009; Ema et al. 2013; Müller et al. 2013). *In vitro* DEP exposure causes T-regulatory cell dysfunction and this impairment is believed to lead to uncontrolled inflammation in exposed hosts (Chiang et al. 2009). DEP also has been shown to suppresses T-helper Type 1 immune responses *in vitro* (Sasaki et al. 2009) and suppress cytokine release from alveolar macrophages (Amakawa et al. 2003). Benzo[a]pyrene (BaP, a major aromatic hydrocarbon in DEP) causes reductions in both Thy 1.2⁺ T-cells and CD45R⁺ B-cells in the spleens of treated mice (Holladay & Smith 1995).

Four nitrophenol ingredients, e.g. 4-nitrophenol, 2-methyl-4-nitrophenol, 4-nitro-3-phenylphenol and



The expression of prostaglandin-E2 and its receptor in the oviduct of Chinese brown frog (*Rana dybowskii*)



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ABSTRACT

The Chinese brown frog (*Rana dybowskii*) has one special physiological phenomenon, which is that its oviduct expands prior to hibernation rather than in the breeding period. In this study, we investigated the immunolocalization and expression levels of prostaglandin-E2 (PGE2), cyclooxygenase (COX)-1 and COX-2, as well as one of its receptor subtypes 4 (EP4) in the oviduct of *Rana dybowskii* during the pre-hibernation and breeding period. PGE2, COX-1, COX-2 and EP4 have been observed in glandular and epithelial cells in the breeding period, whereas only in the epithelial cells during the pre-hibernation. Consistently, the protein levels of COX-2 and EP4 were higher in the pre-hibernation as compared to the breeding period, but the diversity of COX-1 was not obvious. In addition, oviductal PGE2 concentration was also significantly higher in the pre-hibernation. These results suggested that prostaglandin-E2 may play an important autocrine or paracrine role in oviductal cell proliferation and differentiation of *Rana dybowskii* during pre-hibernation.

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1. Introduction

The female reproductive tract undergoes physiological and biochemical changes through the seasonal reproductive cycle [1]. To create a suitable environment for egg transport, the oviduct secretes a variety of factors, including hormones, cytokines and growth factors [2]. Also, oviductal fluid is essential for its reproductive functions [2,3]. Hundreds of secretory molecules are originated from serum as transudate or contributed from an epithelium into the oviductal fluid [2]. As a major secretory product of egg transport, prostaglandins (PGs) have been suggested to be an important factor in maintaining oviductal function and egg development [4].

PGs are a family of the lipid-soluble mediators which mediate a wide range of physiological functions and pathological processes [5–8]. PGs synthesis is a multi-step reaction starting from the arachidonic acid (AA). This pathway is also termed cyclooxygenase (COX) pathway, as COX enzymes play a key role of converting AA into PG precursor PGH₂, which is subsequently converted into different PGs by corresponding synthases. The end-product of this

pathway consists of four kinds of PGs and one thromboxane: prostaglandin E2 (PGE2), prostaglandin D2 (PGD2), prostaglandin F2 (PGF2), prostaglandin I2 (PGI2), and thromboxane A2 (TXA2) [9,10]. Among the PGs, PGE2 has been detected in the female reproductive tissues of all vertebrates [11–14]. PGE2 is also found to be one of the major PGs responsible for acute inflammation and inflammatory disorders [7,8,15] through four distinct receptor subtypes, EP1, EP2, EP3 and EP4 [9]. Among the receptors, EP2 is the least abundant with minority expression in ovary or uterus; the distribution of EP1 mRNA is restricted to a few organs such as kidney, lung and gastrointestinal tract [16]. EP3 and EP4 receptors are widely distributed throughout the organs, and their mRNAs are expressed in almost all mouse tissues [16]. In particular, EP4 signaling is closely related to female reproductive function [17]. As the synthase of PGs, cyclooxygenase (COX) consists of two isoforms: COX-1 and COX-2, which are closely related to physiological and pathological functions, respectively [18]. COX-1 is found to be a constitutively expressed enzyme [18], whereas COX-2 is known to be induced by various cytokines, growth factors, hormones, mitogens and tumor promoters [18,19] and is mainly stimulated by oxytocin [20]. COXs have been associated with inflammatory processes, responding to the presence of various cytokines by elevating its own expression [15,19].

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Seasonal changes of androgen receptor, estrogen receptors and aromatase expression in the medial preoptic area of the wild male ground squirrels (*Citellus dauricus* Brandt)

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Abstract

The wild ground squirrel is a typical seasonal breeder. In this study, using RT-PCR, western blot and immunohistochemistry, we investigated the mRNA and protein expressions of androgen receptor (AR), estrogen receptors α and β (ER α and ER β) and aromatase cytochrome P450 (P450arom) in the medial preoptic area (MPOA) of hypothalamus of the wild male ground squirrel during the breeding season (April), the non-breeding season (June) and pre-hibernation (September). AR, ER α , ER β and P450arom protein/mRNA were present in the MPOA of all seasons detected. The immunostaining of AR and ER α showed no significant changes in different periods, whereas ER β and P450arom had higher immunoreactivities during the breeding season and pre-hibernation when compared to those of the non-breeding season. Consistently, both the protein and mRNA levels of P450arom and ER β were higher in the MPOA of pre-hibernation and the breeding season than in the non-breeding season, whereas no significant difference amongst the three periods was observed for AR and ER α levels. These findings suggested that the MPOA of hypothalamus may be a direct target of androgen and estrogen. Androgen may play important regulatory roles through its receptor and/or the aromatized estrogen in the MPOA of hypothalamus of the wild male ground squirrels.

Introduction

Estrogen and androgen hormones play important roles in brain sexual differentiation and sexual behavior of the vertebrates.¹ The effects of androgens are mediated by androgen receptor (AR) to regulate target gene tran-

scription.² In brain, AR is closely related to male reproductive behavior, and especially in wild seasonal breeding animals AR often has emerged in seasonal variation.³ In addition, androgens can be converted to estrogens by aromatase cytochrome P450 (P450arom), which could potentially change the local estrogen levels.⁴ P450arom is found in various tissues in both females and males, thus estrogens are produced not only in gonads but also in extra-gonadal localizations such as bone,⁵ brain,⁶ adipose tissue,⁶ breast,⁷ and skin.⁸ In brain, by regulating the local estrogen levels, P450arom participates in the sexual differentiation⁹ of brain regions involved in the control of gonadotropin secretion and sexual behavior.¹⁰

By binding to its two nuclear estrogen receptors, estrogen receptor alpha (ER α)¹¹ and beta (ER β),¹² estrogen influences a wide range of biological activities, which is not merely restricted to the development of the reproductive and endocrine systems.^{13,14} In brain, ER α and ER β are abundantly expressed in the hypothalamus.¹⁵ The expression levels of ER α and ER β in hypothalamus are closely related to the reproductive status.¹⁶ AR and P450arom are highly expressed in hypothalamus and limbic system in mammals as well.^{15,17,18} In the medial preoptic area (MPOA) of hypothalamus, a reproduction-related area that primarily controls male sexual behavior,^{19,20} co-expression of AR, ERs and P450arom has been found.^{15,17,18} Meanwhile, the expression of P450arom in the MPOA indicates that androgens may as well be converted into estrogens to regulate hypothalamic function and male sexual behavior. The MPOA P450arom expression and its involvement in the regulation of reproductive behavior of many vertebrates has been demonstrated, including mammals,²¹ birds,²² reptiles²³ and fish.²⁴

The wild ground squirrel (*Citellus dauricus* Brandt) is a typical long-day seasonal breeder whose annual life cycle can be roughly divided into the breeding season (April to May), the non-breeding season (June to September) and hibernation (October to the following March). Our previous studies have found that testicular morphology and function of the wild male ground squirrels gone through robust changes throughout the year, which correlate nicely with the expression profiles of AR, ERs and P450arom.²⁵ Interestingly, unlike other known seasonal breeding rodents, the wild ground squirrels in September, namely pre-hibernation, already show a rise in testosterone level from the non-breeding season, accompanied by revitalized spermatogenesis.^{26,27} To understand the potential impact of androgens and estrogens on hypothalamic function, the present study investigated the expressions of AR, ER α , ER β and P450arom in the MPOA of the

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Key words: AR; ER α ; ER β ; ground squirrel; MPOA; P450arom.

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Contributions: FZ, JW, HZ, YJ participation in experiments performing, data analysis, manuscript drafting; FZ, LZ, JW, XS assistance to sample collection and experiments, participation in manuscript revision; YH, ZY, QW, study design and supervision, manuscript revision. All authors read and approved the final version.

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male wild ground squirrels during the breeding season, the non-breeding season and pre-hibernation.

Materials and Methods

Animals

The wild male ground squirrels that were regarded as adults according to their body weights (242-412 g) were captured on September 27th of 2013 in the pre-hibernation period (n=18), on April 20th after emergence from hibernation in the breeding period (n=15) and on June 9th of 2014 in the non-breeding period (n=16) in Hebei Province, China.

All the procedures on animals were carried out in accordance with the Policy on the Care and Use of Animals by the Ethical Committee, Beijing Forestry University and approved by the Department of Agriculture of Hebei province, China (JNZF11/2007). For the brain samples for immunohistochemistry, wild ground squirrels were weighed and deeply anesthetized with sodium pentobarbital solu-

Seasonal expression of androgen receptor, aromatase, and estrogen receptor alpha and beta in the testis of the wild ground squirrel (*Citellus dauricus* Brandt)

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Abstract

The aim of this study was to investigate the seasonal expression of androgen receptor (AR), estrogen receptors α and β (ER α and ER β) and aromatase cytochrome P450 (P450arom) mRNA and protein by real-time PCR and immunohistochemistry in the wild ground squirrel (WGS) testes. Histologically, all types of spermatogenic cells including mature spermatozoa were identified in the breeding season (April), while spermatogonia and primary spermatocytes were observed in the nonbreeding season (June), and spermatogonia, primary spermatocytes and secondary spermatocytes were found in pre-hibernation (September). AR was present in Leydig cells, peritubular myoid cells and Sertoli cells in the breeding season and pre-hibernation with more intense staining in the breeding season, whereas AR was only found in Leydig cells in the nonbreeding season; P450arom was expressed in Leydig cells, Sertoli cells and germ cells during the breeding season, whereas P450arom was found in Leydig cells and Sertoli cells during pre-hibernation, but P450arom was not present in the nonbreeding season; Stronger immunohistochemical signal for ER α was present in Sertoli cells and Leydig cells during the breeding season; ER β was only expressed in Leydig cells of the breeding season. Consistent with the immunohistochemical results, the mean mRNA level of AR, P450arom, ER α and ER β were higher in the testes of the breeding season when compared to pre-hibernation and the nonbreeding season. These results suggested that the seasonal changes in spermatogenesis and testicular recrudescence and regression process in WGSs might be correlated with expression levels of AR, P450arom and ERs, and that estrogen and androgen may play an important autocrine/paracrine role to regulate seasonal testicular function.

Introduction

In mammalian testes, testosterone appears to be responsible for maintaining adequate blood-testis barrier function,¹ inducing meiosis and postmeiotic development of germ cells^{2,3} and inhibition of germ cell apoptosis.⁴ It has been clearly established that the AR is expressed in Sertoli, Leydig and peritubular cells. However, immunodetection of the AR in testicular germ cells is controversial, with reports indicating its detection and absence, although functional AR in germ cells is not essential for spermatogenesis and male fertility.⁵ Testosterone is converted in target cells to estradiol by the enzyme aromatase. Aromatase is a member of the cytochrome P450 superfamily that catalyzes the conversion of androgens (C19), namely testosterone and androstenedione, into estrogens (C18), estradiol and estrone, respectively. The presence of P450arom in the testes has been reported in numerous species, including American black bears,⁶ raccoon dogs,⁷ Shiba goats,⁸ brown bears,⁹ Göttingen miniature pigs,¹⁰ bank voles,¹¹ rats,¹² mice,¹³ ground squirrels¹⁴ and muskrats.¹⁵ These evidences indicated that estrogens act on the initiation and maintenance of spermatogenesis and on germinal stem cell division and survival in a paracrine/autocrine manner(s).

Estrogen action is displayed by means of two different estrogen receptors (ERs), estrogen receptor-alpha (ER α) and estrogen receptor-beta (ER β), localized in the different testicular cells types. The localization of ERs in testicular cells is not only species-specific but also varies depending on the type of receptor and the developmental stage of the germ cell.¹⁶ In most species analyzed, such as human, rat, cat and dog, ER α and ER β co-localize in spermatogonia, spermatocytes and spermatids as well as in Sertoli, Leydig, and peritubular myoid cells and these locations appeared to change with age in some reports.^{17,18} In other species, such as the boar, ER α and ER β localize separately to spermatogonia/primary spermatocytes and Sertoli cells, respectively.¹⁹ Thus, ER α and ER β , and their localization and function in testicular cells vary depending on the species, cellular developmental stage and type of receptor.

The wild ground squirrel (*Citellus dauricus* Brandt, WGS) is a typical seasonal breeder which has a strict and extremely compressed breeding period from April to May, a long period of sexual dormancy from June to the following March, and a 6-month hibernation (from October to March).^{20,21} The testis and epididymis of this species exhibits a distinct seasonal morphology changes from the breeding season to the nonbreeding season.^{20,23} Our published results have indicated that

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Key words: Wild ground squirrels, testes, seasonal expression, androgen and estrogen receptors, aromatase cytochrome P450, *Citellus dauricus* Brandt.

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Contributions: QL, FZ, SZ, experiments performing, data analysis, manuscript drafting; HZ, XS, samples collection assistance, experiments performing, manuscript revision; YH, ZY, QW study design and supervision, manuscript revision. All authors read and approved the final version.

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immunoreactivity of P450c17 and P450arom in testicular tissues was accompanied by changes of testicular activity during the breeding and nonbreeding seasons.¹⁴ In this study, we investigated the immunohistochemical localization of AR, P450arom, ER α and ER β as well as their mRNA expression in the breeding, nonbreeding seasons and pre-hibernation, to gain insight of the relation between steroid hormones and testicular function throughout the reproductive cycle of WGS.

Materials and Methods

Animals

The wild male ground squirrels were captured by box traps in September 24 (n=12) of 2012 and in April 13 (n=15) and June 27 (n=10) of 2013 in Hebei Province, China. WGSs were thought to be adult based on their body weights (242-412 g). All procedures involving animals were carried out in accordance with the Policy on the Care and Use of

Research Article

Expression of P450arom and Estrogen Receptor Alpha in the Oviduct of Chinese Brown Frog (*Rana dybowskii*) during Prehibernation

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One specific physiological phenomenon of Chinese brown frog (*Rana dybowskii*) is that its oviduct expands prior to hibernation instead of expanding during the breeding period. In this study, we investigated the expression of P450arom and estrogen receptors α and β (ER α and ER β) in the oviduct of *Rana dybowskii* during the breeding period and prehibernation. The results of the present study showed that there were significant differences in both oviductal weight and size with values markedly higher in prehibernation than in the breeding period. P450arom was observed in stromal tissue in both the breeding period and prehibernation. ER α was expressed in stromal tissue and epithelial cells in both periods, whereas ER β could not be detected. The mean protein and mRNA levels of P450arom and ER α were significantly higher in prehibernation as compared to the breeding period. Besides, oviductal content of 17 β -estradiol was also higher in prehibernation than in the breeding period. These results suggested that estrogen may play autocrine/paracrine roles mediated by ER α in regulating the oviductal hypertrophy during prehibernation.

1. Introduction

The female reproductive tract exhibits alterations in structure and function developmentally as well as with seasonal reproductive activity. Oviducts respond to hormonal cues from ovaries with tissue proliferation and differentiation in preparation of transporting and fostering gametes [1]. These responses produce oviductal microenvironments conducive to reproductive success [2]. Oviduct, used in the comparative sense meaning structures derived from the embryonic Müllerian duct, responds to endocrine signals through changes in gene expression, protein synthesis, and morphology with sexual maturation and reproductive activity [3, 4]. Sex steroid hormone receptors in the oviduct receive endocrine signals and regulate growth, differentiation, and protein secretion. Ligand binding of oviductal sex steroid hormone receptors results in a positive feedback that elevates expression levels of sex steroid hormone receptors, priming the tissue to receive further signals in general [5].

Aromatase is a member of the cytochrome P450 superfamily that catalyzes the conversion of androgens (C19), namely, testosterone and androstenedione, into estrogens (C18), estradiol, and estrone, respectively. The enzyme is active in various tissues in both females and males, which means that estrogens are produced not only in gonads but also in extragonadal localizations such as brain, adipose tissue, breast, skin, and bone [6]. Estrogen actions are mediated by two distinct estrogen receptors, estrogen receptor alpha (ER α) and estrogen receptor beta (ER β), both of which regulate the expression of a variety of different genes [7, 8]. In many tissues such as ovary, placenta, brain, and testis, the key genes of estrogen signaling and biosynthesis, *ESR1* (ER α) and *ESR2* (ER β), and *Cyp19* that encodes the enzyme P450arom are coexpressed, suggesting that estrogen acts locally as an autocrine or paracrine factor [9–11]. Disruption of these genes demonstrated that estrogen signaling is not only important for the development and differentiation in the reproductive system, but also in nonreproductive systems [12–16].

Testicular expression of NGF, TrkA and p75 during seasonal spermatogenesis of the wild ground squirrel (*Citellus dauricus* Brandt)

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Abstract

The nerve growth factor (NGF) not only has an essential effect on the nervous system, but also plays an important role in a variety of non-neuronal systems, such as the reproductive system. The aim of this study was to compare the quality and quantity in expression of NGF and its receptors (TrkA and p75) in testes of the wild ground squirrel during the breeding and nonbreeding seasons. Immunolocalization for NGF was detected mainly in Leydig cells and Sertoli cells in testes of the breeding and nonbreeding seasons. The immunoreactivity of TrkA was highest in the elongated spermatids, whereas p75 in spermatogonia and spermatocytes in testes of the breeding season. In the nonbreeding season testes, TrkA showed positive immunostainings in Leydig cells, spermatogonia and primary spermatocytes, while p75 showed positive signals in spermatogonia and primary spermatocytes. Consistent with the immunohistochemical results, the mean mRNA and protein level of NGF and TrkA were higher in the testes of the breeding season than in non-breeding season, and then decreased to a relatively low level in the nonbreeding season. In addition, the concentration of plasma gonadotropins and testosterone were assayed by radioimmunoassay (RIA), and the results showed a significant difference between the breeding and nonbreeding seasons with higher concentrations in breeding season. In conclusion, these results of this study provide the first evidence on the potential involvement of NGF and its receptor, TrkA and p75 in the seasonal spermatogenesis and testicular function change of the wild ground squirrel.

Introduction

The nerve growth factor (NGF) is one kind of neurotrophins (NTs), which are mainly involved in the survival and development of discrete neuronal populations in the central

and peripheral nervous system.¹ The biological function of NGF requires two receptors p75 and TrkA to participate in. These two receptors have many specialties in different aspects. P75 is the low affinity receptor for NGF, which belongs to the tumor necrosis factor receptor superfamily.² TrkA is the high affinity receptor for NGF, which belongs to the tyrosine protein kinase receptor family.³ Accumulating studies to date have suggested that the function of NGF is not only limited to the nervous system, but also extended to the non-nervous systems, including the male and female reproductive systems.^{4,6} In recent years, the studies of NGF and its receptors in reproductive system largely focus on the immunolocalization and expression of NGF system in reproductive organs,^{7,8} the functional role of NGF system in the follicular development^{9,10} and in spermatogenesis.¹¹⁻¹² The studied species range from experimental models, such as rat,^{7,11} mouse¹² and golden hamster,^{13,14} to primate¹⁵ and human.^{16,17} Our previous results indicated that NGF and its receptors may be involved in the regulation of seasonal changes in the ovarian and uterine functions of wild female ground squirrels.¹⁸⁻²⁰ However so far, whether NGF and its receptors also are present or not in the testes of wild rodents and their possible roles in seasonal spermatogenesis remain utterly unknown.

Reproductive strategies of seasonal breeders are adapted to annual changes of the environment, which minimize the animals' energetic efforts for reproduction. The wild ground squirrel (*Citellus dauricus* Brandt) is a typical seasonal breeder, with a short breeding season lasting from April to May and a long period of sexual dormancy from June to the following March.^{21,22} With this model, our laboratory has recently explored the coordinated roles of steroid hormones and local growth factors in the seasonal regulation of the functions of the reproductive organs, such as testis, epididymis, ovary and uterus.^{18-21,23-30} Yet, there are still many limitations in the understanding of the basic mechanisms underlying seasonal changes in spermatogenesis and testicular activity. Thus, the aim of the present study was to determine the regulated expression of NGF and its receptors in testes during the breeding and nonbreeding seasons, and to know the primary role of NGF in seasonal spermatogenesis in the wild ground squirrel.

Materials and Methods

Animals and sample collection

Thirty-eight wild male ground squirrels (23 in breeding season and 15 in non-breeding season), which were thought to be adult based

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Key words: NGF; p75; seasonal spermatogenesis; TrkA; wild ground squirrel.

Conflict of interest: the authors declare no conflict of interest.

Contributions: HZ, YW, JZ, LW, experiments performing, data analysis, manuscript drafting; HZ, QL, XS, assisting in sample collection and all experiments, and in manuscript revision; YH, ZY, QW, study design and supervision, and manuscript revision. All authors read and approved the final version.

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on their body weights (242–412 g), were captured from April to September of 2011 in Hebei Province, China. The animals were decapitated after anesthesia using diethyl ether. Plasma samples were immediately collected and stored at -20°C. The testes were excised from each body after necropsy. Each obtained testis was cut into 2 portions: one portion was fixed in 4% paraformaldehyde in 0.05 M PBS, pH 7.4 for immunohistochemical staining, and the second portion was immediately stored at -80°C until used for Western blot detection and reverse transcription PCR. All the procedures on animals were carried out in accordance with the Policy on the Care and Use of Animals by the Ethical Committee, Beijing Forestry University and approved by the Department of Agriculture of Hebei province, PR China (JNZF11/2007).

Antibodies

Rabbit polyclonal primary antibodies against NGF (0.4 µg/mL, M-20), TrkA (2 µg/mL, 763) and p75 (2 µg/mL, H-92) (Santa Cruz Biotechnology, Santa Cruz, CA, USA) were used for the immunohistochemistry and

SCIENTIFIC REPORTS

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Seasonal Expression of Prolactin Receptor in the Scented Gland of Male Muskrat (*Ondatra zibethicus*)

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Han Cao, Liang Wang, Shuo Zhang, Lu Lu, Xia Sheng, Yingying Han, Zhengrong Yuan & Qiang Weng

Prolactin (PRL) has numerous actions in mammalian biological systems including mammary development and biological processes. The aim of this study was to investigate the seasonal changes of prolactin receptor (PRLR) expression in the scented gland of muskrat during the breeding and nonbreeding seasons. Histologically, glandular cells, interstitial cells and excretory tubules were identified in the scented glands in both seasons, whereas epithelial cells were sparse in the nonbreeding season. PRLR was observed in glandular cells of scented glands during the breeding and nonbreeding seasons with stronger immunostaining during the breeding season. Consistent with the immunohistochemical results, both the mean of protein and mRNA levels of PRLR were higher in the scented glands of the breeding season, and relatively lower level in the nonbreeding season. In addition, differential seasonal changes were also detected in the expression profile of microRNAs (miRNAs) in the scented gland of muskrat. Besides, plasma PRL concentration was remarkably higher in the breeding season than that in the nonbreeding season. These results suggested that muskrat scented gland was the direct target organ of PRL, and stronger expression of PRLR in scented glands during the breeding season indicated that PRL may directly regulate scented glandular function of the muskrats.

Prolactin (PRL) is mainly synthesized and secreted by the lactotroph cells of the pituitary¹. Native PRL is secreted as a protein of approximately 23 kDa, cleavage of the full-length product by cathepsin D results in 16 kDa N-terminal PRL². More than 300 separate actions have been reported in various vertebrates, including effects on water and salt balance, growth and development, endocrinology and metabolism, brain and behavior, reproduction, and immune regulation and protection^{3–6}. Circulating PRL is also detected in males, although it is present at lower levels than in females. In males, PRL is known to influence reproductive functions but the significance and mechanisms of PRL action in male organs and tissues are poorly understood.

PRL mediates its physiologic functions through the engagement of prolactin receptor (PRLR), a member of the cytokine receptor superfamily. PRLR is a transmembrane protein comprising an extracellular domain, a transmembrane domain and an intracellular domain. Multiple isoforms of membrane-bound PRLR resulting from alternative splicing of the primary transcript have been identified³. These different PRLR isoforms (short and long) differ in the length and composition of their cytoplasmic tail. Most of them are similar in their extracellular domain, but differ in the intracellular part⁷. Thus, multiple isoforms potentially can activate distinct intracellular signaling events. Generally, the most abundant PRLR is the long isoform, whereas other intermediate and short forms also exist. The long receptor isoform was studied in detail, and specific functions of the other PRLR isoforms are relatively less investigated⁶. Upon ligand binding and sequential dimerisation, it activates multiple signaling systems including JAK2/STAT5, STAT3, MAPK p44/42 and PI3K pathways^{3,7–10}. PRLR expression has been reported in a wide

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Predictive assessment in pharmacogenetics of *XRCC1* gene on clinical outcomes of advanced lung cancer patients treated with platinum-based chemotherapy

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Published data have shown inconsistent results about the pharmacogenetics of *XRCC1* gene on clinical outcomes of advanced lung cancer patients treated with platinum-based chemotherapy. This meta-analysis aimed to summarize published findings and provide more reliable association. A total of 53 eligible studies including 7433 patients were included. Patients bearing the favorable TrpTrp and TrpArg genotypes of Arg194Trp were more likely to better response rates to platinum-based chemotherapy compared to those with the unfavorable ArgArg genotype (TrpTrp+TrpArg vs. ArgArg: odds ratio (OR)=2.02, 95% CI, 1.66–2.45). The GlnGln and GlnArg genotypes of Arg399Gln were significantly associated with the poorer response rates compared to those with the ArgArg genotype (GlnGln +GlnArg vs. ArgArg: OR=0.68, 95% CI, 0.54–0.86). The GlnGln genotype might be more closely associated with shorter survival time and higher risks of death for patients (GlnGln vs. ArgArg: hazard ratio (HR)=1.14, 95% CI, 0.75–1.75). Our cumulative meta-analyses indicated a distinct apparent trend toward a better response rate for Arg194Trp, but a poorer response rate in Arg399Gln. These findings indicate a predictive role of *XRCC1* polymorphisms in clinical outcomes. The use of *XRCC1* polymorphisms as predictive factor of clinical outcomes in personalized chemotherapy treatment requires further verification from large well-designed pharmacogenetics studies.

Lung cancer, a major serious public health problem, is one of the most common malignant tumors and has become the leading cause of cancer-related deaths in the world¹, with more than one million deaths from this disease annually^{2,3}. There are two main types of lung cancer: non-small cell lung cancer (NSCLC) and small cell lung cancer (SCLC), of which NSCLC accounts for approximately 80%–85% and nearly 70% of patients present with the locally advanced stages (such as stage IIIB or IV) or metastatic disease at the time of diagnosis, losing the opportunity of surgical resection and making curative surgery impossible^{3–9}. Although intensive effort has been made to improve the efficacy of lung cancer diagnosis and therapy in the last decades, the overall five-year survival rate still remains only about 15% and even lower in China^{1,2}.

The treatment of lung cancer patients is surgery for early stages, whereas chemotherapy regimen is the main conventional therapeutic method for locally advanced stages and metastatic cancers. Currently, the platinum-based chemotherapy is one of the most extensively accepted and used treatments in advanced lung cancer patients, which has been shown to improve overall survival (OS)^{10–12}. However, individual

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RESEARCH ARTICLE

Open Access



Isolation of a novel bio-peptide from walnut residual protein inducing apoptosis and autophagy on cancer cells

Sihui Ma^{1,2}, Di Huang^{1,2}, Mengxin Zhai^{1,2}, Lubing Yang¹, Sen Peng¹, Changxu Chen¹, Xiaoru Feng¹, Qiang Weng¹, Bolin Zhang^{1,2} and Meiyu Xu^{1,2*}

Abstract

Background: Walnut is unique because they have a perfect balance of n-6 and n-3 polyunsaturated fatty acids. The increasing market demand of walnut lipids results in the large amount of the oil extraction residue. The walnut residue is rich in nutritional proteins, and the uneconomic use of the by-product discouraged the development of walnut industry. Anticancer peptides have recently received attention as alternative chemotherapeutic agents that overcome the limits of current drugs. The aim of this study was to investigate whether anticancer bioactive peptide is contained in walnut.

Methods: Walnut residual protein was hydrolyzed separately by five different proteases. The sequential purification of the hydrolysates was carried out by ultra-filtration, gel filtration chromatography and RP-HPLC to obtain a cancer cell growth inhibitory peptide. Cell cycle distribution, Annexin V-FITC/PI double staining, TUNEL assay, western blot and immunofluorescence for LC3-II assay were used to detect apoptosis and autophagy on cells. Cytokine production was measured by ELISA kits, macrophage phagocytosis was measured by neutral red uptake assay, nitric oxide production was measured by Griess reagent.

Results: The hydrolysates of walnut residual protein produced by papain under the optimal conditions (5 % substrate concentration and an enzyme-substrate ratio of 10 % at temperature 60 °C for 3 h), showed significant growth inhibitory activity on MCF-7. The amino acid sequence of the purified peptide was identified as CTLEW with a molecular weight of 651.2795 Da. It is a novel bio-peptide with an amphiphilic structure. CTLEW induced both apoptosis and autophagy on MCF-7 cells, inhibited the cancer cells growth of Caco-2 and HeLa significantly, but did not show any cytotoxic activity against non-cancerous IEC-6 cells. Moreover, the bio-peptide enhanced proliferation and IL-2 secretion of spleen lymphocytes, promoted phagocytosis and NO production of macrophages.

Conclusion: These results suggested that a novel bio-peptide, CTLEW inducing apoptosis and autophagy on MCF-7 cells can be released from walnut residual protein through papain hydrolyzing under the certain condition. The bio-peptide shows selective inhibition towards cancer cells growth and immunomodulatory activity.

Keywords: Walnut residual protein, Bio-peptide, Apoptosis, Autophagy, Cancer cells

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Iron(III) reduction-induced phosphate precipitation during anaerobic digestion of waste activated sludge



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ABSTRACT

Iron(III) reduction-induced phosphate precipitation during anaerobic digestion of waste activated sludge from a wastewater treatment plant was investigated for phosphorus removal and possible recovery. The digestion of sludge with Fe(III) amendments was performed in batch assays using hematite and ferrihydrite as the iron sources. Aqueous phosphate concentrations as high as 316 mg/L (as P) were observed in the Fe(III)-free controls after 30 d of digestion, demonstrating waste activated sludge to be an excellent material for phosphorus recovery. Ferrihydrite-Fe(III) was effectively reduced during the digestion, whereas the reduction of hematite-Fe(III) was insignificant. Phosphate removal in the Fe(III) amended sludge was closely related to the extent of Fe(III) reduction. Compared with the controls, 53% of aqueous phosphate in the ferrihydrite-amended sludge was removed as Fe(III) reduction occurred. The analyses of the phosphate and Fe(II) flows indicate that the removed aqueous phosphate was generally via Fe(II) bounded precipitates.

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RESEARCH

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Seasonal changes in expression of nerve growth factor and its receptors TrkA and p75 in the ovary of wild ground squirrel (*Citellus dauricus* Brandt)

Ben Li¹, Xia Sheng¹, Lihong Bao², Shiyang Huang¹, Qinglin Li¹, Yuning Liu¹, Yingying Han¹, Gen Watanabe³, Kazuyoshi Taya³ and Qiang Weng^{1*}

Abstract

The aim of this study was to investigate the presence of nerve growth factor (NGF) and its receptors tyrosine kinase A (TrkA) and p75 in the ovaries of the wild ground squirrels during the breeding and nonbreeding seasons. In the breeding period, NGF, TrkA and p75 were immunolocalized in granulosa cells, thecal cells, interstitial cells and luteal cells whereas in the nonbreeding period, both of them were detected only in granulosa cells, thecal cells and interstitial cells. Stronger immunostaining of NGF, TrkA and p75 were observed in granulosa cells, thecal cells and interstitial cells in the breeding season compared to the nonbreeding season. Corresponding for the immunohistochemical results, immunoreactivities of NGF and its two receptors were greater in the ovaries of the breeding season then decreased to a relatively low level in the nonbreeding season. The mean mRNA levels of NGF, TrkA and p75 were significantly higher in the breeding season than in the nonbreeding season. In addition, plasma gonadotropins, estradiol-17 β and progesterone concentrations were significantly higher in the breeding season than in the nonbreeding season, suggesting that the expression patterns of NGF, and TrkA and p75 were correlated with changes in plasma gonadotropins, estradiol-17 β and progesterone concentrations. These results indicated that NGF and its receptors, TrkA and p75 may be involved in the regulation of seasonal changes in the ovarian functions of the wild ground squirrel.

Keywords: Ground squirrel, NGF, Ovary, p75, TrkA

Introduction

The nerve growth factor (NGF) belongs to a family of related proteins required for the survival, maintenance, and development of discrete neuronal populations in the central and peripheral nervous systems [1-3]. It is also believed that NGF not only has an effect on the nervous system, but also plays an important role in a variety of non-neuronal system, such as immune, cardiovascular and endocrine systems [4-6]. The effect of NGF has been shown to be mediated through specific membrane receptors high-affinity tyrosine kinase A (TrkA), which is responsible for its biological activities [7,8]. Furthermore, the effect of NGF is also mediated via low affinity receptor p75 that also functions as other neurotrophins' receptor [9]. When p75 and TrkA

receptors are co-expressed, p75 increases the sensitivity of the TrkA receptor and its signaling efficiency [10,11].

It is now well known that NGF and its receptors are expressed in the mammalian ovary, including women [12-14], rats [14,15], golden hamsters [16-18], cows [19], sheep [20] and Shiba goats [21]. More and more evidences have indicated that NGF signaling plays a critical role in the development of mammalian ovary, oogenesis and folliculogenesis [22-24], in an auto- and/or paracrine manner. In our previous studies of the golden hamsters, NGF and its two receptors TrkA and p75 were present in ovaries, oviducts and uteri, demonstrating that NGF, TrkA and p75 have important autocrine and paracrine regulatory roles in the function of reproductive organs during the estrous cycle [16,25,26]. Data to support this concept in wild animals, however, is very limited. To study the basic mechanisms of NGF regulation of ovarian function during the breeding and nonbreeding seasons within the annual

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Immunolocalization of NGF and its receptors in ovarian surface epithelium of the wild ground squirrel during the breeding and nonbreeding seasons

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Abstract

The ovarian surface epithelium (OSE) plays an important role in normal ovarian physiology. During each reproductive cycle, the OSE takes part in the cyclical ovulatory ruptures and repair. The aim of this study was to investigate the immunolocalization of nerve growth factor (NGF) and its receptors, tyrosine kinase A (TrkA) and p75, in the OSE cells of the wild ground squirrels during the breeding and nonbreeding seasons. There were marked variations in ovarian weight and size between the breeding and the nonbreeding seasons. Histologically, cuboidal cells and squamous cells were identified in the OSE of both seasons. Yet, stronger immunostaining of NGF, TrkA and p75 were observed in cuboidal cells and squamous cells in the breeding season as compared to the nonbreeding season. In addition, plasma gonadotropin concentrations were higher in the breeding season than in the nonbreeding season, suggesting that the expression patterns of NGF, TrkA and p75 in the OSE were correlated with changes in plasma gonadotropins. These findings suggested that NGF and its receptor TrkA and p75 may be involved in the regulation of seasonal changes in the OSE of wild ground squirrel.

Introduction

The ovarian surface epithelium (OSE) is a single mesothelial layer of cuboidal and squamous cells, which is derived from the coelomic layer along with the lining of the peritoneal cavity.¹ Cell proliferation occurs at the epithelial surface above the developing preovulatory

follicle to accommodate the increase in follicular size, and again after ovulation, to repair the surface.² Electron microscopy of normal human ovaries reveals that the epithelium consists of two distinct cell types, cuboidal type A cells and squamous type B cells, each occupying discrete zones in the epithelium. These two cell types are observed in both mouse^{3,4} and human OSE.⁵ Cuboidal cells may divide and migrate to cover the wound site caused by ovulation; and squamous cells would be expected to increase as the number of ovulations increased.^{4,5} Human OSE appears to differ from mouse OSE in that human type B cells are associated with past ovulation episodes. During the reproductive life of a woman, invagination of the surface epithelium into the cortical stroma gives rise to epithelial crypts and inclusion cysts.⁶ These structures are considered preneoplastic and may facilitate malignant transformation of entrapped OSE by generating a microenvironment enriched with growth factors, cytokines and hormones.^{7,8} The OSE cells also secrete chymotrypsin-like and elastase-like peptidases, metalloproteases and plasminogen activator inhibitor, which may facilitate ovulatory rupture *in vivo*.⁹ Notably, the OSE expresses integrins that bind to laminin, collagens, fibronectin and vitronectin, and these interactions may play a role in the adhesion, spreading, proliferation and matrix reconstitution of normal OSE following post-ovulatory ruptures. As the ovary is a rich source of multiple hormones, and normal OSE and ovarian carcinomas secrete and have receptors for hormones, growth factors and cytokines, these factors are strong candidates to regulate normal OSE physiology and the transformation and progression of ovarian cancers.⁶

Nerve growth factor (NGF) is one kind of neurotrophins (NTs) which are mainly involved in the survival and development of discrete neuronal populations in the central and peripheral nervous system.¹⁰ The biological function of NGF requires two receptors: p75 and tyrosine kinase A (TrkA). P75 is the low affinity receptor for NGF and belongs to the tumor necrosis factor receptor superfamily.¹¹ TrkA is the high affinity receptor for NGF and belongs to the tyrosine protein kinase receptor family.¹² Accumulating studies to date suggest that the function of NGF is not only limited to the nervous system, but also extends to non-nervous systems, including the male and female reproductive systems.¹³⁻¹⁵ Evidence indicates that NGF and its receptors play a critical role in development of the mammalian ovary, oogenesis and folliculogenesis.^{16,21} However, the expressions of NGF and its receptors TrkA and p75 in the OSE of a seasonal breeder are unclear.

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Keywords: ground squirrel, NGF, OSE, p75, TrkA.

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Contributions: QW, experiments conceiving and design; LB, QL, XS, experiments performing; YL, YH, data analysis; LB, QW, manuscript design and writing. All authors approved the final version.

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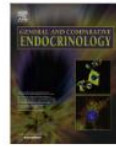
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The wild ground squirrel (*Citellus dauricus* Brandt) is a typical seasonal breeder which have a strict and extremely compressed breeding period (for females, it consists of estrous period and pregnancy) from April to May and a long period of sexual dormancy from June to the following March including a 6-month hibernation period.²² The wild female ground squirrel exhibits estrus immediately after emergence from hibernation in spring, and has a gestation period of 28 days.^{23,24} Although many observations on the regulatory roles of NGF and its receptors on ovarian function exist, the mechanisms of ovarian function and especially its role in the seasonal ovarian function changes, such as OSE cell survival and differentiation are not well understood. Our previous study found that immunoreactivities of NGF, TrkA and p75 in the ovary were high in the breeding season and then decreased in the nonbreeding season, suggesting that they may be involved in regulation of seasonal ovarian function changes in the wild ground squirrel.²⁵ To test that hypothesis, we evaluated the morphology of OSE and the immunolocalization of NGF and its receptors TrkA and p75 in OSE of the wild ground squirrel during breeding and nonbreeding periods and thereby gained a better understanding of the relationship between NGF system and OSE function changes in the wild ground squirrel.



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journal homepage: www.elsevier.com/locate/ygcenSeasonal expression of androgen receptor in scented gland of muskrat (*Ondatra zibethicus*)

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ABSTRACT

Muskrat is a seasonal breeder, males of which secrete musk from paired perineal scented glands found beneath the skin at the ventral base of the tail for attracting female during the breeding season. The aim of this study was to investigate the seasonal changes of expression of androgen receptor (AR) in the scented gland of muskrat during the breeding and nonbreeding seasons. Histologically, glandular cells, interstitial cells and excretory tubules were identified in scented glands in both seasons, whereas epithelial cells were sparse in the nonbreeding season. AR was observed in glandular cells of scented glands during the breeding and nonbreeding seasons with stronger immunostaining during the breeding season compared to the nonbreeding season. Consistent with the immunohistochemical results, AR protein level was higher in the scented glands of the breeding season, and then decreased to a relatively low level in the nonbreeding season. The mean mRNA level of *Ar* was significantly higher in the breeding season than in the nonbreeding season. In addition, plasma gonadotropins and testosterone concentrations were remarkably higher in the breeding season than those in the nonbreeding season. These results suggested that muskrat scented gland was the direct target organ of androgen, and stronger expression of AR in scented glands during the breeding season suggested that androgens may directly influence scented glandular function of the muskrats and also courtship behavior as we inferred.

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1. Introduction

Androgens mediate a wide range of developmental and physiological responses and are especially crucial in male sexual differentiation, pubertal sexual maturation, the maintenance of spermatogenesis and male gonadotropin regulation (Keller et al., 1996; McLachlan et al., 1996; Roy et al., 1999). As one of the most potent and important natural androgens, testosterone, which is responsible for inducing meiosis and inhibiting apoptosis in the germ cell, is mainly produced by Leydig cells of testis and binds

to the androgen receptor (AR) modulating gene transcription in various cells (Welsh et al., 2009). Androgens also regulate sexually dimorphic characteristics and processes in extragonadal sites, such as growth of facial, body and pubic hair, enlargement of vocal chords, development of muscle strength, and masculine behavior (Mostaghel et al., 2012; Quigley et al., 1995). It is widely accepted that ablation of the androgenic gland at a certain stage of development sexual differentiation in crustaceans could result in the loss of male-like behavior, demasculinization and physiological shifts and even sex reversal to female (Affalo et al., 2006; Barki et al., 2006). In mammals, testosterone concentration may be associated with both current reproductive activity and paternal behavior such as incubation, infant carrying and provisioning (Nunes et al., 2001; Onyango et al., 2013; Stoehr and Hill, 2000).

The effects of androgens are mediated through AR, a 110-kDa ligand-inducible nuclear receptor with domains for androgen binding, nuclear localization, dimerization, DNA binding, and transactivation (Quigley et al., 1995; Zhou et al., 1994). AR is expressed not only in male and female reproductive organs, but

Abbreviations: AR, androgen receptor; CNS, central nervous system; DHT, 5 α -dihydrotestosterone; dNTP, deoxy-ribonucleotide triphosphate; EB, ethidium bromide; FSH, follicle stimulating hormone; GSI, gonadosomatic index; HE, hematoxylin-eosin; HVC, high vocal center; LH, luteinizing hormone; POA, preoptic area; RIA, radioimmunoassay; RT-PCR, reverse transcription-polymerase chain reaction.

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Immunoreactivities of PPAR γ 2, leptin and leptin receptor in oviduct of Chinese brown frog during breeding period and pre-hibernation

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Abstract

The Chinese brown frog (*Rana dybowskii*) is a special amphibian with one unique physiological phenomenon, which is that its oviduct expands prior to hibernation, instead of during the breeding period. In this study, we investigate the localization and expression level of PPAR γ 2, leptin and leptin receptor proteins in oviduct of *Rana dybowskii* during breeding period and pre-hibernation. There were significant variations in oviductal weight and size, with values much lower in the breeding period than in pre-hibernation. PPAR γ 2 was observed in stromal and epithelial cells in both periods. Leptin was immunolocalized in epithelial cells in both periods, whereas leptin receptor was detected only in stromal cells. Consistently, the protein levels of PPAR γ 2, leptin and leptin receptor were higher in pre-hibernation as compared to the breeding period. These results suggested that oviduct was the target organ of leptin, which may play an important paracrine role in regulating the oviductal hypertrophy during pre-hibernation.

Introduction

Oviduct is a dynamic organ that goes through significant morphological, biochemical, and physiological modifications throughout the reproductive cycle. It is not only a passive channel for gamete and embryo transport, but also encompasses a highly active secretory organ involved in several critical reproductive events, such as estrous cycle and ovulation.¹ Oviduct is regulated by a wide variety of factors, including locally synthesized molecules working in an collaborative, synergistic, or antagonistic manner to regulate different oviductal functions, such as gene expression, protein synthesis, morphology with sexual maturation and reproductive activity.² Oviductal fluid is essential for the oviduct to perform its reproductive functions,³ which

offers an optimal microenvironment for biological functions that contribute to sperm capacitation, final oocyte maturation, fertilization and early embryo development.^{4,5} Oviductal fluid is consisted of hundreds of macromolecules which can be secreted from oviduct epithelium or serum transudate.^{6,7}

The Chinese brown frog (*Rana dybowskii*) is a unique amphibian species in northeastern China. It is a seasonal breeder with the habit of seasonal migration between mountain and wetland. *Rana dybowskii* is a famous economic species which has been used widely in the Traditional Chinese Medicine.⁸ The hibernation for *Rana dybowskii* takes place from October to February, which is followed by the breeding period ranging from February to June depending on the latitude and altitude. Interestingly, one unique physiological phenomenon of *Rana dybowskii* is that its oviduct expands during pre-hibernation but not during the breeding period. Besides, dried oviduct of the female *Rana dybowskii*, Oviductus *Ranae*, is one of the best-known and highly valued oriental foods and Chinese crude drugs, which is recorded in the Pharmacopoeia of the People's Republic of China.⁹ Traditional Chinese medicine holds that Oviductus *Ranae* can nourish the yin, moisten the lung and replenish the kidney essence.¹⁰ Meanwhile, Oviductus *Ranae* is mainly composed of proteins and lipid, which are up to 50% or more.¹¹

Vast published literature has been made in our understanding of adipocyte differentiation and adipocyte-specific gene expression. Peroxisome proliferator-activated receptor (PPAR) γ is a ligand-activated transcription factor and a member of the nuclear hormone receptor superfamily. It has been proven to be involved in directing expression of fat-specific genes and in activating the program of adipocyte differentiation.¹² PPAR γ can also induce trans-differentiation from fibroblasts and myoblasts to adipocytes.^{13,14} Besides, PPAR γ has two main isoforms: PPAR γ 1 and PPAR γ 2.¹⁵ Adipose tissue is the most abundant site for both isoforms.¹⁶ The difference is that PPAR γ 2 is restricted in fat,¹⁷ whereas PPAR γ 1 is predominant in other tissues.¹⁸ Adipose tissue contributes to the regulation of energy homeostasis, secreting a large number of active adipokines.¹⁹ Leptin is one of the best-characterized adipokines, which affect carbohydrate and lipid metabolism and energy.²⁰ Leptin is a 16-kDa polypeptide hormone coded by the *obese (ob)* gene.²¹ In addition to regulating energy homeostasis, leptin is also a vital hormone/cytokine for a number of diverse physiological processes such as reproduction, angiogenesis, inflammation, and immune function.²² The leptin receptor (Ob-R, also known as LEP-R, LR) was first isolated from mouse choroid plexus by expression cloning and is a member of the interleukin-6 receptor family of class I

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Key words: Leptin, leptin receptor, oviduct, PPAR γ 2, *Rana dybowskii*.

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Contributions: YL, JW experiments performing, data analysis, manuscript drafting; SH, YH, YS, XS sample collection and experiments assistance, participation in manuscript revising; MX, QW, study design and supervision, manuscript revising. All authors read and approved the final version.

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cytokine receptors.²³ Ob-Rb is the long form of the leptin receptor and has a long cytoplasmic region containing several motifs required for signal transduction.²⁴ Leptin binding to this receptor induces conformational changes in the intracellular receptor domain.²⁵ Many studies have shown that dietary intake and fat stores regulate the production of leptin, which then enters the circulatory system and binds to leptin receptor in multiple tissues, modulating numerous other physiological processes, including body temperature, energy regulation, immune reaction, reproduction and development.^{26,27} Leptin and its receptor have also been shown to express in ovary and testis,^{28,29} as well as in several other tissues of the reproductive tract.³⁰

Our previous study has shown that *c-kit* and proliferating cell nuclear antigen (PCNA) had higher expressions in the pre-hibernation oviduct, which suggested that as the intrinsic regulator including the *c-kit* receptor might play a regulatory role in oviductal cell proliferation.³¹ In order to elucidate the relationship between leptin and oviductal hypertrophy during pre-hibernation, this study investigated the expression of PPAR γ 2, leptin and leptin receptor proteins in the oviduct of *Rana dybowskii* during the breeding and pre-hibernation periods.

Research Article

Immunostimulatory Activity of Protein Hydrolysate from *Oviductus Ranae* on Macrophage *In Vitro*

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Oviductus Ranae is the dry oviduct of *Rana chensinensis*, which is also called *R. chensinensis* oil. *Oviductus Ranae* is a valuable Chinese crude drug and is recorded in the Pharmacopoeia of the People's Republic of China. The aim of this study was to investigate the immunostimulatory activity of protein hydrolysate of *Oviductus Ranae* (ORPH) and to assess its possible mechanism. Immunomodulatory activity of ORPH was examined in murine macrophage RAW 264.7 cells. The effect of ORPH on the phagocytic activity of macrophages was determined by the neutral red uptake assay. After treatment with ORPH, NO production levels in the culture supernatant were investigated by Griess assay. The mRNA and protein expressions of inducible nitric oxide synthase (iNOS) were detected by RT-PCR and Western blotting. The production of TNF- α , IL-1 β , and IL-6 after treatment with ORPH was measured using ELISA assay. In addition, NF- κ B levels were also investigated by Western blot. The results showed that ORPH enhanced the phagocytosis of macrophage, increased productions of TNF- α , IL-1 β , IL-6, and NO in RAW 264.7 cells, and upregulated the mRNA and protein expression of iNOS. Besides, NF- κ B levels in RAW 264.7 cells were elevated after ORPH treatment. These findings suggested that ORPH might stimulate macrophage activities by activating the NF- κ B pathway.

1. Introduction

Macrophages are a type of differentiated tissue cells that originate as blood monocytes. The cells have several functions such as the removal of cell debris, the killing of pathogenic microorganisms, and the processing and presentation of antigens to lymphocytes [1, 2]. Macrophages are the first cells to recognize invading foreign bodies and are central to cell mediated and humoral immunity. Therefore, the activation of macrophages is a key event for effective innate and adaptive immunity. It is reported that activated macrophages can defend against pathogen invasion by secreting proinflammatory cytokines and releasing some inflammatory molecules such as tumor necrosis factor- (TNF-) α , interleukin- (IL-) 1 β , interleukin- (IL-) 6, or nitric oxide (NO) [3]. NO, as a free-radical gas, is synthesized by inducible nitric oxide synthase (iNOS) and mediates diverse functions, including vasodilation, neurotransmission, immunoresponses, and inhibition

of platelet aggregation and of extracellular matrix production [4, 5]. NO has been identified as the major effector molecule involved in the destruction of tumor cells by activated macrophages [6]. Moreover, the involvement of NO during nonspecific host defense, macrophage-mediated killing, and the inhibition of the proliferation of microorganisms and tumor cells both *in vitro* and *in vivo* has previously been demonstrated [7].

Nuclear factor κ B (NF- κ B) is a transcriptional factor that regulates a battery of genes that are critical to innate and adaptive immunity, cell proliferation, inflammation, and tumor development. In macrophages, NF- κ B, in cooperation with other transcription factors, coordinates the expression of the genes encoding TNF- α , IL-1 β , IL-6, and IL-8 [8]. Moreover, NF- κ B plays a critical role in the activation of immune cells by upregulating the expression of many cytokines essential for the immune response [9]. NF- κ B activation also results in the upregulation of antiapoptotic genes thereby

cDNA CLONING AND SEQUENCE DETERMINATION OF THE PHEROMONE BIOSYNTHESIS ACTIVATING NEUROPEPTIDE FROM THE SEABUCKTHORN CARPENTERWORM, *Holcocerus hippophaecolus* (LEPIDOPTERA: COSSIDAE)

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Seasonal Changes in Immunoreactivity of Inhibin/Activin Subunits in the Epididymis of Wild Ground Squirrels (*Citellus dauricus* Brandt)

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Abstract. The inhibin/activin subunits (α , β_A and β_B) have been found in epididymal tissue of many mammals, but there have been no data available for wild seasonal breeders so far. The aim of this study was to investigate the immunoreactivities of inhibin/activin α , β_A and β_B subunits in the epididymis of wild ground squirrels during the breeding and nonbreeding seasons. Immunohistochemistry and Western blotting were performed to detect the epididymal immunolocalizations and immunoreactivities of the three subunits. Strong immunostaining of α subunit was present in the interstitial part of the caput epididymis and epithelial parts of the corpus epididymis and cauda epididymis during the breeding season, whereas no α subunit was found in the nonbreeding season. β_A and β_B subunits were expressed in all cell types of the epithelium throughout the whole seasonal cycle, and immunostaining in the breeding season was likely stronger compared with that of the nonbreeding season. These results suggested that the epididymis might be a potential source of inhibin and activin in the wild male ground squirrel, and the secretion of epididymal inhibin and activin showed distinct seasonal changes. Furthermore, inhibin and activin might function as paracrine and/or autocrine factors that have an effect on the epididymis.

Key words: Epididymis, Immunoreactivity, Inhibin/activin subunits, Wild ground squirrel

(J. Reprod. Dev. 59: 302–307, 2013)

The mammalian epididymis is derived from the anterior Wolffian (or mesonephric) duct and serves a critical function in sperm maturation and acquisition of the capacity to fertilize [1, 2]. At birth, the epididymis consist mainly of the epididymal duct and interstitial tissue, and it must then undergo elongation, expansion, coiling and segmentation to morph from a straight tube to an elaborately convoluted organ [3]. As a main male accessory reproductive organ, the development of a fully differentiated epididymis is dependent not only on androgens but also requires a mesenchyme-epithelium interaction to determine the regional specialization of the epithelium [4, 5]. Thus some mesenchyme-derived factors involved in the mesenchyme-epithelium interaction were thought to have a functional role in this process.

A number of paracrine factors involved in the control of proliferation and differentiation of various types of cells have been identified, including members of the transforming growth factor β (TGF- β) family, which are essential for the development and functional control of the male reproductive system [6–9]. Activins and inhibins are members of the TGF- β family, initially characterized by their ability to regulate FSH secretion from the pituitary [10, 11]. They are dimeric glycoproteins formed by two of three different subunits (α , β_A and β_B). Inhibins consist of either of the β -subunits dimerized

with a common α -subunit (α - β_A and α - β_B ; inhibin A and inhibin B, respectively). Activins are dimers of β -subunits (β_A - β_A , β_A - β_B and β_B - β_B ; activin A, activin AB and activin B, respectively). There is also evidence that inhibin and activin are not only expressed in the testis but also in other tissues of the male reproductive tract, e.g., the prostate, seminal vesicles and epididymis [12]. In addition, previous studies have shown the expression of mRNA and protein of inhibin/activin subunits in the epididymis of the mouse, monkey, ovine and human [5, 13–18]. Inhibin B was suggested to have a possible role in epididymal function or an effect on the epididymis parallel to that of testosterone [19]. Furthermore, β_A subunits were proven to be mesenchyme-specific factors that act collectively with testosterone to facilitate epididymal coiling by stimulating epithelial proliferation in the mouse [5].

The wild ground squirrel (*Citellus dauricus* Brandt) is a typical seasonal breeder with a short sexually active period in April and May that is followed by a long period of sexual dormancy from June to March [20]. The testis and epididymis of this species exhibits distinct seasonal morphology changes from the breeding season to the nonbreeding season [21–24]. Our published results have indicated that seasonal changes in the distribution of inhibin/activin α , β_A and β_B subunits and activin signaling proteins were accompanied by changes in testicular activity in male ground squirrels and other mammals [21, 22, 25–29]. However, little is known about the role of inhibin/activin subunits in the epididymal tissue of this wild species. Thus, the aim of the present study was to investigate the localization of inhibin/activin subunits in the epididymis during the breeding and nonbreeding seasons, and to elucidate the relationship between the

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Pathways of phosphate uptake from aqueous solution by ZnAl layered double hydroxides

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ABSTRACT

ZnAl layered double hydroxides (LDHs) were prepared by urea hydrolysis-based coprecipitation for removing phosphate from aqueous solutions. The chemical formula of the product was determined as $\text{Zn}_{5.54}\text{Al}_{3.02}(\text{OH})_{8.73}(\text{CO}_3)_{0.57}\text{Cl}_{5.66} \cdot 7.84\text{H}_2\text{O}$. Chloride ion was the major interlayer anion of the ZnAl LDHs. Adsorption of phosphate onto the ZnAl sorbent over the entire study period was not in close agreement with pseudo-first-order or pseudo-second-order models. The adsorption can be divided into two steps. A fast adsorption was observed during the first 10 h with a marked increase in the concentration of Cl^- in the bulk solution. This indicated that the adsorption of phosphate was largely attributed to the ion exchange between phosphate and the interlayer Cl^- . A second fast adsorption of phosphate occurred after 10 h. During this period, the pH increased slowly, whereas the Cl^- concentration was stable. The uptake of phosphate was likely attributed to $\text{OH}^-/\text{H}_2\text{PO}_4^-/\text{HPO}_4^{2-}$ ion exchange as well as surface adsorption/complexation. Acidic conditions favored adsorption of phosphate by ZnAl LDHs, which is consistent with the pH increases during the adsorption. Coexisting anions, e.g., SO_4^{2-} and CO_3^{2-} , are competitive ions for the adsorption of phosphate. The results verify the contribution of ion exchange and surface adsorption/complexation in the removal of phosphate by ZnAl LDHs.

Key words | adsorption, layered double hydroxides, pathway, phosphate, ZnAl

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INTRODUCTION

Removal of phosphate from waste streams by adsorption has attracted increasing attention in recent years (Chitrakar *et al.* 2006; Das *et al.* 2006; Karaca *et al.* 2006; Cheng *et al.* 2009). The use of an adsorptive process not only reduces consumption of chemicals and sludge production during phosphate removal, but also enables recovery of phosphate via desorption (Kuzawa *et al.* 2006). Materials studied for adsorptive removal of phosphate include minerals (e.g., goethite, dolomite), industrial byproducts (e.g., fly ash, blast furnace slag), and metal oxides/hydroxides (i.e., aluminium oxide, iron oxide) (Seida & Nakano 2002; Cheng *et al.* 2009).

Layered double hydroxides (LDHs), also called hydrotalcite-like compounds, have been shown to be efficient adsorbents for separation of phosphate from aqueous solutions (Das *et al.* 2006) and also real streams (Chitrakar *et al.* 2005; Cheng *et al.* 2009). The formula of these compounds can be described as $[\text{M}_1^{2+}{}_x\text{M}_2^{3+}{}_y(\text{OH})_z][\text{A}^{n-}]_{x/ny}\cdot n\text{H}_2\text{O}$, where M_1^{2+} and M_2^{3+} denote divalent and trivalent metal

cations, respectively, and A^{n-} is the intercalated anion. The exchangeability of interlayer anions and the high-density positive charge of the sheets from the isomorphic substitution of M_1^{2+} by M_2^{3+} were generally believed to be responsible for the high capacity of LDHs for phosphate removal (Cheng *et al.* 2010). Since LDHs are a group of compounds with great compositional diversity, the mechanisms for phosphate removal could also vary among compounds. For example, the released metal cations and/or hydroxides were shown to play a critical role during the enhanced uptake of phosphate by LDHs containing iron (Seida & Nakano 2002). More recently, it was illustrated that removal of triphosphate by MgFe-Cl-LDHs was mainly due to surface adsorption and near-edge intercalation, while its uptake by CaFe-Cl-LDHs could be attributed to dissolution of LDHs and the subsequent precipitation of calcium phosphate (Zhou *et al.* 2011). Overall, the interaction between phosphate and LDHs is currently far from well understood. In addition, LDH

Seasonal Changes in Immunoreactivity of Activin Signaling Component Proteins in Wild Ground Squirrel Testes

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Abstract. The seasonal spermatogenesis and localization of inhibin/activin subunits (alpha, betaA, betaB) in the testes of wild ground squirrel has been previously described; however, the expression pattern of activin receptors and cytoplasmic signaling SMADs has not been detected in any seasonal breeders. The objective of this study was to investigate the abundance and cellular localization of activin signaling components in testes of the wild ground squirrel during the breeding and nonbreeding seasons. The immunolocalizations of ActRIIB (activin type II receptor B) and activin-related SMADs (phospho-SMAD2/3, SMAD4 and SMAD7) were observed by immunohistochemistry. Total proteins were extracted from testicular tissues in the breeding and nonbreeding seasons and were used for Western blotting analysis for ActRIIB and SMADs. Immunoreactivities of activin signaling components were greater in the testes of the breeding season, and then decreased to a relatively low level in the nonbreeding season. ActRIIB and related SMADs were widely spread in the active testes, while spermatogonia were the predominant cellular sites of activin signal transduction during arrested spermatogenesis. The dynamic regulation of activin type II receptor and SMADs indicated that the activin signal pathway played an important paracrine role in seasonal spermatogenesis of the wild ground squirrel. Furthermore, the distinct localizations and immunoreactivity of ActRIIB and SMADs might suggest different functions of activin in seasonal spermatogenesis.

Key words: ActRIIB, SMAD, Spermatogenesis, Testes, Wild ground squirrel

(J. Reprod. Dev. 58: 126–131, 2012)

Seasonal reproduction is common among mammals at all latitudes, even in the deep tropics [1]. Seasonal changes of testicular function and spermatogenesis in wild animals are governed by the influence of many growth factors, including members of the transforming growth factor β (TGF- β) superfamily, which is defined as a group of over 40 ligands, such as TGF- β s, inhibins and activins, bone morphogenetic proteins (BMPs), Müllerian inhibiting substance (MIS) and growth and differentiation factors (GDFs) [2].

Ligands of the TGF- β superfamily control many aspects of cell physiology through conserved signal transduction pathways [3]. Activin, which acts through two transmembrane serine/threonine kinases receptors, a type II receptor (ActRIIA or ActRIIB) and a type I receptor (ALK4 or ALK7), displays a high affinity for the type II receptors and does not interact with the isolated type I receptor [4, 5]. Assembly and activation of the heteromeric receptor complex results in phosphorylation of the intracellular transducers of the activin signal, the SMAD proteins [6]. SMADs exist as three subgroups: the receptor-regulated SMADs (R-SMADs), the common SMAD (co-SMAD) and the inhibitory SMADs (I-

SMADs). Activin binds tightly to the ectodomain of the type II receptor first; this binding allows the subsequent incorporation of the type I receptor, forming a large ligand-receptor complex involving a ligand dimer and four receptor molecules. Thereafter, the phosphorylated receptors stimulate R-SMADs (SMAD2 and 3) to accumulate in the nucleus as heteromeric complexes with the Co-SMAD, of which SMAD4 is the only member. In the nucleus, the SMADs associate with one of the many DNA binding partners and various transcriptional coactivators or corepressors, thereby positively or negatively regulating gene expression. In contrast, the I-SMADs (SMAD6 and 7) counteract the effects of the R-SMADs and thus antagonize activin signaling [4–7]. In addition, it is increasingly apparent that TGF- β -related proteins activate not only SMADs but also other signaling pathways. These pathways regulate SMAD-mediated responses, yet also induce SMAD-independent responses [8].

The expression of inhibin/activin subunits have been studied in several seasonal breeders, indicating that seasonal changes in testicular activity are correlated with changes in spermatogenesis and testicular distribution of inhibin/activin subunits [9–13]. Our previous study also demonstrated significant season-related changes in inhibin/activin subunits localization in the wild ground squirrel (*Citellus dauricus* Brandt) [14]. However, much less is known about the expression of activin receptors and cytoplasmic SMADs in the testes of seasonal breeders [15]. Two of the ActRIIB

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Expression of nerve growth factor and its receptors TrkA and p75 in the uterus of wild female ground squirrel (*Citellus dauricus* Brandt)

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ABSTRACT

In this study, we investigated the presence of nerve growth factor (NGF) and its receptors tyrosine kinase A (TrkA) and p75 in the uterus of the wild ground squirrels during the estrous period, early pregnancy and non-breeding period. In the estrous period and early pregnancy, NGF and TrkA were immunolocalized in stromal cells, luminal epithelial cells, glandular cells and smooth muscle cells whereas in the non-breeding period, both of them were detected only in luminal epithelial cells and glandular cells, but not in stromal cells or smooth muscle cells. Stronger immunostaining of NGF and TrkA was observed in luminal epithelial cells and glandular cells in the estrous period and early pregnancy as compared to the non-breeding period. p75 was immunolocalized only in luminal epithelial and glandular cells during the estrous period, early pregnancy and non-breeding period. The intensity of the immunohistochemical signals for p75 did not vary significantly in the estrous period, early pregnancy and non-breeding period. The mean mRNA levels of NGF and TrkA and p75 were significantly higher in the estrous period and early pregnancy as compared to the non-breeding period. Besides, plasma estradiol-17 β and progesterone concentrations were higher in the estrous period and early pregnancy than in the non-breeding period, suggesting that the expression patterns of NGF and TrkA are correlated with changes in plasma estradiol-17 β and progesterone concentrations. These results indicate that NGF and its receptor TrkA may be involved in the regulation of seasonal changes in the uterine functions of wild female ground squirrels.

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1. Introduction

Nerve growth factor (NGF) belongs to a family of proteins known as neurotrophins that are important for many physiological processes such as cell survival, maintenance and development of discrete neuronal populations in the central and peripheral nervous systems [21,33]. The multiple effects of NGF are mediated via its receptors [29,37,7]. Binding of NGF to the high affinity membrane-bound receptor tyrosine kinase A (TrkA) leads to TrkA dimerization and autophosphorylation of tyrosine residues

[19,18]. Phosphorylation of TrkA leads to activation of second messenger cascades, such as mitogen-activated protein kinase and phosphatidylinositol-3 kinase that are involved in essential pathways for cell survival and differentiation [42,14]. NGF also binds to the low affinity receptor p75 [7].

The density of uterine sympathetic nerves shows phases of degeneration and regeneration during the natural oestrous cycle. Even more, uterine sympathetic nerves degenerate during normal pregnancy and regenerate following delivery [3]. Pregnancy-induced uterine denervation is of physiological significance as it reduces myometrial contractility and thus prevents preterm labor [15,23]. On the other hand, much evidence has suggested that the steroid hormone-induced growth of uterine endometrial cells is mediated in an autocrine or paracrine manner by polypeptide growth factors synthesized by the uterus [6]. Previous studies have shown that in experimental and domestic animal species, NGF and its receptors TrkA and p75 are expressed in the female reproductive system and exert their biological roles in many related processes including uterine growth and proliferation [11,1,32,39–41]. Data

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Seasonal Changes in Morphology and Immunoreactivity of PDGF-A and its Receptor PDGFR- α in the Epididymis of Wild Ground Squirrels (*Citellus dauricus* Brandt)

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Abstract. The platelet-derived growth factor (PDGF) system is expressed and can exert its biological role in the male reproductive system including the maintenance of morphological structure and function of the epididymis. The aim of this study was to clarify the relationship between the PDGF system and seasonal changes in morphology of the wild ground squirrel epididymis during the breeding and nonbreeding seasons. Hematoxylin-eosin (HE) staining was used to observe the epididymal morphology and histology. Immunohistochemistry and Western blotting were performed to detect the immunoreactivities of PDGF-A and B and PDGFR- α . Significant seasonal changes in epididymal morphology were observed in the breeding and nonbreeding seasons. The proportions of the three compartments (interstitial tissue, epithelium and lumen of the duct) revealed distinct variances. Strong immunostaining of PDGF-A was present in the myoid cell and on the sperm in the breeding season, whereas there was a faint signal in the myoid cell in the nonbreeding season. PDGFR- α was expressed in all cell types of the epithelium throughout the whole seasonal cycle, and immunostaining of PDGFR- α in the breeding season was significantly stronger compared with that of the nonbreeding season. PDGF-B was not detected in the epididymis of wild ground squirrels. These results suggested that seasonal morphological changes in epididymis were correlated with immunoreactivities of PDGF-A and its receptor PDGFR- α and that PDGF-A and PDGFR- α might function as paracrine, autocrine or apocrine factors in wild ground squirrels.

Key words: Epididymis, Immunoreactivity, PDGF-A, PDGFR-A, Wild ground squirrel

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The mammalian epididymis plays an important role in preparing male germ cells for fertilization [1]. On the basis of histological and ultrastructural differences, the epididymis can be grossly divided into three regions including the caput, corpus and cauda epididymis. Each region of the epididymis has a different function: the caput and corpus carry out early and late sperm maturational events, respectively, while the cauda region primarily serves as a storage site for functionally mature spermatozoa [2]. As a main male accessory reproductive organ, the epididymis is highly responsive to androgen. Castration could induce a remarkable decrease in weight and function of the epididymis [3]. Besides, recent studies on the ERKO [4, 5] and anti-estrogen [6, 7] effects on male reproduction showed that estrogen also plays an important role in maintaining the function of the epididymis.

It is now widely reported that a group of polypeptide growth factors play vital roles in mediating the androgen/estrogen-regulated process [8–12]. The platelet-derived growth factor (PDGF) is one of

them. PDGFs are members of the PDGF/vascular endothelial growth factor (PDGF/VEGF) family, which comprises a series of 30- to 34-kd homodimers and heterodimers formed by a combination of 4 polypeptides, PDGF-A, B, C and D, and bind to two different receptors, α and β [13, 14]. PDGF-A and B have been proved to play an important role in several reproductive tissues. In the mouse uterus and vagina, PDGF-A and B act as potential mediators of estrogen action [15]. In males, through complex interactions, PDGF-A and B could play a leading role in ontogenesis and testicular pathophysiology [16]. In addition, in *Pdgfr- α ^{-/-}* mice, circulating testosterone was not detectable, confirming that the spermatogenic arrest and germ line apoptotic regression in these animals were mediated by androgen deficiency [17]. The tissue-specific expression patterns of the two isoforms of PDGF-A mRNA were identified in mouse epididymis [18]. Furthermore, with PDGF-A, PDGF-B and PDGF receptor β deficient mice, Basciani *et al.* found that the PDGF systems (mainly refer to PDGF-A and B) were involved in the maintenance of morphological and functional control of this organ [19].

The wild ground squirrel is a typical seasonal breeder that has a breeding season from April to May, followed by a long period of sexual dormancy from June to the following March [20]. The seasonal switch of the reproductive system between the breeding and nonbreeding seasons provides us a unique model to study the

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ORIGINAL ARTICLE

Immunolocalization of steroidogenic enzymes and their expression during the breeding season in the testes of wild raccoon dogs (*Nyctereutes procyonoides*)

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ABSTRACT

The objective of this study was to investigate immunolocalization of steroidogenic enzymes 3 β HSD, P450c17 and P450arom and their expression during the breeding season in wild male raccoon dogs. The testicular weight, size and seminiferous tubule diameters were measured, and histological and immunohistochemical observations of testes were performed. The messenger RNA expression (mRNA) of 3 β HSD, P450c17 and P450arom was measured in the testes during the breeding season. 3 β HSD was found in Leydig cells during the breeding and non-breeding seasons with more intense staining in the breeding season. P450c17 was identified in Leydig cells and spermatids in the breeding season, whereas it was present only in Leydig cells in the non-breeding season. The localization of P450arom changed seasonally: no immunostaining in the non-breeding season; more extensive immunostaining in Leydig cells, Sertoli cells and elongating spermatids in the breeding season. In addition, 3 β HSD, P450c17 and P450arom mRNA were also expressed in the testes during the breeding season. These results suggested that seasonal changes in testicular weight, size and seminiferous tubule diameter in the wild raccoon dog were correlated with spermatogenesis and immunoreactivity of steroidogenic enzymes and that steroidogenic enzymes may play an important role in the spermatogenesis and testicular recrudescence and regression process.

Key words: immunohistochemistry, mRNA, raccoon dog, steroidogenic enzymes, testes.

INTRODUCTION

Reproductive strategies of seasonal breeders are adaptations to annual changes in the environment and they minimize the animals' energetic efforts for reproduction. Mature males show synchronized cycles of testicular growth and involution between breeding and non-breeding periods (Bronson & Heidemann 1994). Seasonal changes in spermatogenesis, morphology of the testis and peripheral testosterone concentrations have been reported in numerous species (Komatsu *et al.* 1997; Tsubota *et al.* 1997, 2001; Hayakawa *et al.* 2010; Zhang *et al.* 2010). In these animals, immunohistochemical studies on testicular tissues have demonstrated that the distributions of immunoreactivities for steroidogenic enzymes in testicular tissue are associated with seasons and species. Steroid biosynthesis is accomplished by the actions of two

major families of enzymes. The first are the hydroxylase enzymes, encoded by genes belonging to the cytochrome P450 superfamily. The second family, the steroid dehydrogenase enzymes, belong to one of two distinct groups, the shortchain alcohol dehydrogenase/reductase family or the aldo-keto reductase superfamily. Together, the P450 and dehydrogenase enzymes are necessary for steroidogenesis in the gonads, placenta and adrenals (Hinshelwood 1998).

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Immunohistochemical Localization of Inhibin/Activin Subunits in the Wild Ground Squirrel (*Citellus dauricus brandt*) Ovary

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Abstract. The intraovarian function of gonadally produced inhibin and activin has been extensively studied in experimental models for decades, yet their presence and function have been rarely reported in wild rodents. With our seasonal breeding model, the wild ground squirrel, we aimed to investigate the possible roles of these peptides in the seasonal folliculogenesis. Immunohistochemical staining and Western blotting have been used to detect the cellular localization and expression patterns of inhibin/activin subunits (α , β_A and β_B). In the breeding season ovary, all three subunits were present in granulosa cells, theca cells of antral follicles and interstitial cells, with the strongest immunostaining in granulosa cells. Following ovulation, the corpora lutea become a major site of inhibin/activin synthesis. In the nonbreeding season ovary, inhibin/activin α and β_A subunits were weakly immunopositive in granulosa cells of early stage follicles, while β_B subunit was undetectable. The expression level of inhibin/activin subunit proteins were generally higher in the ovaries of the breeding season, and then decreased to a relatively low level during the nonbreeding season. The dynamic expression of inhibin/activin subunits indicated that they might play important paracrine and/or autocrine roles during the seasonal folliculogenesis of the wild ground squirrel.

Key words: Folliculogenesis, Immunohistochemistry, Inhibin/activin subunits, Ovary, Wild ground squirrel

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Inhibin and activin are prototypical members of the transforming growth factor β (TGF β) superfamily of ligands and receptors, which are temporally and spatially widespread and functionally diverse [1–3]. Inhibin is composed of an α -subunit disulfide linked to a β subunit, and the particular isoform of inhibin is named for the β subunit present in that molecule (inhibin A, α/β_A , and inhibin B, α/β_B). Activins are homodimers of the inhibin β subunits (activin A, β_A/β_A , activin B, β_B/β_B , and activin AB, β_A/β_B) [4–6]. Biological roles for activin have been proposed in a number of reproductive organs including the gonads, pituitary, and uterus, where it regulates processes such as folliculogenesis, spermatogenesis, and pregnancy, while the primary role of inhibin appears to be antagonism of inhibin/activin signaling in many cells, including pituitary gonadotrope FSH synthesis and ovarian theca and testicular Leydig cell androgen production [7–9]. In the ovary, inhibin and activin, mainly produced by granulosa cells, are thought to be involved in many intraovarian roles during folliculogenesis [10]. Activin and several other TGF- β superfamily ligands play key roles in germ cell survival, in primordial follicle assembly and in follicle growth from the preantral to mid-antral stages, and exert paracrine actions on theca cells to attenuate

LH-dependent androgen production in small- to medium-sized antral follicles [11, 12]. Changes in intrafollicular activins may contribute to dominant follicle selection by modulating both FSH- and IGF-dependent signaling pathways in granulosa cells. Activin may also play a positive role in oocyte maturation and acquisition of developmental competence. In addition to its endocrine feedback to suppress FSH secretion, increased output of inhibin by the selected dominant follicle may upregulate LH-induced androgen secretion that is required to sustain a high level of estradiol secretion during the preovulatory phase [11–13].

On the other hand, accumulating information has also been gained on the role of the inhibin/activin system in ovarian regulation in nonmammalian vertebrates, which exhibits a considerable overlap with that in mammals [12, 14]. However, little is known in terms of the functional involvement of the inhibin/activin system in seasonal folliculogenesis in a wild rodent. The wild ground squirrel (*Citellus dauricus* Brandt) is a typical seasonal breeder with a short sexually active period in April and May, followed by a long period of sexual dormancy from June to the following March [15]. Previously, we have detected the immunoreactivity of inhibin/activin subunits, activin type II receptor, activin-related SMADs and steroidogenic enzymes (P450c17 and P450arom) in the testis of the wild ground squirrel and revealed an important paracrine role of the activin signal in seasonal spermatogenesis [16–18]. The present study aimed to investigate the immunoreactivity of inhibin/activin subunits in the ovarian recrudescence and regression during the breeding and

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Seasonal Changes in Immunoreactivity of Vascular Endothelial Factor and its Receptors VEGFR1 and VEGFR2 in the Uterus of Wild Ground Squirrels (*Citellus dauricus* Brandt)

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Abstract. In this study, we investigated the immunoreactivity of vascular endothelial growth factor (VEGF) and its receptors flt-1 (VEGFR1) and the kinase domain receptor (KDR/Flk-1, VEGFR2) in the uteri of the wild ground squirrels during the estrous period, early pregnancy and nonbreeding period. Cellular localizations of VEGF, VEGFR1 and VEGFR2 were detected by immunohistochemistry, and total proteins were extracted from uterine tissue in the estrous period, early pregnancy and nonbreeding period for Western blotting analysis. In addition, plasma estradiol-17 β and progesterone concentrations were measured by radioimmunoassay. Stronger positive staining of VEGF was found in luminal epithelial cells and glandular cells, and its receptors (VEGFR1 and VEGFR2) were observed in stromal cells in the estrous period and early pregnancy compared with the nonbreeding period. The protein levels of VEGF, VEGFR1 and VEGFR2 were significantly higher in the estrous period and early pregnancy as compared with the nonbreeding period. Besides, plasma estradiol-17 β and progesterone concentrations were higher in the estrous period and early pregnancy than in the nonbreeding period, suggesting that the immunoreactivities of VEGF, VEGFR1 and VEGFR2 were correlated with changes in plasma estradiol-17 β and progesterone concentrations. These results suggested that VEGF and its receptors may be involved in the regulation of seasonal changes in the uterine functions of wild female ground squirrels.

Key words: Uterus, VEGF, VEGFR1, VEGFR2, Wild ground squirrel

(J. Reprod. Dev. 58: 537–543, 2012)

During the reproductive cycle, the uterine endometrium undergoes a precisely timed complex sequence of physiological and morphological changes in preparation for implantation. These changes are controlled primarily by the ovarian steroid hormones 17 β -estradiol (E₂) and progesterone [1]. During pregnancy, blood flow to the uterus is increased dramatically to meet the rising demands of the growing fetus. Endocrine control of this phenomenon is complex but includes in part the action of many growth factors [2, 3]. Vascular endothelial growth factor (VEGF) is a protein with angiogenic activity and a potent stimulator of microvascular permeability [4, 5]. It plays an important role in physiological and pathological neovascularization via its receptors Flt1/VEGFR1 and kinase insert domain containing region (KDR)/VEGFR2, both of which have tyrosine kinase activity [6]. In reproductive organs, VEGF is required for normal ovarian angiogenesis and endometrial growth throughout the ovulatory cycle in humans [7, 8] and rodents [9, 10]. The expression of VEGF and

its receptors has been demonstrated in the endometrium in humans and in experimental and domestic animals throughout the menstrual cycle, with an upregulation in the late proliferative and luteal phases [11–15], periods that correspond to angiogenesis and an increase in vascular permeability [16]. However, the expression of VEGF and its receptors VEGFR1 and VEGFR2 in the endometrium of a seasonal cycle breeder has not been clarified. To study the basic mechanisms of VEGF regulation of uterine function changes during the breeding and nonbreeding seasons, the wild female ground squirrel may offer a useful model without any manipulations.

The wild ground squirrel (*Citellus dauricus* Brandt) is a typical seasonal breeder that has a strict and extremely compressed breeding period (for females, it consists of the estrous period and pregnancy) from April to May and a long period of sexual dormancy from June to the following March that includes a 6-month hibernation period [17]. The wild female ground squirrel exhibits estrus immediately after emergence from hibernation in spring, and has a gestation period of 28 days [18, 19]. Although many observations have been reported recently concerning the regular roles of VEGF and its receptors on uterine function, there are still limitations in understanding the mechanisms of uterine function, especially the roles of VEGF and its receptors VEGFR1 and VEGFR2 in the seasonal uterine function

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RESEARCH

Open Access

Immunoreactivities of androgen receptor, estrogen receptors, p450arom, p450c17 proteins in wild ground squirrels ovaries during the nonbreeding and breeding seasons

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Abstract

The aim of this study was to elucidate the regulatory role of androgen in the follicular development of wild female ground squirrels. Immunohistochemical staining of FSHR, LHR, P450c17, P450arom, androgen receptor (AR), estrogen receptors (ERa and ERb) were executed in ovaries of female ground squirrels from both breeding and nonbreeding seasons. In addition, total ovarian proteins were extracted from the ovaries of squirrels from breeding and nonbreeding seasons, and Western blot analysis were performed in order to probe for FSHR, LHR, P450c17, P450arom, AR, ERa and ERb. The results of immunohistochemical staining and Western blotting of P450c17 showed that there was no significant difference between the breeding and nonbreeding seasons. It was found that granulosa cells expressed P450arom during the breeding season. In contrast, there was no positive staining of P450arom in the nonbreeding season. There was no significant difference in immunoreactivity of AR between the breeding and nonbreeding seasons. However, the immunoreactivities of ERa and ERb were both significantly reduced in the nonbreeding season compared to the breeding season. The positive stains of FSHR and LHR were found in the granulosa cells and theca cells of the ovaries of the breeding and nonbreeding seasons. In addition, the Western blotting results of FSHR and LHR showed a significant reduction in the nonbreeding season compared with the breeding season. These findings suggested that androgen might be predominantly converted into estrogen in order to regulate the follicular development via binding of estrogen receptors during the breeding season, whereas androgen might predominantly directly bind androgen receptor to regulate the follicular development during the nonbreeding season in the ovaries of wild female ground squirrels.

Keywords: Androgen receptor, Ovary, P450c17, P450arom, Wild ground squirrels

Introduction

The major stages of ovarian folliculogenesis were formation of the primordial follicle; recruitment into the growing pool to form a primary, secondary, and tertiary follicle; and lastly ovulation and subsequent formation of a corpus luteum (CL) [1]. These physiological progressions were under the regulation of hypothalamic-pituitary-

gonad (HPG) axis [2]. GnRH from the hypothalamus stimulated the anterior pituitary to secrete follicle-stimulating hormone (FSH) and luteinizing hormone (LH), which acted on the ovary to promote folliculogenesis and the concomitant synthesis of estradiol [3]. Following follicular recruitment was the gonadotropin-independent stage, a state in which preantral follicular development did not require stimulation by the pituitary gonadotropins [1]. Subsequent to this was the gonadotropin-dependent stage, which was when preantral follicles grew to antral follicles. Thereafter, secretion of FSH by the pituitary promoted further granulosa cell proliferation and survival. Ovulation of the dominant

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发明名称：一种基于区块链的种质资源数据高效可信存储方法

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申请日时发明人：袁峥嵘;李鑫伟;张延峰;孙玉婷;张哲培

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证书号第6284222号



发明专利证书

发 明 名 称：一种基于希尔伯特曲线的聚类索引方法

发 明 人：王新阳;孙宇;陈志泊;孙俏;许福

专 利 号：ZL 2021 1 0785517.6

专 利 申 请 日：2021年07月12日

专 利 权 人：北京林业大学

地 址：100083 北京市海淀区清华东路35号

授权公告日：2023年08月29日

授权公告号：CN 113434511 B

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其他事项参见续页

证书号第2373956号



发明专利证书

发明名称：一种污水强化除磷方法

发明人：程翔；陈兵；孙德智；刘佳琪

专利号：ZL 2014 1 0641499.4

专利申请日：2014年11月13日

专利权人：北京林业大学

授权公告日：2017年02月08日

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局长
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证书号第 12428520 号



实用新型专利证书

实用新型名称：一种光偏振态检测系统

发 明 人：刘彦君;李鑫伟;王琪瑶;黄紫璐;杨洋;刘芯竹

专 利 号：ZL 2020 2 1033122.8

专利申请日：2020 年 06 月 08 日

专 利 权 人：北京林业大学

地 址：100083 北京市海淀区清华东路 35 号

授权公告日：2021 年 02 月 02 日

授权公告号：CN 212458661 U

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第 1 页 (共 2 页)

其他事项参见续页

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证书号： 软著登字第14887040号

软件名称： 激光除草机器人的杂草结构识别系统
V1.0

著作权人： 北京林业大学

权利取得方式： 原始取得

权利范围： 全部权利

登记号： 2025SR0230842

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2025年02月10日

中华人民共和国国家版权局 计算机软件著作权登记证书

证书号： 软著登字第12948823号

软件名称： 肌肉组织切片扫描图像纤维细胞计量系统
V1.0

著作权人： 中国农业科学院北京畜牧兽医研究所(中国动物卫生与
流行病学中心北京分中心);安徽省农业科学院畜牧兽
医研究所;北京林业大学

权利取得方式： 原始取得

权利范围： 全部权利

登记号： 2024SR0544950

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2024年04月23日

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计算机软件著作权登记证书

证书号： 软著登字第12883177号

软件名称： 高精度、智能化肌肉组织切片扫描图像肌纤维面积和
密度计量软件
V1.0

著作权人： 北京林业大学;中国农业科学院北京畜牧兽医研究所
(中国动物卫生与流行病学中心北京分中心);安徽省农
业科学院畜牧兽医研究所

开发完成日期： 2024年01月19日

首次发表日期： 未发表

权利取得方式： 原始取得

权利范围： 全部权利

登记号： 2024SR0479304

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2024年04月09日

中华人民共和国国家版权局

计算机软件著作权登记证书

证书号： 软著登字第12933454号

软件名称： 一种面向荧光染色牛肌肉组织切片扫描图像的肌纤维
信息提取系统
V1.0

著作权人： 北京林业大学;中国农业科学院北京畜牧兽医研究所
(中国动物卫生与流行病学中心北京分中心);安徽省农
业科学院畜牧兽医研究所

开发完成日期： 2024年01月23日

首次发表日期： 未发表

权利取得方式： 原始取得

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登记号： 2024SR0529581

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2024年04月19日

中华人民共和国国家版权局 计算机软件著作权登记证书

证书号： 软著登字第13027835号

软件名称： 基于深度模型的肌肉组织切片扫描图像肌内膜厚度计
量软件
V1.0

著作权人： 安徽省农业科学院畜牧兽医研究所;中国农业科学院北京
畜牧兽医研究所(中国动物卫生与流行病学中心北京
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权利取得方式： 原始取得

权利范围： 全部权利

登记号： 2024SR0623962

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2024年05月09日

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证书号： 软著登字第13755643号

软件名称： 珍稀濒危野生动植物识别APP
[简称：动植物识别APP]
V1.0

著作权人： 北京林业大学

权利取得方式： 原始取得

权利范围： 全部权利

登记号： 2024SR1351770

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2024年09月11日

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证书号： 软著登字第13298060号

软件名称： 古树名木智慧保护管理系统
V1.0

著作权人： 北京林业大学

权利取得方式： 原始取得

权利范围： 全部权利

登记号： 2024SR0894187

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2024年06月28日

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证书号： 软著登字第13632144号

软件名称： 珍稀濒危野生动物图像预处理及少样本数据集生成系统
V1.0

著作权人： 北京林业大学

权利取得方式： 原始取得

权利范围： 全部权利

登记号： 2024SR1228271

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2024年08月22日

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计算机软件著作权登记证书

证书号： 软著登字第12495392号

软件名称： 泛癌与铜死亡关联分析数据库软件
[简称：CuPCA]
V1.0.0

著作权人： 北京林业大学;袁峥嵘;徐义舒;马振书;叶家铭;张龙

开发完成日期： 2023年09月29日

首次发表日期： 未发表

权利取得方式： 原始取得

权利范围： 全部权利

登记号： 2024SR0091519

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2024年01月12日

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计算机软件著作权登记证书

证书号： 软著登字第11556454号

软件名称： 基于 bootstrap 和 Arduino 的室内空气质量远程监测系统
[简称：室内空气质量远程监测系统]
V1.0

著作权人： 北京林业大学

开发完成日期： 2023年05月31日

首次发表日期： 2023年05月31日

权利取得方式： 原始取得

权利范围： 全部权利

登记号： 2023SR0969281

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2023年08月23日

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计算机软件著作权登记证书

证书号： 软著登字第11616529号

软件名称： 基于Python的光纤耦合对准软件
[简称： 光纤耦合对准软件]
V1.0

著作权人： 北京林业大学

开发完成日期： 2023年06月16日

首次发表日期： 2023年06月21日

权利取得方式： 原始取得

权利范围： 全部权利

登记号： 2023SR1029356

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2023年09月07日

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计算机软件著作权登记证书

证书号： 软著登字第9080065号

软件名称： 古树名木健康诊断与预警系统
[简称： 古树诊断预警App]
V1.0

著作权人： 北京林业大学

开发完成日期： 2021年10月01日

首次发表日期： 未发表

权利取得方式： 原始取得

权利范围： 全部权利

登记号： 2022SR0125866

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No. 10100013



2022年01月19日

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证书号： 软著登字第9080026号

软件名称： 平原生态林巡护养护Web管理平台
[简称：平原生态林巡护养护]
V1.0

著作权人： 北京林业大学

开发完成日期： 2021年11月15日

首次发表日期： 未发表

权利取得方式： 原始取得

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No. 10093977



2022年01月19日

2 424

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证书号： 软著登字第7280143号

软件名称： 木质部横截面显微图像导管细胞计量系统
[简称：导管细胞计量系统]
V1.0

著作权人： 北京林业大学

开发完成日期： 2020年01月27日

首次发表日期： 2020年01月27日

权利取得方式： 原始取得

权利范围： 全部权利

登记号： 2021SR0557517

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No. 07795828



2021年04月19日

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证书号： 软著登字第5894742号

软件名称： 基于LabVIEW系统的玻璃类型检测软件
[简称： 玻璃类型检测软件]
V1.0

著作权人： 北京林业大学

开发完成日期： 2020年06月15日

首次发表日期： 未发表

权利取得方式： 原始取得

权利范围： 全部权利

登记号： 2020SR1016046

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No. 06332526



2020年08月31日

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证书号： 软著登字第5713174号

软件名称： 基于Arduino单片机的光偏振态检测系统软件
[简称：光偏振态检测系统软件]
V1.0

著作权人： 北京林业大学

开发完成日期： 2020年02月26日

首次发表日期： 未发表

权利取得方式： 原始取得

权利范围： 全部权利

登记号： 2020SR0834478

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No. 06115294



2020年07月27日

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计算机软件著作权登记证书

证书号： 软著登字第5713188号

软件名称： 基于LabVIEW系统的光偏振态检测软件
[简称：光偏振态检测软件]
V1.0

著作权人： 北京林业大学

开发完成日期： 2020年02月16日

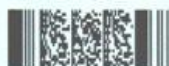
首次发表日期： 未发表

权利取得方式： 原始取得

权利范围： 全部权利

登记号： 2020SR0834492

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No. 06115296



2020年07月27日

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证书号： 软著登字第3632340号

软件名称： 大一新生的掌中宝手机客户端软件
[简称：大一新生的掌中宝APP]
V1.0

著作权人： 北京林业大学

开发完成日期： 2019年01月01日

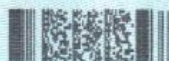
首次发表日期： 2019年01月03日

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权利范围： 全部权利

登记号： 2019SR0211583

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计算机软件著作权登记证书

证书号：软著登字第 BJ44500号

软件名称：基于手机摄像的大气能见度信息采集软件
V1.0

著作权人：北京林业大学

开发完成日期：2017年12月20日

首次发表日期：2018年03月20日

权利取得方式：原始取得

权利范围：全部权利

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(按首字母排序)

金奖		
1	储“液”拔萃基于沿海绿色能源的全液冷储能技术 领军者	广东海洋大学
2	醇真——基于新型工程菌构建的紫杉醇绿色高效生 产技术	山东中医药大学
3	基于“炭-菌协同”机制的生态修复材料设计与水体 净化性能优化研究	扬州职业技术大学
4	基于农业废弃物的耐候型粉体蛋白胶黏剂创新研发	山东农业大学
5	净益求禽——禽白血病病毒磁微粒化学发光抗原检 测首创者	山东农业大学
6	粮安无忧——鸟害智能防护装置	河套学院
7	“零醇 π 动力”基于传质-反应耦合的无醇啤酒乙醇 脱除与风味物质保留技术研究	湖南农业大学
8	秦风绿账：咸阳生态家底精算与乡村振兴新引擎	咸阳市规划设计研 究院
9	水智瞳——合成生物学赋能环境治理：基于工程酵 母的 水体新型污染物检测仪器研发	北京林业大学



中国国际大学生创新大赛（2025）

北京赛区

获奖证书

二等奖

项目名称：水智瞳——合成生物学赋能环境治理：基于工程酵母的水体新型污染物检测仪器研发

项目负责人：史心怡

项目成员：刘佳凡、方思为、任祎峻、梁璐

指导老师：张浩林、程瑾、闫磊

推荐学校：北京林业大学

在中国国际大学生创新大赛（2025）北京赛区荣获二等奖。

编号：2025100333



“青创北京”2025年“挑战杯”首都大学生课外学术科技作品竞赛获奖名单



序号	赛道	奖项	项目名称	负责人	团队成员	指导教师
23	青聚 AI	一等奖	智绘河图——地理数据可视化系统赋能生态可持续发展	林文卫 230401808	钟函芮 220401615、刘子吟 230405126、刘宜伶 220401117、杨昊田 231002814、杨婧涵 230401923、李吟瑜 230401912、王雨彤 240401320、肖晚 220404218	李小勇 王少荣
24	青聚 AI	一等奖	基于机器学习算法鉴定月季花瓣类胡萝卜素代谢的关键基因	赵李洋 240204117	无	于超
25	青聚 AI	一等奖	智森鹰眼——人工智能林业监测与管理系统	李卓然 230401709	钟铭铭 230601321、朱子辛 231401230、高天白 230101321、靳佳凝 220101524、毛嘉妮 220403106、张严方 220405122、高宸轩 230413104	张晓丽
26	青聚 AI	一等奖	水智瞳——合成生物学赋能环境治理：基于工程酵母的水体新型污染物检测仪器研发	史心怡 230506109	史心怡 230506109、刘佳凡 220506107、梁璐 220413117、方思为 220602122、彭琳涵 221301117、任伟峻 230413106	张浩林
27	青聚 AI	二等奖	基于 PLUS-InVEST 模型的白洋淀上游流域生态修复协同技术实施效应模拟评估及生态服务功能潜力分析	刘鸿渝 220301306	陈方丹 220603207、徐元晟 220301201、马秉怡 220401213、史益铭 220401217、郭馨泽 221701203、李佳聪 220301307、陶昱安 220301303、杨健熙 240707103	王平 冯天骄 徐子涵
28	青聚 AI	二等奖	H ₂ Oasis 氢洲——基于深度学习的藻类产氢技术优化	邹心维 231702119	王靖涵 230501302、张玉立 230201425、刘雨萱 230501117、杨婧涵 230401923、黄聆 230401907、鲁瑞玉 240401311、吕鑫鑫 231401310、齐晓嫣 241401619、赵佳佳 230203215	陈明 陈佳
29	青聚 AI	二等奖	参智绘景——AI 赋能三维公园设计系统	何越衡 210203122	邢家怡 230205523、韩文菁 220201518、余林迅 220205623、袁璐 230404122	赵晶
30	青聚 AI	二等奖	“液”态森瞳“林”景绘映——基于液态金属传感林木智能诊断与监测系统	郭非凡 230707118	周雅琪 230701522、周洋 220701708、王国庆 220701902、高佳云 230405214	王磊

首页 科协简介 学会组织 学术交流 科学普及 科创服务 人才高地 党建引领 信息公开

2025北京科学传播大赛获奖名单公示

信息来源：北京科普发展与研究中心 发布时间：2025-08-29

2025北京科学传播大赛全部赛道评审于2025年8月24日完成。现将《2025北京科学传播大赛获奖名单》公布如下，公示期3个工作日，2025年8月29日至2025年9月2日。

公示期内，任何单位或个人对公布结果持有异议，可通过书面形式向组委会提出。书面内容应包括异议人的姓名、身份证明、单位、联系电话，注明质疑内容并提供翔实的依据材料。经查明，确有弄虚作假者，将取消其获奖成绩。

联系邮箱：kxcbdsgf@163.com

附件：

科学演讲大赛获奖名单

作品名称	参赛单位/作者	奖项
马兰的来信	北京钱学森中学 肖畅	一等奖
故宫屋顶的防雷密码	中国社会科学院大学 尹涛	一等奖
水域救援服——生命的最后保险	中国消防救援学院 杨尚宗	二等奖
重生的西南之龙——鳄蜥	北京林业大学 司洛宁	二等奖

荣誉证书

徐义舒

荣获第四届森林生物学国际论坛青年学术“玉兰奖”评选活动
三等奖
特发此证，以资鼓励。

森林生物学国际论坛组委会（代章）

2024年10月



获奖证书

张玉蛟、钱科而、刘建楠、罗敏桑、朱萃菲 同学：

在首届北京林业大学“勉励杯”大学生创新创业
大赛中，你们的项目 科兴夏河一牦牛藏羊科技小院，助力乡村振兴新征程
荣获

优秀奖

特颁此证，以资鼓励，并致祝贺！

北京林业大学创新创业学院



北京林业大学

BEIJING FORESTRY UNIVERSITY



中国国际大学生创新大赛 (2024)

北京赛区

获奖证书

二等奖

项目名称：水智瞳——精准治理水体内分泌干扰物的绿色酵母
水质检测仪器研发

项目负责人：刘佳凡

项目成员：梁璐、杨喜晴、方思为、秦邀、吴天圻、邹锦瑜、
郑佳宁、杨舒喻、邓静怡、冯玮、任祎峻、蒋铁泓、
邵康靖、张严方

指导老师：张浩林、闫磊、张名扬、程瑾

推荐学校：北京林业大学

在中国国际大学生创新大赛 (2024) 北京赛区荣获二等奖。

编号：2024100386





CULSC 第九届全国大学生生命科学竞赛（科学探究类）

获奖证书

获奖项目：冬眠达乌尔黄鼠睾丸自噬水平的变化与调控机制研究

获奖学生：李宇嘉 王树天 罗宇轩 张玉蛟 牛羽丰

指导老师：杨迪 袁峥嵘

获奖单位：北京林业大学

获奖类型：一等奖

证书号：CULSC2024KY0022



全国大学生生命科学竞赛委员会

二〇二四年七月

CULSC



CULSC 第九届全国大学生生命科学竞赛（科学探究类）

获奖证书

获奖项目：Cupca-泛癌与铜死亡关联分析联合数据库

获奖学生：徐义舒 朱苹菲 孙萌 顾翔然

指导老师：袁峥嵘 甘芝霖

获奖单位：北京林业大学

获奖类型：三等奖

证书号：CULSC2024KS0071

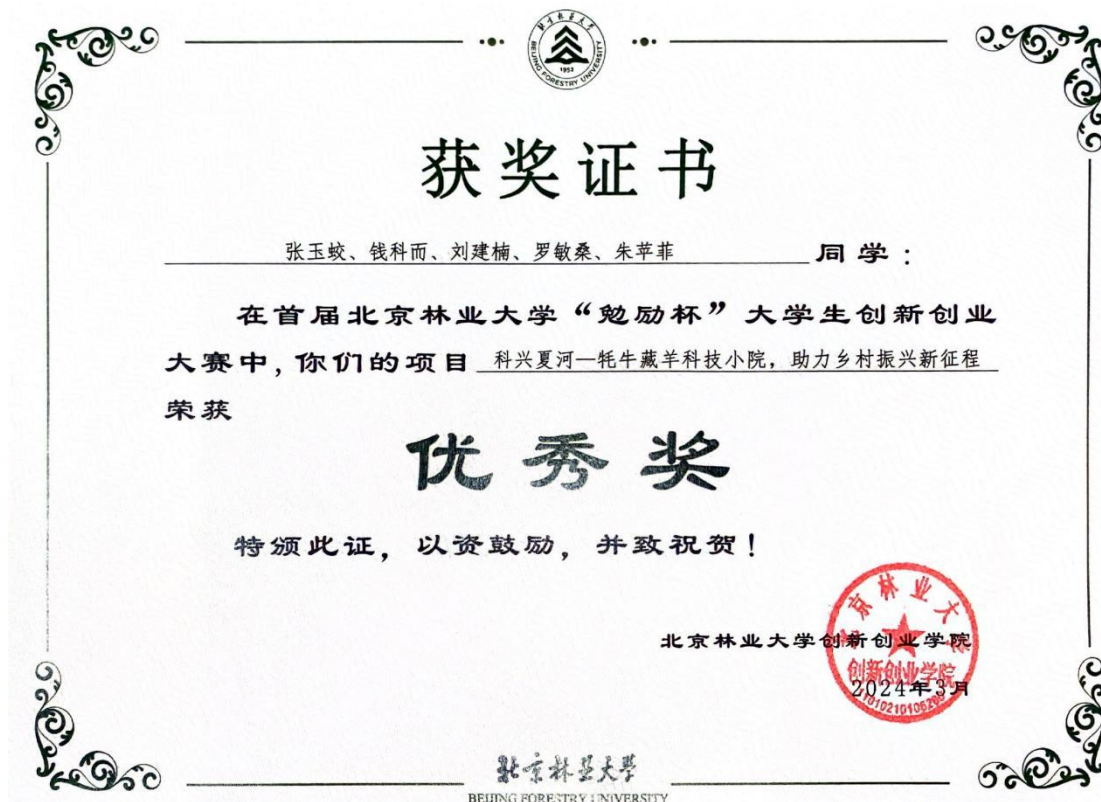


全国大学生生命科学竞赛委员会

二〇二四年七月

CULSC









第九届中国国际“互联网+”大学生创新创业大赛
北京赛区复赛高教主赛道

获奖证书

三等奖

项目名称：水域锐眸——针对水体内分泌干扰物的活细胞微量检测仪器

创 始 人：刘佳凡

项目成员：黄萌、王楚寒、张屹轩、龙捷、耿若涵、卢桐宇、董羽越、
邓培妍、牛艺璇、罗俪灵、张晨、陈智雅

指导老师：张浩林、程瑾、翁强、薛永基、韩莹莹、袁峥嵘

推荐学校：北京林业大学

在二〇二三年第九届中国国际“互联网+”大学生创新创业大
赛北京赛区复赛中荣获三等奖。

编号：2023100774







“青创北京”2023年“挑战杯”
首都大学生课外学术科技作品竞赛

获奖证书

徐义舒、马振书、叶家铭、杨蕊嘉、李宏旭、彭芑、李明卉

同学

你(们)的项目 CuPCA: 泛癌与铜死亡相关基因关联分析数据库

在“青创北京”2023年“挑战杯”首都大学生课外学术科技作品竞赛主体赛荣获

二等奖

高校名称: 北京林业大学

指导教师: 袁峥嵘、甘芝霖、程瑾

特颁此证, 以资鼓励。



获奖证书

北京林业大学第十三届“梁希杯”
大学生课外学术科技作品竞赛

银奖

项目：CuPCA：泛癌与铜死亡相关基因关联分析数据库

团队人员：徐义舒 马振书 宋丰成 杨蕊嘉

彭 芃 李宏旭 李明卉（共7人）



二〇二三年三月

获奖证书

北京林业大学第十三届“梁希杯”
大学生课外学术科技作品竞赛

铜奖

项目：麝鼠肠道微生物结构和功能的季节性变化

团队人员：宋丰成 李宏旭 徐义舒 彭 芃

郑然希 马书宝（共6人）



二〇二三年三月

获奖证书

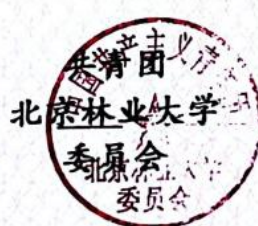
北京林业大学第十三届“梁希杯”
大学生课外学术科技作品竞赛

优秀奖

铁死亡相关基因

项目：在肝细胞癌中的表达及其预后价值

团队人员：李宏旭 宋丰成 彭 芃 徐义舒（共4人）



二〇二三年三月



荣誉证书

HONORARY CREDENTIAL



北京林业大学 许福老师：

您指导的梁澳康、梁澳康、吴鹏同学在“2023年第五届全国高校计算机能力挑战赛”中，成绩优异，荣获人工智能挑战赛本研组全国决赛一等奖，被评为：

优秀指导老师

特发此证，以资鼓励。

全国高等学校计算机教育研究会
全国高校计算机能力挑战赛组委会
2023年12月

编号: JTS_70109792117FT



2022年华北五省（市、自治区）及港澳台 大学生计算机应用大赛

在2022年华北五省（市、自治区）及港澳台大学
生计算机应用大赛中，经评审获得 本科组
二 等奖，特发此证。

作品名称：首都全民义务植树智慧管理系统

参赛院校：北京林业大学

参赛学生：陈与珩 杨博迪

指导教师：许福

北京市教育委员会（代章）

二〇二二年十一月



第八届中国国际“互联网+”大学生创新创业大赛
北京赛区复赛高教主赛道

获奖证书

一等奖

项目名称：麝香酮革命-生物合成麝香酮

创始人：谢文倩

项目成员：范思洁、高清净、姜姍、张香炜、贺婧悦、刘小语、
朱蕊苑

指导老师：张浩林、翁强、韩莹莹、袁峥嵘、何玥

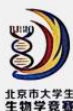
推荐学校：北京林业大学

在二〇二二年第八届中国国际“互联网+”大学生创新创业
大赛北京赛区复赛中荣获一等奖。



编号：2021100072





荣誉证书

第八届北京市大学生生物学竞赛

获奖项目：神经生长因子对小鼠肝脾发育及功能影响探究

获奖者：王乐，谭惠文，贾玉蓉，朱赫，张译心

指导教师：韩莹莹

获奖单位：北京林业大学

获奖等级：一等奖

证书编号：BIO20221133



荣誉证书

第八届北京市大学生生物学竞赛

获奖项目：早期母婴分离应激对雄性小鼠睾丸功能的影响

获奖者：董子敬，高山子，林怡，刘昱雯

指导教师：胡庆，高福利

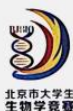
获奖单位：北京林业大学

获奖等级：二等奖

证书编号：BIO20221151







荣誉证书

第八届北京市大学生生物学竞赛

获奖项目：神经生长因子对小鼠肝脾发育及功能影响探究

获奖者：王乐，谭惠文，贾玉蓉，朱赫，张译心

指导教师：韩莹莹

获奖单位：北京林业大学

获奖等级：一等奖

证书编号：BIO20221133





CULSC

全国大学生生命科学竞赛

2022, 科学研究类

获奖项目

神经生长因子对小鼠肝脾发育
及功能影响探究

获奖学生

王乐、谭惠文、贾玉蓉、
朱赫、张译心

指导教师

韩莹莹

获奖单位

北京林业大学

获奖等级

二等奖

证书编号

CULSC2022KE0334



第三届北京市大学生节能减排低碳减排社会实践与科技竞赛

优秀指导教师

指导老师：程翔

指导项目：治理河湖富营养化之利器：装载MgO水凝胶球的鸟粪石原位结晶反应墙

在2021年“第三届北京市大学生节能减排低碳减排社会实践与科技竞赛”
获得荣誉称号，特发此证。

北京市教育委员会
二〇二一年十一月



荣誉证书

授予

于凡 同学（指导老师：许福）荣获2021全国大学生软件测试大赛总决赛

三等奖

开发者测试 个人赛

特发此证，以资鼓励！

证书编号：2021CN00A1036
大赛官网：moocetest.org

全国信息技术标准化技术委员会
软件与系统工程分技术委员会
2021年11月20日





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：麝鼠泌香腺中类固醇激素合成酶的季节性表达与调控

获奖者：王郁、徐露霞、钟佳慧、谭静怡、谭惠文

指导老师：张浩林、翁强

获奖单位：北京林业大学

获奖类型：一等奖（创新类）

证书号：CULSC2021CY0118

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，创新创业类）

获奖证书

获奖项目：血管内皮生长因子及其受体影响野生达乌尔黄鼠前列腺中的季节性增生

获奖者：陈迪、安晓宇、周粤、刘昱雯、王梓源

指导老师：翁强、许美玉

获奖单位：北京林业大学

获奖类型：三等奖（创新类）

证书号：CULSC2021CS0546

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，创新创业类）

获奖证书

获奖项目：瘦素参与调节野生达乌尔黄鼠睾丸活性季节性变化

获奖者：朱珏宇、刘宇欣、张紫雯、田育坤、王昊宇

指导老师：许美玉、韩莹莹

获奖单位：北京林业大学

获奖类型：三等奖（创新类）

证书号：CULSC2021CS0566

全国大学生生命科学竞赛委员会

二〇二〇年十一月





获奖证书

第十一届“挑战杯”首都大学生课外学术 科技作品竞赛

高校名称: 北京林业大学

作品名称: 神经生长因子对卵巢早衰的治疗功效研究

团队成员: 丁 霄、安晓宇、肖叶涛、周 粤、王 乐、朱 赫

指导教师: 韩莹莹、翁 强、

二等奖



二〇二一年五月



荣誉证书

第七届北京市大学生生物学竞赛

获奖项目：汽车尾气中内分泌干扰物对卵巢内 DNA 甲基化酶及 DNA 甲基化的影响

获奖者：王都、钟佳慧、谭静怡、谭惠文、袁晓洁

指导教师：张浩林、翁强

获奖单位：北京林业大学

获奖等级：二等奖

证书编号：BIO20211515

北京市教育委员会
2021年9月



荣誉证书

第七届北京市大学生生物学竞赛

获奖项目：早期母婴分离对雌雄小鼠 HPA 轴活性及海马体内炎症反应的影响差异

获奖者：刘昱雯、杨汶津、杨芃、李佳倩、胡清扬

指导教师：翁强、张浩林

获奖单位：北京林业大学

获奖等级：三等奖

证书编号：BIO20211587

北京市教育委员会
2021年9月



荣誉证书

第六届北京市大学生生物学竞赛

获奖项目：大熊猫应激状态与肠道微生物群落相关性研究

获奖者：肖一峰 王乃秋 韩莹莹 钟佳慧 王昊宇

指导教师：袁峥嵘 林浩林

获奖单位：北京林业大学

获奖等级：三等奖

证书编号：BIO20201724



荣誉证书

第六届北京市大学生生物学竞赛

获奖项目：围卵巢脂肪介导雌性生殖毒理作用研究

获奖者：赵立玮 丁霄 安晓宇 肖叶涛

指导教师：韩莹莹 袁峥嵘

获奖单位：北京林业大学

获奖等级：三等奖

证书编号：BIO20201717





优秀奖	小路晓路美丽乡村旅游信息公益平台	邱梦洁	温亚利
	“识鸟绘影”——面向湿地自然保护区水鸟生态智能	李鸿婧	王晗
	普通话与方言推广计划	潘晴	
	自韵常青家具定制有限责任公司	乔子津	刘毅
	基于互联网+人工智能的濒危野生动物灭绝风险评估与预警平台设计	张雪莹	袁峥嵘
	农汇——会“讲故事”的助农程序	夏薇佳	李小勇
	“智瞳”——基于边缘识别的野生动物智能自助观测	李峥嵘	张军国
	优种通——用户专属的优良种子引育管家	靳承卓	薛永基
	安租家具——打造回收利用一体化 家具租赁新模式	孙芊玥	陈凯
	静出女性旅游服务有限公司	林泳鸿	
	“证好由你”大学生个性化考证规划项目	谭航	
	绘生绘设——“电子绘本+沉浸式科普教育”助力儿童	李珊	侯宁
	林慧测——便携式苗木胸径测量系统	谢晴晴	李华晶



高等学校国家级实验教学示范中心
联席会

NATIONAL DEMONSTRATION CENTER FOR EXPERIMENTAL TEACHING

证书

为表彰第五届全国大学生生命科学创新创业大赛优秀成果
奖获得者，特颁发此证书。

作品名称：达尔黄鼠前列腺季节性增生与回缩：前列腺素 E 合成酶及
受体表达

获 奖 者：申雨瑶 赵立玮 肖一峰 刘源

学 校：北京林业大学

获奖等级：一等奖(创新类)

证书编号：NDC2020CXC00201

教育部高等学校生物技术、生物工程专业教学指导委员会

教育部高等学校食品科学与工程类专业教学指导委员会

高等学校国家级实验教学示范中心联席会

《高校生物学教学研究》编辑部

2020 年 8 月 23 日



高等学校国家级实验教学示范中心
联席会

NATIONAL DEMONSTRATION CENTER FOR EXPERIMENTAL EDUCATION

证书

为表彰第五届全国大学生生命科学创新创业大赛优秀成果
奖获得者，特颁发此证书。

作品名称：防御素在附睾：野生达乌尔黄鼠附睾中 SPAG11A 的季节性
表达

获 奖 者：张紫雯 刘沛 项思佳 闫帅廷 冯小航

学 校：北京林业大学

获奖等级：一等奖(创新类)

证书编号：NDC2020CXC00202

教育部高等学校生物技术、生物工程专业教学指导委员会

教育部高等学校食品科学与工程类专业教学指导委员会

高等学校国家级实验教学示范中心联席会

《高校生物学教学研究》编辑部

2020 年 8 月 23 日

证书



全国大学生创新创业实践联盟
National College Student Alliance for Innovation & Entrepreneurship Practice

编号: 202003062

袁峥嵘、张浩林、韩莹莹
高福利、翁强 同志:

您的论文《国家级线下一流本科课程
建设与改革实践研究——以动物生理学课
程为例》，在第三届全国大学生创新创业
实践联盟年会暨第四届双创实践新技术高
峰论坛优秀论文评比中荣获:

三等奖

全国大学生创新创业实践联盟
2020年12月30日



高等学校国家级实验教学示范中心
联席会

证书

为表彰第四届全国大学生生命科学创新创业大赛优秀成果
奖获得者，特颁发此证书。

作品名称：雌激素在雄性生殖道：达乌尔黄鼠附睾内雌激素的合成及潜
在作用

获 奖 者：齐鸿煜 王艺 张春娇 郭媛媛 范思洁 施锦欣

学 校：北京林业大学

获奖等级：一等奖(创新类)

证书编号：NDC2019CXCXY00095

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
教育部高等学校食品科学与工程类专业教学指导委员会
高等学校国家级实验教学示范中心联席会
《高校生物学教学研究》编辑部

2019年7月19日



高等学校国家级实验教学示范中心
联席会

证书

为表彰第四届全国大学生生命科学创新创业大赛优秀成果
奖获得者，特颁发此证书。

作品名称：催产素在雄性小鼠附睾形态与功能的季节性变化中的作用研究

获 奖 者：肖一峰 张紫雯 申雨瑶

学 校：北京林业大学

获奖等级：二等奖(创新类)

证书编号：NDC2019CXCXY00440

教育部高等学校生物技术、生物工程专业教学指导委员会

教育部高等学校食品科学与工程类专业教学指导委员会

高等学校国家级实验教学示范中心联席会

《高校生物学教学研究》编辑部

2019 年 7 月 19 日



高等学校国家级实验教学示范中心
联席会

证书

为表彰第四届全国大学生生命科学创新创业大赛优秀成果
奖获得者，特颁发此证书。

作品名称：脂联素介导围卵巢脂肪调节卵巢发育

获 奖 者：庄皓桐 杨佳伊 项思佳 闫帅廷 赵立玮 刘源

学 校：北京林业大学

获奖等级：三等奖(创新类)

证书编号：NDC2019CXCXY00987

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

教育部高等学校食品科学与工程类专业教学指导委员会

高等学校国家级实验教学示范中心联席会

《高校生物学教学研究》编辑部

2019年7月19日



北京市大学生生物学竞赛荣誉证书

北京林业大学

汤泽齐 余文洋 张紫雯 申雨瑶 冯小航 同学：

你们的项目 冬眠期黄鼬体内能量储存：脾大
输卵管内的糖原合成与脂肪代谢机制 在第五届北京
市大学生生物学竞赛实验设计竞赛单元中表现优秀，
荣获北京市二等奖。

指导老师：葛强 张洁林



BIO20191482



北京市大学生生物学竞赛荣誉证书

北京林业大学

张春娇 郭媛媛 范思洁 齐晓媛 王艺 同学：

你们的项目 机动车尾气中3-甲基-4-硝基苯酚干扰时钟基因影响卵巢内分泌发育时序 在第五届北京市大学生生物学竞赛实验设计竞赛单元中表现优秀，荣获北京市二等奖。

指导老师：张洁林 苗颖



BIO20191438



北京市大学生生物学竞赛荣誉证书

北京林业大学

张博 熊凯悦 应皓帆 吴佳明 程佳鑫 同学：

你们的项目 移风第一梯队 在第五届北京市大学生生物学竞赛奇思妙想竞赛单元中表现优秀，荣获北京市三等奖。

指导老师：韩莹莹



BJO20191345

荣誉证书

高校：北京林业大学

作品：基于野生达乌尔黄鼠动物模型研究前列腺增生与回缩机制

作者：翁强 王艺 齐鸿煜 张春娇 郭媛媛 范思洁

荣获第十届“挑战杯”首都大学生课外
学术科技作品竞赛

二等奖

特发此证，以兹鼓励。



二〇一九年六月

荣誉证书

高校：北京林业大学

作品：小鼠卵巢微环境影响雌性性腺发育机制研究

作者：董 强 庄皓桐 杨佳伊 赵立彤 刘 源

荣获第十届“挑战杯”首都大学生课外
学术科技作品竞赛

三等奖

特发此证，以兹鼓励。



二〇一九年六月

荣誉证书

高校：北京林业大学
作品：动物交配吸引机制探索：麝鼠犁鼻器性激素受体与气味受体表达研究
作者：翁强 张紫雯 肖一峰 崔楚若 冯小航 申雨瑶

荣获第十届“挑战杯”首都大学生课外
学术科技作品竞赛

三等奖

特发此证，以兹鼓励。



二〇一九年六月



创新引领未来 科技成就梦想

北京林业大学第十一届
“梁希杯”大学生课外学术科技作品竞赛

一等奖

项目：卵巢局部代谢微环境影响雌性性腺
发育机制研究

队员：庄皓桐

杨佳伊 赵立玮 刘 源

特发此证，以资鼓励

共青团
北京林业大学
委员会

北京林业大学
教务处

北京林业大学
党委研究生
工作部

北京林业大学
科技处

二零一九年五月



创新引航青春 科技成就梦想

北京林业大学第十一届
“梁希杯”大学生课外学术科技作品竞赛



项目：动物交配吸引机制探索：雄性麝鼠
犁鼻器性激素受体与气味受体表达研究

队员：张紫雯

冯小航 崔楚若

申雨瑶 肖一峰

特发此证，以资鼓励

共青团
北京林业大学
委员会

北京林业大学
教务处

北京林业大学
党委研究生
工作部

北京林业大学
科技处

二零一九年五月



创新引航青春 科技成就梦想

北京林业大学第十一届
“梁希杯”大学生课外学术科技作品竞赛



项目：基于达乌尔黄鼠动物模型研究前列腺增生与回缩机制

队员：王 艺

齐鸿煜 张春娇

郭媛媛 范思洁

特发此证，以资鼓励

共青团
北京林业大学
委员会

北京林业大学
教务处

北京林业大学
党委研究生
工作部

北京林业大学
科技处

二零一九年五月



第二届全国大学生生命科学竞赛

获奖证书

获奖项目：雄性麝鼠犁鼻器气味受体表达研究

获奖者：王子谊 张书豪 刘佳妮 陈鹏宇 张潇航

指导教师：翁强 张浩林

获奖单位：北京林业大学

获奖等级：三等奖

证书号：CULSC201803034

教育部高等学校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)》

二〇一八年十一月



第二届全国大学生生命科学竞赛

获奖证书

获奖项目：基于黄鼠动物模型研究前列腺增生与回缩机制

获奖者：张岩 齐鸿煜 肖一峰 王艺 黄璨

指导教师：张浩林 翁强

获奖单位：北京林业大学

获奖等级：三等奖

证书号：CULSC201803032

教育部高等学校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)》

二〇一八年十一月

荣誉证书

北京林业大学王子谊、张书豪、刘佳妮、陈鹏宇、张潇航同学：

在第四届北京市大学生生物学竞赛之生物学实验设计竞赛中表现优秀，荣获“北京市大学生生物学实验设计竞赛”一等奖。

指导教师：翁强、张浩林

特发此证，以资鼓励。

证书编号： 20181065



荣誉证书

北京林业大学张岩、齐鸿煜、肖一峰、王艺、黄璨同学：

在第四届北京市大学生生物学竞赛之生物学实验设计竞赛中表现优秀，荣获“北京市大学生生物学实验设计竞赛”一等奖。

指导教师：张浩林、翁强

特发此证，以资鼓励。

证书编号： 20181050





获奖证书



北京林业大学

王语涵 朱曼雨 张琳 郭婷 许恒源 黄璵 汤泽齐 同学：

你（们）的作品《天然无耐药性抗炎活性物质新探索--东北林蛙皮肤活性肽调节巨噬细胞免疫功能研究》在第十五届“挑战杯”中国银行全国大学生课外学术科技作品竞赛中荣获

三等奖

指导教师：翁强

特颁此证，以兹鼓励。



荣誉证书

高校：北京林业大学

作品：东北林蛙皮肤活性肽调节巨噬细胞免疫功能研究

作者：王淑娟、郭 婷、肖恒源、黄 璐、陈泽丹

荣获第九届“挑战杯”首都大学生课外学
术科技作品竞赛

一 等 奖

特发此证，以兹鼓励。



二〇一七年八月

荣誉证书

高校：北京林业大学

蟹广素通过内分泌、自分泌或旁分泌调节野生达马二醇鼠

作品：附睾中精子成熟研究

作者：朱俊雨、王子涵、杨一超、金文洋、张译航

荣获第九届“挑战杯”首都大学生课外学
术科技作品竞赛

二 等 奖

特发此证，以兹鼓励。



二〇一七年八月

第九届“挑战杯”首都大学生课外学术科技作品竞赛获奖名单 三等奖

作品内部编号	作品名称	类别
112845	液体和光纤通信中超短光脉冲的变系数非线性数理方程的解析符号计算及实验	数理
111961	高分辨率遥感影像阴影检测光谱比二次修正算法	数理
113186	圆周运动综合演示和测量仪研制	数理
112905	冰湖溃决灾害风险评估与预警系统研究--以一带一路枢纽地区新疆为例	数理
113189	测量刚体转动惯量实验改进装置的制作	数理
113068	农产品碳标签：探索与实践	生命科学
112902	可吸收生物修复膜	生命科学
112944	非对准情况下静脉穿刺针力测量初步实验研究	生命科学
113352	大兴简易便携式西瓜包装	生命科学
112462	SAP102在生后不同年龄大鼠与APP/PS1转基因小鼠海马中的动态表达变化	生命科学
112383	北京某体检人群代谢综合征组分数目与高尿酸血症发生的关联性分析	生命科学
112950	关于疾病大分子的体外检测方法	生命科学
112614	一种自平衡担架	生命科学
112825	不同提取方法下金银花木犀草苷含量比较研究	生命科学
112110	夫西地酸生物合成途径的前体物质研究	生命科学
112256	3-甲基-4-硝基苯酚干扰小鼠卵巢细胞增殖与凋亡调控的研究	生命科学
113207	3-O-(3-甲氧基肉桂酰)-甘草次酸酯对HepG2细胞体外抑制作用的研究	生命科学
112916	一种智能仿生空中驱鸟器的研究	生命科学
113288	基于NBD疏解的高效H2S分子探针的设计及应用	生命科学
112997	激光雷达树木轮廓扫描仪	生命科学
112847	家用式人工耳蜗植入儿童声源定位能力训练系统	生命科学
113174	一种含可微波炉加热陶瓷珠子的热暖袋	生命科学
112946	冬凌草叶水提取物对α-葡萄糖苷酶抑制作用的研究	生命科学
112764	茉莉酸对番茄花粉育性的影响初探	生命科学
113242	牛角地黄汤对金黄色葡萄球菌外毒素分泌表达的影响	生命科学
112673	一种护发生发的组合物及其制备方法	生命科学
113328	在酿酒酵母中基于2A系统的β-胡萝卜素的生物合成研究	生命科学
113410	甜菊糖醇注射剂对糖尿病小鼠血糖调节作用	生命科学



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一等奖

奖项：一等奖

1952

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节巨噬细胞免疫功能研究

队员：王语涵、汤泽齐、郭婷、许恒源、黄璨

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党委研究生
科技处

北京林业大学

北京林业大学
党委研究生
科技处

北京林业大学
党委研究生
科技处

〇 一 七 二 五 月



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一等奖

奖项：一等奖

1952

项目：“催产素”通过内分泌、自分泌或旁分泌调节野生达乌尔黄鼠精子成熟研究

队员：朱曼雨、王子谊、杨起、余文洋、张潇航

特发此证，以资鼓励





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二等奖

奖项：二等奖

1952

项目：3-甲基-4-硝基苯酚干扰小鼠卵巢

细胞增殖与凋亡调控的研究

队员：张琳、张书豪、张岩、陈鹏宇

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北京林业大学委员会

教务处

〇 一 七 年 五 月

荣誉证书

高校：北京林业大学

作品：东北林特精油量效促进巨噬细胞免疫功能作用

作者：王守强、黄睿、邓钰

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术科技作品竞赛

一等奖

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二〇一五年七月

荣誉证书

高校：北京科技大学

作品：内分泌学新发现：内乳素调节垂体前叶腺分泌腺垂体功能

作者：张欣 李晚晴 侯洋 郝博威

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术科技作品竞赛

三等奖

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二〇一五年七月

荣誉证书

高校：北京科技大学

作品：机动车尾气中硫氧化物对发动机排放功能研究

作者：岳天祥、王晨璐、赵月、唐增旗、杨锐

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术科技作品竞赛

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二〇一五年七月

荣誉证书

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二〇一四年八月

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北京林业大学

张凤伟 孙荣洋 李晓晴 陆博 伍潇潇 王亚超 吕天泽 同学：

你（们）的作品《内分泌学新发现：垂体调节小鼠泌乳素分泌性类固醇激素》在第十三届“挑战杯”全国大学生课外学术科技作品竞赛中荣获

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指导教师：翁强

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2013年10月

荣誉证书

第七届“挑战杯”首都大学生课外学术科技作品竞赛

高 校：北京林业大学

作 品：内分泌学新发现：垂体调节大鼠泌乳素分泌性类固醇激素

作 者：张凤伟、孙荣淳、李晓晴、陆博、伍潇潇、王亚超、吕天泽

指导老师：翁强、鲍伟东

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二〇一三年六月

荣誉证书

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高 校：北京林业大学

作 品：脂肪源瘦素功能新发现：冬眠前期促进黄鼠精子形成作用

作 者：潘彦勋、赵可、赵怡阳、王宇、钟卓珩、吴为、郝博威

指导老师：翁强、许美玉

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二〇一三年六月

荣誉证书

作品名称：内分泌学新发现：垂体调节麝鼠香腺分泌性类固醇激素

指导教师：翁强

作者：张凤伟 郝博威 李晓晴 吕天泽 陆博 德格晋

荣获北京林业大学第八届“梁希杯”课外学术科技作品竞赛

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二〇一三年四月

荣誉证书

作品名称：脂肪源瘦素功能新发现：冬眠前期促进黄鼠精子形成作用

作者：潘彦勋 赵可 赵怡阳 王宇 钟卓珩 吴为

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二〇一三年四月



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许福 舒志 张威 编著

- ① 本书内容深入浅出，循序渐进，由浅入深，由易到难，先介绍有关知识和技术，再以实例说明其开发应用。
- ② 本书可作为高等院校计算机专业及相关专业的教材，也可供从事计算机工作的工程技术人员参考。

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SAMS

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(美) Kevin Hoffman 著
李虎 许福 王晓博 等译



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China Machine Press

师心如风育新苗 科教融合铸匠魂

中国网 2025-07-03 15:24:52 32.5万

当科教兴国战略在新时代沃土中深植根系，一批深耕教育一线的科研工作者正以创新实践勾勒人才培养的新图景。北京林业大学生物科学与技术学院教授袁峥嵘，便是其中以"科教融合、协同育人"模式破题的探索者。在动物基因组学与生物信息学领域深耕多年，将科研创新与人才培养深度耦合，让实验室的"真题"成为学生成长的"养料"，用跨学科思维为青年科研者打开视野，在树木树人的育人征程中，书写着"知山知水，树木树人"的北林篇章。

科教融合：让科研"真题"成为育人"活教材"

在国家大力推进"科教融汇"的政策导向下，科研项目对人才培养的潜在价值愈发显著。国家自然科学基金"单细胞多组学整合解析麝鼠香囊腺发育和泌香功能"等国家级或省部级科研项目被拆解为数十个"科研小课题"，成为本科生实践的"练兵场"。



鸟鸣啾啾，树叶沙沙，北京通州张家湾集体林场的科技小院里十分热闹，这里的生物多样性实验室刚投入使用。

5月22日，国际生物多样性日当天，张家湾镇中心小学的学生们在科技小院入驻团队指导下，操作显微镜观察花粉结构，学习植物知识并制作标本。“我刚才观察了油松花粉。植物对我们的生活非常重要，每个人都应该做些力所能及的事，让身边的环境更加美好。”五年级学生姚金宸兴奋地说。

科技小院负责人、北京林业大学生物科学与技术学院副院长程瑾接受《民生周刊》记者采访时表示，生物多样性是人类社会赖以生存和发展的重要基础，我们是生物多样性的守护者和受益者。人人参与生物多样性保护，具有重要意义。



菁菁校园

校工会赴兄弟高校调研学习北京市青教赛、青管赛组织和参赛经验

发布时间：2025-06-23

- 分享 -



为调研学习北京市青教赛、青管赛组织和参赛经验，深入推动我校“北京高校青年教师先进教研工作室”建设。近日，校工会常务副主席韩俊彦带队，邀请理学院党委书记李万福，理学院党委副书记、院长王爱文一同赴北京林业大学、中国矿业大学（北京）、北京科技大学进行调研交流。



“种子银行”为物种延续提供保障 | 科技助力，守护多样之美

时间：2025-05-22 19:55:32 来源：中国环境APP 作者：中环报见习记者鲁昕

种质资源也成遗传资源，是生物多样性的基础。近年来，各国通过建立种质资源库、研究基因编辑技术等方式，探索基因技术在生物多样性特别是遗传多样性方面的应用，为物种的延续提供科技帮助。



让古树与人和谐共生

本报记者 向子丰

针对读者关心的古树保护相关问题,记者采访了北京林业大学信息学院(人工智能学院)院长许福、南京大学城市科学研究院执行院长胡小武、中国建筑科学研究院有限公司规划设计中心副主任冯新刚。

记者:一些地方的古树因为不知道树龄而未列入保护,怎么测算古树年龄?如何让这些未鉴定的古树被大家看见?

许福:比较常见的树龄鉴定方法有年轮法、生长锥法、回归估测法、碳

14测定法等。年轮法和生长锥法会对古树造成伤害,回归估测法、碳14测定法误差较大。目前我们在研究利用光谱影像技术扫描树木内部结构,就像在医院做CT一样,实现树龄无损精准鉴定。

今年将开展第三次古树名木资源普查,这次普查的要求是“应保尽保”,包括以往没有纳入保护范围或者没有进行鉴定挂牌保护的古树。而且将通过无人机、AI(人工智能)等手段在普查中快速识别树种、树冠尺

寸,结合环境数据推算树龄,预计会新增大量古树记录。

记者:从我们了解到的案例看,保护古树存在不少困难和问题,为什么会出现这样的情况?

许福:部分地区缺乏古树名木专项养护资金,巡护投入人力有限。另外,古树名木保护法规不完善,《古树名木保护条例》实施后,还要进一步完善地方配套细则,强化考核机制,建议将古树保护纳入各地林长制的考核标准中。

胡小武:一方面,古树养护得好看不出“成绩”,没养护好也似乎无人问责。有的地方政府对古树保护重视不够。另一方面,在古树保护工作中,林业、住建、文旅等多部门“多头管理”,权责不清晰。此外,在《古树名木保护条例》出台前,处罚上限较低,违法成本不高。

同时,在古树保护过程中,古树保护方案制定没有群众参与。尤其在没有居民避让古树的情况下,势必会增加一部分成本,没有明确这部分成本由谁负担,导致居民对保护古树缺乏热情,甚至产生抵触心理。这些都需要相关部门平衡好生态保护与生活需求的关系,增强公众对古树名木的保护意识。

记者:如果古树保护与城市建设、城镇化发展出现冲突,应当如何协调树与人的关系?

冯新刚:在城市规划和建设中,

应尽量避免让古树保护范围,但也不能使古树沦为景观“孤岛”,尽可能让人的生活与古树名木和谐共生。可以通过提高技术手段,实现保护与发展的平衡。如通过规划方案优化、工程技术创新和科学保育技术的构建,最大限度降低对古树名木的影响。

许福:古树与居民区共存时,应当优先进行安全评估,可以适当修剪影响建筑的枝干,这其实也是对古树的一种保护。当古树影响到居民生活时,可以通过补偿机制协调保护与民生的关系,比如村民宅基地上的古树由政府出资养护,为村民置换新的宅基地。

古树不仅有生态价值,也有历史文化价值,是重要的绿色文物。要通过创新利用,挖掘古树的文脉,比如建设古树名木数字博物馆,让更多人了解古树、爱护古树。



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“水!水!水!”在云南西双版纳体验“泼天的欢乐”

- “在德宏‘样样好’”体验背后的文旅融合之路
- 第十七届云茶博览交易会将于4月25至28日在昆明举办
- 昆明阳宗海风景名胜区“暖阳”志愿服务品牌发布
- 共赴“舍不得的丽江” 开启旅居丽江的诗意生活
- 云南西双版纳欢庆傣历新年 点燃春日激情

在专题报告环节,中国科学院生态环境研究中心研究员欧阳志云、植物研究所研究员马克平、昆明分院研究员周杰、西南林业大学研究员郭辉军、国家林草局西南林业调查规划院生态价值评估处处长张天星、北京林业大学教授许福和张志翔、中国科学院西双版纳热带植物园研究员曹敏、昆明动物研究所研究员蒋学龙、昆明植物研究所研究员伊廷双和李嵘、云南大学教授耿宇鹏等12位专家,分别围绕国家公园建设的政策和经验、高黎贡山国家公园核心价值、智慧林业、高黎贡山动物多样性、植物多样性和种质资源保存、生物多样性动态监测等方面作报告,分享了生物多样性研究领域的最新进展,探讨了加强国家公园建设、促进生物多样性保护与区域生态产品价值转化路径和对策,为活动注入了浓厚的学术氛围和前瞻性的思考。同时,杨祝良研究员和耿长安研究员参加了“生物多样性保护与产业高质量发展”平行活动,围绕高黎贡山的大型真菌资源与保护利用、草果的化学和功效研究及开发前景作报告分享。

国家林业和草原局应急揭榜挂帅项目验收

北京青年报客户端 2025-03-26 16:12

3月25日，国家林业和草原局应急揭榜挂帅项目“野生动植物和古树名木鉴定技术及系统研发”验收会举行。北京青年报记者了解到，该项目自2023年1月启动实施以来，在野生动植物精准识别和古树名木无损精准鉴定方面取得重要突破。其中，树龄鉴定技术有望为全国第三次古树名木普查等场景提供重要技术支撑，跨平台的野生动植物智能识别App已在我国多个国家公园和自然保护区示范应用。



据项目负责人、北京林业大学信息学院（人工智能学院）院长许福介绍，项目组创建了多场景古树名木树龄鉴定技术体系。在北京、江西、云南等地采集了5万余株古树名木信息，构建了古树名木健康体检数据库。

在此基础上，项目组设计了古树树龄光谱成像无损检测方法。“新技术攻克了树龄鉴定误差大、易对树木造成损伤等技术难题。”许福说。

此外，项目组建成了多生物特征的野生动物智能识别样本库和知识库，以及不同物候特征的珍稀濒危野生植物智能识别样本库和知识库，构建了包含108种野生动物和110种珍稀濒危野生植物的AI训练样本库，同时构建了云端在线野生动植物智能识别模型和移动端离线野生动植物智能识别模型。



9:17

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推荐





程瑾
北京林业大学
生物科学与技术学院
教授

"昆虫皇后" "食肉兰花" "美人杀手"

01:53

 胡利娟

一直以来，对于兰花螳螂出色的“伪装术”，人们猜测它的形态是模拟兰花花朵而演化。近日，发表在期...



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评论

乡村振兴 南开力量 | 科技帮扶助力夏河畜牧业高质量发展

来源：和美南开
2023-08-07 14:00

来源：和美南开



近日，南开区科技局与北京林业大学合作、依托津甘东西部科技协作项目申报的甘南夏河牦牛藏羊科技小院成功入选2023年首都高校师生服务乡村振兴行动计划。通过科技帮扶引导养殖户科学开展杂交改良，杂交后的犏牛产奶性能和生长性能均有所增加。通过集成早期妊娠诊断等先进技术，提升牦牛杂交改良效率1倍以上。

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生物学院“北京高校青年教师创新教研工作室”揭牌

来源：生物学院 发表时间：2023/07/27

近日，我校首个“北京高校青年教师创新教研工作室”揭牌仪式在生物楼310会议室举行。校工会常务副主席、生物学院负责人、教师工作部相关负责人、教务处相关负责人、创新教研工作室负责人及青年教师代表出席揭牌仪式。



校工会常务副主席指出，校工会将会同学校相关部门，为工作室建设保驾护航，并对工作室的建设工作提出希冀与要求。她强调，创新工作室的建设不仅要面向学院、学校，更要面向北京市大胆建设和创新探索，力争打造出具有自主特色的创新工作室，为高校青年教师发展开辟新范

《育见》——一颗种子的“太空之旅”

2023/06/30 11:28

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绿满万物生，北京城市副中心打造

🔖

🔄



东郊湿地园

北京林业大学生物科学与技术学院教授、博士生导师程瑾指出：“林地面积的增加、植物种类的丰富，使得各种昆虫数量与种类逐渐上升，又进一步为昆虫食性的鸟类和兽类的繁殖与扩张提供了重要食物来源。林地蓄水保水的效果促进了大型真菌的生长繁殖。水质条件的改善为水生植物与底栖动物的繁荣提供了条件。副中心大量的城市公园与湿地公园也保存了一定规模的生物资源，曾在通州分布较少的弓喙苔草、毛鞘苔草（耐旱地被，有较高的观赏价值）在城市绿心公园均有分布。”

副中心之所以生物多样性如此丰富，离不开林长制的保驾护航。今年3月，通州区发布的第1

中国绿色守望者

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赞

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写留言

CCTV-17农业农村频道 致富经

《致富经》 20220712 夏日冰冰凉 第6集 夏日里的“冷”美食

来源：央视网 2022年07月12日 22:14



城市里常见的植物是由谁决定的？

新周刊 2022-03-30 00:41

过去的20年，中国城市绿化建设呈现出高速发展的态势。2015年后每年千亿元以上的资金被投入到各大城市绿化项目之中，全国城市建成区绿化覆盖率整体呈稳步上升趋势。但是，城市绿化率和人均绿化面积的提升并不能直接说明城市绿化质量提高。

伴随中国城市化的发展，城市绿化成为了城市结构中最为重要的构成元素之一。但在探索过程中，城市绿化也走过很多弯路：南方植物一路北迁、热带植物不考虑适应性地栽种、外来植物无节制地培育等不科学的绿化方式，导致城市地域性生态特色变得模糊，城市与城市越来越相似，城市里的植物变得无趣而刻板。城市绿化刻意营造的生态环境，让人有种“不自然”的违和感。



什么才是好的城市绿化案例？城市里常见的植物是由谁决定的？南方与北方城市植物的选择需要考虑哪些因素？《新周刊》采访了北京林业大学生物科学与技术学院教授程瑾，从植物的角度谈谈中国城市绿化中的植物、城市与人之间共生共存的关系。程瑾教授认为，北京冬奥会赛场的建设是中国城市绿化转型中最值得参考的案例之一。

CCTV-17农业农村频道 致富经

《致富经》 20210903 南鳄北养 多样赚钱

来源：央视网 2021年09月03日 23:52



“以榜样的力量引领人 着眼国家战略需求培养人”



中央教育电视台在全国教育新闻联播节目报道了《动物生理学》课程“以榜样的力量引领人 着眼国家战略需求培养人”的课程思政成果。

澎湃号-政务 >

北林大支教教师程瑾：一生难忘的草原筑梦之行

北京林业大学 >
北京林业大学官方澎湃号

2020-06-08 20:25 北京

2019年7月，在国家脱贫攻坚的重要时刻，我有幸成为了北京林业大学教育扶贫服务团的一员，前往学校对口帮扶地区开展为期一年的支教服务工作。从那一刻起，内蒙古兴安盟科尔沁右翼前旗



北林焦点 绿色要闻 专题报道 校园动态 教学科研 媒体矩阵 媒体北林 党建思政 绿色人物 观点言论 北林报 图说北林 视

2025年10月12日 星期日



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韩莹莹：不忘育人初心，站稳三尺讲台

来源：生物学院 发表时间：2019/04/11



马尾辫、框架眼镜、干净温暖的笑容，初见韩莹莹老师，她便给我留下了干练、朴素又平易近人的印象。

入职五年，韩老师曾先后四次参加学院组织的青年教师教学基本功比赛初赛，今年终于突出重围，进入学校决赛并斩获特色组第一名。此后，她也将作为林大教师的代表，参加北京市级青教赛的角逐。

第二届“大创”成果展示与经验交流会总结会召开

【发布日期：2015-06-17 点击数：1697】

2015年6月15日上午，第二届北京林业大学大学生创新创业训练成果展示与经验交流会总结会在二教扇形报告厅召开。骆有庆副校长出席会议并讲话。教务处、学生处、招生就业处、校团委负责人、教学督导、各学院分管教学工作副院长、教学秘书、教师及学生代表等参加了总结会。



总结会上，翁强教授代表指导教师做了《“创新活动”之花》的主题发言；动画11班曹琦代表参与大学生创新创业训练计划的同学分享了《北京绿像素设计工作室》的创新创业之路；电气11-2班曹芳菲代表参与学科竞赛的同学重温了所在团队《缘起物联网，让梦想飞翔》的故事。



中国绿色时报：北林大学生入选科技创新团队

发表时间：(2014-05-08)

本报讯记者铁铮报道在团中央新近公布的大学生“小平科技创新团队”名单中，北京林业大学生物学院学生的一支团队榜上有名，他们将获中国青少年科技创新奖励基金的支持。这支团队名为“北林”野生动物生殖奥秘探索创新团队，是首都高校入选的5支团队之一。

据了解，邓小平同志的亲属捐献出邓小平生前全部稿费，委托团中央等设立了中国青少年科技创新奖励基金。基金主要用于支持中国青少年科技创新活动。2014年，基金面向全国大学生遴选支持百支在学术研究、科技竞赛、成果转化等方面取得突出成绩或有较大潜力的大学生科技创新团队，命名为“小平科技创新团队”。

“北林”野生动物生殖奥秘探索创新团队的前身，是在2005年成立的野生动物生殖生理学实验小组。这支团队自2008年成立以来，立足于揭示野生动物特殊的生殖生理学机理，在翁强教授的指导下，有60多名本科生依托国家、北京市和学校的大学生科技创新项目，探索和发现野生动物生殖生理学奥秘，取得了一批创新研究成果，多次获得大学生科研创新成果奖。

中國綠色時報

CHINA GREEN TIMES

報頭題字 江澤民 全國綠化委員會 國家林業局 主管 中國綠色時報社 主辦

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2014 年

3月21日

星期五 第3959期

北林大創新實驗室培養生物學人才

本報訊 為培養具有創新思維和綜合競爭力的複合型應用型人才,近年來,北京林業大學國家植物生物學基礎通過建立大學生物創新實驗室,不斷探索實地創新型人才培養模式,進一步提高了學生的專業知識水平和實踐動手能力。

學校和生物科學與技術學院為創新實驗室建設配備了高水平的專業團隊,通過定期討論會、大學生物創新培訓班,建設創新實驗室網站,開展高水平國內外學術交流等,提高學生參與創新實踐活動的興趣。北林野生動物生態實驗室創新團隊就是其中一支優秀的學生科研團隊。該實驗室自2008年建立以來,先後有40多名在校本科生物學專業、北京自然學校的大學生物技術創新班、國家和北京野生動物保護生物學實驗班取得了突出的創新研

究成果。

目前,北林野生動物生態實驗室創新團隊已在美國《科學引文索引》(SCI)期刊上發表研究論文15篇,21人次獲得國際學業以第一作者發表創新科研成果,2人次獲得國際學業優秀獎,3人次獲全國優秀生物學子獎,20多名學生赴美國、加拿大、歐洲、澳洲等地一流大學和科研機構從事生物學領域研究。北林大生物學院教授劉義強是該實驗室的指導教授。他承擔著3項教育部國家大學生物創新實驗設計題目和3項本科人才創新培養基金的指導任務。劉義強認為,大學生本身并不缺乏科研創造能力,關鍵的是要建立起科學的大學生物創新實驗培養機制和科研創新運行機制,積極引導和培養學生。(義強)

北林報

雁頭顯字，溫費

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□ 2012年10月16日 星期三

□ 第 363 期

□ 國內統一刊號 CN11-0814/G2

培养创新人才的“样板田”

● 有人认为,在北大,学生应以学业为重,没时间和精力从事科研活动。更有人认为,科研成果,均来自其他国家的植物生物学家。北大生物学院的领导教师却给出了截然不同的答案。

刘松中,在北大创新实验班培养的本科生,他掌握知识扎实,综合素质高,创新能力强,综合素质高,现已成为该领域学术的领军创新人才。

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2012年10月16日

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毕业本科生代表（99 人）

姓名	年级	毕业去向	个人业绩成果
郭子铭	2021 级	清华大学攻读博士学位	发表 SCI 论文 1 篇，申请专利 2 项。在校期间曾担任党建办公室主席团成员等。连续两年获国家奖学金、优秀学生一等奖学金、三好学生、优秀学生干部、校级文体和学术优秀奖学金等；曾获北京市优秀毕业生、北京市三好学生，参与三项市级校级科研项目，获得北京市大学生生物学实验设计竞赛一等奖，全国大学生生命科学竞赛二等奖等。
史可	2021 级	北京大学攻读博士学位	发表 SCI 论文 1 篇。在校期间曾担任生苑学生事务中心主席团成员等；连续三年获国家奖学金、优秀学生一等奖学金、校级三好学生、校级优秀学生干部、校级文体优秀奖学金等；曾获北京市优秀毕业生、北京市三好学生、“达标创优”优秀共青团员、学术优秀奖学金等；主持 2 项动物生殖生理学项目，参与 1 项植物分子项目，获国家级、市级奖项以及北京市级大创优秀结题；志愿北京时长 403h，曾参与服贸会、北半马等活动；连续四年代表学校参加首都高校比赛，曾获健美操比赛北京市第三名，拓展比赛单项北京市第二名等奖项。
徐义舒	2021 级	美国加州大学伯克利分校攻读博士学位	主要研究方向为计算机科学，医学工程方向 PhD，本科期间在 Database 等期刊发表 SCI 论文 2 篇。曾获得学术优秀奖学金，优秀学生二等奖奖学金，国际森林论坛玉兰奖，全国大学生实验设计竞赛三等奖，北京市挑战杯二等奖，北京市大学生实验设计竞赛二等奖，梁希杯银奖，全美大学生建模比赛 H 奖等。
张玉蛟	2021 级	浙江大学攻读博士学位	主要研究方向为基础医学，在 Life 等期刊发表学术论文 2 篇。在校期间获得全国大学生英语竞赛二等奖、生命科学竞赛一等奖、优秀学生二等奖、学术优秀奖学金、文体优秀奖学金，志愿时长 300h。
毛馨艺	2021 级	同济大学攻读硕士学位	主要研究方向为生物信息方向，发表 SCI 论文 1 篇，中文核心期刊 1 篇。在校期间曾获国家奖学金、全国大学生数学竞赛二等奖、全国大学生英语竞赛二等奖、北京市大学生生物学知识竞赛二等奖等 4 项国家级、8 项省部级、23 项校级荣誉奖励。
莫岚	2021 级	中山大学攻读硕士学位	研究方向为基础医学（分子医学）。在校期间曾获优秀学生二、三等奖学金，全国大学生生物竞赛三等奖和北京市大学生生物竞赛二等奖。

刘诗佳	2021 级	中山大学攻读硕士学位	主要研究方向为干细胞与再生。在校期间曾获优秀学生一等奖学金。
宋宗胜	2021 级	东南大学攻读硕士学位	在校期间曾担任理学院电子信息科学与技术专业 21-1 班班长，本科期间总学分积专业排名第二。曾获优秀学生一等、二等奖学金、学术优秀奖学金；在全国大学生蓝桥杯电子竞技中获省级二等奖、全国大学生数学建模竞赛中获省级二等奖；2023 年参加大学生创新创业项目，以北京市级立项，2024 年以良好结题；担任班长期间，工作勤勉尽责，获“三好学生”、“优秀学生干部”等荣誉称号。
邱万理	2021 级	北京大学攻读硕士学位	在校期间保研学分积和综合成绩均为专业第一，曾获国家奖学金，国家励志奖学金、优秀学生一等、三等奖学金、学术优秀奖学金；曾获全国大学生机器人大赛超级对抗赛全国赛三等奖、区域赛一等奖、高校联盟赛三等奖、电子设计竞赛北京市二等奖等；曾任开拓者机器人协会副会长、电子 23 级新生学业辅导员、北林森林狼电控组长，数学建模社宣传部部长。
宋语涵	2021 级	北京航空航天大学攻读硕士学位	在校期间曾任生科 21 班文艺宣传委员，北京林业大学校主持团骨干。曾获优秀学生二等奖学金、学术优秀奖学金等荣誉；主持国家级大学生创新创业项目并获优秀结题，全国大学生生物学知识竞赛三等奖、北京市大学生物理实验竞赛一等奖、诺维信杯首都高校生命科学竞赛三等奖等。
常琮朝	2021 级	北京航空航天大学攻读硕士学位	在校期间曾任本科计算机党支部副书记、信息学院党建办公室执行主席；以计算机大类与答辩双第一的成绩获国家奖学金；主持一项国家级大创项目；获全国大学生数学竞赛国三、美国大学生数学建模大赛 H 奖等奖项；带领班级获活力团支部与优良学风班称号；主持校招办的云观校活动，多平台直播观看人数超 15 万。
王天宇	2021 级	中国科学院大学攻读硕士学位	发表 SCI、软件著作权等 4 项科研成果。在校期间曾任校第二课堂办公室分管主席，23 级新生学业辅导员，高等数学助教和班级宣传委员；获优秀学生一等奖学金，学术优秀奖学金等 8 项奖学金；获评三好学生和优秀学生干部。在科创上，取得 2 项国家级、7 项省部级与 2 项校级竞赛奖项。
许升	2020 级	天津大学攻读硕士学位	主要研究方向为固体废物资源化。在校期间曾获优秀先进个人、北京市节能节水低碳减排竞赛一等奖等。

李宇宸	2020 级	北京林业大学 攻读硕士学位	主要研究方向为环境中新污染物的筛查与归趋，发表 SCI 论文 1 篇。现任研究生专硕党支部书记。
严梦灿	2020 级	清华大学攻读 硕士学位	主要研究方向为环境中新污染物筛查与分析；发表 SCI 论文一篇。现担任清华大学 SIGS 科普讲师团成员一职。
宋丰成	2020 级	北京林业大学 攻读硕士学位	主要研究方向为肉牛遗传育种，本科期间在 <i>Animals</i> 等期刊发表 SCI 论文 6 篇。曾获北京市挑战杯三等奖等奖项。
穆圣衡	2020 级	清华大学攻读 博士学位	发表 SCI 论文 1 篇。在校期间曾任生科 20 理科基地班班长；曾主持国家级大学生创新创业训练项目；曾获宝钢优秀学生奖、国家奖学金、优秀学生一等奖学金等荣誉奖项，也曾获全国大学生生命科学竞赛国家级二等奖、全国大学生英语竞赛国家级二等奖、连续三届获得北京市大学生生物学竞赛一等奖。
郑然希	2020 级	北京林业大学 攻读硕士学位	主要研究方向为基因编辑育种，在 <i>Current Bioinformatics</i> 发表 SCI 论文 1 篇。在校期间加入中国大学生“西部计划”研究生支教团项目前往内蒙古自治区兴安盟科尔沁右翼前旗支教。
于越	2020 级	清华大学攻读 博士学位	发表 SCI 论文 1 篇。在校期间连续三年获优秀学生一等奖学金、学术优秀奖学金等荣誉奖项。参与并获得全国大学生数学竞赛国家级二等奖、北京市大学生数学竞赛一等奖、北京市大学生生物学竞赛二等奖、全国大学生英语竞赛国家级二等奖等。
闫凌霄	2020 级	清华大学深圳 国际研究生院 攻读硕士学位	在校期间全学程学分积排名专业第一，曾获国家励志奖学金、优秀学生一等奖学金、学术优秀奖学金、社团活动奖学金、三好学生等 10 次荣誉；在学科竞赛上累计获得 13 次国家级和省部级奖项；主持一项北京市级大创项目并通过结题验收、以骨干成员身份参与一项国家级大创项目；曾担任理学院电子本科生党支部组织委员、电子爱好者协会会长、北林森林狼竞技机器人协会社团骨干、理学院女子篮球队队长；志愿北京时长 140h。
许照乘	2020 级	慕尼黑工业大 学攻读硕士学 位	在校期间连续三年获得校级优秀学生二等奖学金，以及校级三好学生、校级优秀班干部等荣誉；专业成绩优秀，拥有国家级奖项 4 个，曾获全国大学生数学竞赛二等奖、全国大学生物理实验竞赛三等奖、北京市大学生数学竞赛二等奖，以及若干校级奖项；曾任院学生会文艺部部长团成员、院排球队经理、班级学习委

			员。
李宏旭	2020 级	上海科技大学 攻读硕士学位	在 <i>Frontiers in Oncology</i> 等期刊发表 SCI 论文 3 篇。在校期间曾获优秀学生三等奖学金、梁希杯优秀奖等。
周健	2020 级	北京师范大学 攻读硕士学位	发表 EI 论文 1 篇。在校期间曾任信息学院计算机 201 班, 担任班长, 曾获优秀学生奖学金、学术优秀奖学金、校级三好学生、校级优秀学生干部等奖项; 带领班级取得“活力团支部”、“北京市先锋杯”等荣誉。曾参与北京市大学生创新创业项目, 北京林业大学科技创新计划项目; 曾获得美国大学生数学建模竞赛 Meritorious Winner 等奖项。
陈森达	2020 级	同济大学攻读 硕士学位	在校期间曾任信息学院计算机 202 班团支书。曾任计算机类 205 班宣传委员、校科协活动部部长; 54 门课程 90 分以上, 22 门课程 95 分以上; 曾获北京市优秀毕业生、三好学生、优秀学生干部等 8 项荣誉称号以及新生专业特等奖学金、优秀学生奖学金、学术优秀奖学金等 7 次奖学金; 专业成绩优异, 保研至同济大学; 热爱科研, 主持北京市级大创, 竞赛累计获得国家奖项 4 次, 省市级奖项 8 次; 文体突出, 曾获文体优秀奖学金; 参加志愿服务, 在疫情防控志愿服务中获优秀志愿者称号。
赵文斯	2020 级	北京师范大学 攻读硕士学位	在校期间曾任本科计算机党支部副书记、班级团支书等职务, 主持一项校级大创项目, 曾获北京市优秀毕业生、优秀党员、三好学生、优秀学生干部、优秀团支书等荣誉称号以及优秀学生奖学金等奖学金。积极参与志愿活动, 曾作为志愿者参与 2023 年中国国际服务贸易交易会。
李懿帆	2020 级	浙江大学攻读 硕士学位	在校期间曾任信息学院学生会体育部副部长、触控未来科创社团团支书、高等数学助教等。全学程学分积及综合排名第一, 曾获优秀学生一等奖学金、学术优秀奖学金、文体优秀奖学金、社团活动奖学金、三好学生, 北京市优秀毕业生等; 竞赛累计获得国家奖项 4 项, 省市级奖项 5 项, 校级奖项 7 项。
刘艾琳	2020 级	北京交通大学 攻读硕士学位	在校期间连续三年获优秀学生二等奖学金、学术奖学金, 现已保研至北京交通大学。曾获校优秀团员、三好学生、优秀干部、社会实践优秀个人等荣誉, 曾获第 15 届全国三维数字化

			创新设计大赛特等奖、第16届中国大学生计算机设计大赛一等奖、第十届全国大学生数字媒体科技作品及创意竞赛三等奖等；曾任院学生会传媒部副部长，数媒202班长，曾带领班级获院优良学风班，校优秀班集体称号。
袁毅慧	2020级	中国科学院大学攻读硕士学位	在校期间曾担任北林青春视频部主编、本科信息党支部宣传委员、信息201班权益委员；曾获北京市优秀毕业生、三好学生、优秀学生干部等4次荣誉称号和优秀学生奖学金、学术优秀奖学金等5次奖学金；曾作为志愿者参与2021年中国国际服务贸易交易会、服务保障中国共产党成立100周年庆祝活动，并获得优秀个人的称号。
赵美琪	2020级	中国科学院大学攻读硕士学位	在校期间曾任信息20-2班宣传委员；曾获北京市优秀毕业生、三好学生、优秀学生干部等6项荣誉称号；连续三年荣获国家奖学金、优秀学生一等奖学金，并获学术优秀奖学金、陈谋询奖学金等；曾任国家级大创项目主持人、院就业事务中心活动部部长、计算机导论助教等。
周兆福	2020级	中国科学院大学攻读硕士学位	在校期间曾担任学习委员、体育委员、学生党支部组织委员、信息学院男子足球队副队长；多次荣获优秀学生二等奖学金、校级三好学生等。2022年北京冬奥会期间，担任赛会志愿者，在主媒体中心为各国媒体提供交通保障服务；在竞赛方面，曾获第十四届全国大学生数学竞赛二等奖、2022团体程序设计天梯赛全国总决赛团队三等奖，以及第十四届蓝桥杯全国软件和信息技术专业人才大赛北京赛区三等奖。
谈天柱子	2020级	北京邮电大学攻读硕士学位	在校期间连续四年学分绩位列专业第一，曾担任物联网网工联合党支部支委、信息学院学生事务中心外宣部部长等，获北京市优秀毕业生、优秀学生一等奖学金、学术优秀奖学金等，主持一项大创项目并良好结题，获第十二届APMCM亚太地区大学生数学建模竞赛一等奖、2022年“挑战杯”首都大学生创业计划竞赛主赛道金奖等奖项，参与“左林右舍”“林里寻物”等校园常用小程序开发。
谢宜珊	2019级	北京大学攻读博士学位	主要研究方向为生物化学。在校期间曾获国家奖学金、优秀学生一等奖学金、二等奖学金、三好学生、校级优秀毕业生等荣誉奖项。
王梓源	2019级	中国科学院大学攻读硕士学位	主要研究方向为微生物生态学。在校期间曾任北京林业大学博物馆志愿服务团团团长；曾获得优秀学生一、二等奖学金，校级三好学生，优

			秀共青团员等荣誉。
张艺涵	2019 级	香港大学攻读硕士学位	在校期间担任电子 191 班班长、理学院电子本科生党支部组织委员；曾主持一项国家级大创，参加第七届全国物理实验竞赛获全国三等奖；履职尽责，团结向上，带领班集体获得“北京市先进基层组织”、“北京林业大学十佳班集体”等荣誉称号；曾获北京市优秀毕业生、北京林业大学三好学生、优秀学生干部、优秀学生奖学金等多项荣誉。
赵东辰	2019 级	英国爱丁堡大学攻读硕士学位	在校期间曾担任电子 192 班长。曾荣获 2019、2020、2021 学年校级优秀学生干部，2019、2021 学年校级三好学生等荣誉称号，荣获优秀学生三等奖学金、学术奖学金等。在 21 年全国电子设计竞赛中斩获北京市二等奖。积极参与实践活动，疫情期间多次担任社区志愿者，参加北林“A4210 光盘行动志愿者”活动，并多次去敬老院、孤儿院等参加校外志愿活动；2021 年代表理学院参加第三十五次校学生代表大会。
冯子阳	2019 级	香港中文大学攻读硕士学位	在校期间荣获国家奖学金、优秀学生一等奖学金、校级三好学生、校级优秀学生干部等。曾获 2021 年美国数学建模大赛 Finalist 奖、2021 年亚太数学建模大赛 First Prize 奖、第十二届全国大学生市场调查与分析大赛北京市一等奖以及梁希杯铜奖等。
武玲	2019 级	北京师范大学攻读硕士学位	发表 SCI 论文 2 篇，申请软件著作权 1 部。在校期间曾获北京市优秀毕业生、三好学生、优秀学生干部等 6 项荣誉称号以及国家奖学金、优秀学生奖学金等 6 次奖学金；竞赛方面，曾获得蓝桥杯三等奖、全国大学生数学竞赛三等奖等；科研方面，主持一项北京市级大创项目并以优秀结题。
孙语泽	2019 级	清华大学攻读硕士学位	发表 EI 论文 3 篇。在校期间参与国家重点研发计划两项，主持国家级大创项目优秀结题；曾获得中国大学生计算机设计大赛全国二等奖，知识图谱应用大赛全国一等奖，中国大学生团体程序设计竞赛全国二等奖等多项程序设计类奖项；带领信息学院获得院史第一次运动会奖项大满贯，各项体育赛事屡破佳绩；带领班级团队不断努力学习，坚持开展志愿服务活动，获得校十佳班集体等称号。个人获珠峰奖学金、学术奖学金等荣誉，连续三年被评为

			校级三好学生、优秀学生干部。
刘博	2019 级	中国传媒大学 攻读硕士学位	在校期间多次优秀学生奖学金二等奖三等奖，连续三年被评为校级三好学生，两年被评为优秀学生干部；同时也曾获得 ACM 校内赛二等奖，美国大学生数学建模大赛 H 奖，虚拟现实技术与应用创新大赛三等奖等奖项
韩用功	2019 级	北京邮电大学 攻读硕士学位	发表 EI 论文 2 篇。在校期间荣获优秀学生一等奖学金 2 次、优秀班干部 3 次，三好学生 2 次、获得北京林业大学 ACM 大赛一等奖与二等奖，蓝桥杯北京市三等奖，参与两项国家级大创。
席紫藤	2019 级	北京航空航天大学 攻读硕士学位	在校期间曾任信息学院本科物联网网工联合党支部副书记，连续三年荣获校级三好学生、优秀学生干部等称号，多次获得优秀学生奖学金、学术优秀奖学金等荣誉；参加专业类相关竞赛，累计获得国家级奖项 4 次，省市级奖项 2 次，校级奖项 1 次。曾任信息学院党建办公室组培部部长
米永艺	2019 级	武汉大学攻读 硕士学位	在校期间曾获国家奖学金、优秀学生一等奖学金，陈谋询信息专业奖学金、新科鹏举奖学金；曾获 2022 年“挑战杯”北京市金奖、“互联网+”北京市三等奖、2021 年团体程序设计天梯赛北京市三等奖；曾任信息学院学生会体育部副部长、信息 192 班心理委员；曾获三好学生、优秀团员、优秀心理委员、学期长跑明星、校园健康学子、校园运动达人等荣誉称号。
陈一凡	2019 级	浙江大学攻读 博士学位	主要研究方向为 miRNA 介导的细胞通讯及相关生物信息学工具开发。在校期间专业成绩第二，获优秀学生二等奖学金，全国大学生生命科学实验竞赛三等奖；曾赴哈萨克斯坦阿拉木图植物生物学和生物技术研究所做口头报告。
陈天厚	2018 级	深圳大学攻读 硕士学位	主要研究方向为锂离子电池粘结剂的开发与应用；申请专利 1 项。在校期间曾获北京市节能减排低碳减排大赛一等奖等荣誉。现担任巴斯夫广东湛江一体化基地生产工艺管培生一职。

刘旭豪	2018 级	美国西北大学 攻读硕士学位	主要研究方向为 RNA 治疗领域；在 <i>Journal of Affective Disorders</i> 等期刊发表 SCI 论文 2 篇。在校期间曾主持国家级大学生创新创业项目。曾担任默沙东（MSD）细胞研究专员；现担任礼来公司（Eli Lilly & Co.）高级生物学家，隶属于基因医学部门。
张雪莹	2018 级	荷兰阿姆斯特丹大学攻读硕士学位	主要研究方向为自噬基因在动物繁殖期的功能差异及基于深度学习的野生动物监测识别；在 <i>Animals</i> 等期刊发表 SCI 论文 3 篇。在校期间曾任院学生会外联部部长；曾主持国家级大学生创新创业训练项目，毕业论文被评为校级优秀论文。毕业后于天津某药企项目协调管理部门任职。
安晓宇	2018 级	清华大学攻读博士学位	主要研究方向为结构生物学。在校期间曾任校学生自律委员会骨干。曾获得国家奖学金，北京市三好学生，优秀学生一、二等奖学金，学术优秀奖学金，优秀学生干部等荣誉，获得北京市大学生生物学竞赛一等奖、二等奖、三等奖。
陈颖铎	2018 级	北京理工大学攻读硕士学位	在校期间曾担任电子 181 班班长、学生公寓自律委员会常务主席、粤港文化协会团支书、电子爱好者协会副会长；同时攻读北京大学国家发展研究院经济学辅修项目；曾获得北京市优秀毕业生、北京市三好学生、优秀学生干部、优秀学生奖学金等多项荣誉；在各级各类竞赛中总计获得 17 个奖项，并主持一项国家级大创项目。
周粤	2018 级	澳门大学攻读博士学位	主要研究方向为耐药性癌症细胞的诊断与治疗。在校期间曾获得优秀学生干部，国家奖学金，一等学业奖学金，学术奖学金，北京市大学生生物学竞赛一等奖、二等奖、三等奖，北京市优秀毕业生；曾任生物学院就业助理团外联部主席，生物 21 班学业辅导员，校学生公寓自律与管理外联部部长。
曹泽昊	2018 级	中国科学院大学攻读硕士学位	发表 SCI 论文 1 篇。在校期间获 6 项国家级及以上学科竞赛奖项，3 项省级竞赛奖项，11 项奖学金，7 项软件著作权，数十项校级及以下奖项。曾任“林里校园”微信平台（原“林次元口袋”）第一批开发组成员。
张宇哲	2018 级	北京邮电大学攻读硕士学位	在校期间获得国家奖学金、校级一等二等优秀学生奖学金、珠峰奖学金，连续三年被评为校级三好学生，两年被评为校级优秀学生干部。

姜文娟	2018 级	北京林业大学 攻读硕士学位	发表学术论文 3 篇。在校期间获得专业学科竞赛奖项 7 项,积极参与中华人民共和国成立 70 周年群众联欢活动、北京林业大学献血志愿服务等。曾获学业一等奖学金、优秀研究生干部、学术创新奖等荣誉。现在恒丰银行任职。
瞿小龙	2018 级	北京林业大学 攻读博士学位	发表学术论文 10 余篇;参与国家自然科学基金面上项目“基于多模态知识图谱推理的胃癌前疾病风险预警方法研究”和教改项目、横向项目若干;获得国家级/省部级学术竞赛奖项 10 余项。在校期间积极参与国际学术会议、志愿活动和社会实践,曾获国家奖学金、优秀研究生、优秀学生干部、北京市优秀社会实践团队等荣誉。
胡若涵	2018 级	中国人民大学 攻读硕士学位	在校期间曾获得 2019-2020 学年国家奖学金、优秀学术奖学金、一等奖学金等荣誉。积极参加科研竞赛,参与一项国家级大创,曾获全国大学生数字媒体科技作品及创意竞赛一等奖,MathorCup 高校数学建模挑战赛全国一等奖,美国大学生数学建模竞赛二等奖,北京市大学生动漫设计竞赛一等奖,北京市计算机设计大赛二等奖等奖项。
刘方舟	2018 级	中国科学院大学 攻读硕士学位	发表 EI 论文 2 篇,申请软件著作权 2 项。在校期间曾获计算机设计大赛国三、北二,美赛建模 H 奖,两篇一作、省部级大创结题一项在研,优秀学生二等三等奖学金、学术优秀奖奖学金,优秀学生干部、三好学生、2019 国庆服务保障“优秀个人”。
杜泽涛	2018 级	上海科技大学 攻读硕士学位	在校期间获蓝桥杯三等奖,互联网+创新创业大赛三等奖,主持一项国家级大学生创新创业项目,分别获校级一等奖、二等奖,优秀学生干部,优秀班干部,担任物联网 18 班团支部书记。
蒋妙妙	2018 级	北京交通大学 攻读硕士学位	在校期间曾获达标创优五四红旗优秀团支部书记、校三好学生、校优秀学生干部、北京市优秀毕业生、优秀学生二等奖学金、学术优秀奖奖学金、陈谋询信息专业奖学金等多项荣誉,获第十一届全国大学生数学竞赛二等奖,第四届虚拟现实技术及应用创新作品展优秀奖、三等奖。
王祺	2018 级	北京林业大学 攻读硕士学位	申请专利 2 项。在校期间荣获 10 余项国家级、省级及校级竞赛奖项,连续 3 年获评校级三好学生、优秀学生奖学金、学术优秀奖奖学金等,积极参与校院级和党支部组织的各项活动,带领班级获评北京林业大学“十佳优秀班集体”。

			目前在中国地质调查局油气资源调查中心任职。
崔可	2017 级	北京林业大学攻读硕士学位	主要研究方向为流域磷污染控制；已发表 SCI 论文 1 篇。现就职于理想汽车。
郭诗曼	2017 级	香港大学攻读博士学位	主要研究方向为病原微生物及噬菌体。在校期间曾任生物 17-3 班长、生科 17 副班长，院学生会传媒部部长；曾获得北京市优秀本科毕业论文，北京林业大学优秀本科毕业论文，优秀学生二、三等奖学金，优秀学生干部等荣誉。
宋悦	2017 级	河北省廊坊市疾病预防控制中心	在校期间曾任生物 171 班长、生科 17 团支书，校青协副主席，曾获优秀学生干部等荣誉。现担任河北省廊坊市疾病预防控制中心微生物检验师一职。
闫帅廷	2017 级	清华大学攻读博士学位	在校期间曾获国家奖学金、优秀学生一等奖学金、三好学生、优秀毕业生、优秀团员、全国大学生生命科学创新创业大赛一等奖、全国大学生生命科学创新创业大赛三等奖等荣誉奖项。
刘昊	2017 级	北京林业大学攻读硕士学位	在校期间担任研信息 2023 第一党支部书记，曾获“中国大学生自强之星”、北京市三好学生、北京林业大学研究生“党员标兵”等。现于中央办公厅任职。
杨楚峤	2017 级	北京大学攻读硕士学位	在校期间曾获得国家奖学金，校优秀学生一等奖学金，并获得优秀学生干部，优秀团员等荣誉称号。
谢艺嘉	2017 级	清华大学攻读博士学位	在校期间专业成绩第一；获国家奖学金（三次）、宝钢优秀学生奖学金、北京市优秀毕业生、全国大学生生命科学竞赛一等奖、全国大学生创新创业大赛一等奖等。
王冰蓉	2016 级	北京林业大学攻读硕士学位	主要研究方向为污水磷吸附去除材料；发表 SCI 论文 2 篇，申请专利 1 项。现担任上海塑料研究所工程师一职。
谭金宜	2016 级	英属哥伦比亚大学攻读博士学位	研究方向为真菌遗传学；以共同第一作者的身份在国际顶级学术期刊 Science 杂志发表论文。在校期间曾任生物 16 班长、北京林业大学交响乐团副团长，校艺术团事务监察主任，是“青兰计划”成员与艺术骨干，获得国家奖学金，北京市优秀毕业生，优秀学生一、二等奖学金，校级三好学生，优秀学生干部等荣誉。
王艺	2016 级	清华大学攻读博士学位	在校期间曾获国家奖学金、优秀学生一等奖学金、优秀学生干部、三好学生等荣誉称号。现于清华大学附属中学工作。

齐鸿煜	2016 级	浙江大学攻读博士学位	在校期间曾获国家奖学金、优秀学生一等奖学金、进步奖学金等，优秀学生干部、三好学生等荣誉称号。现于首都师范大学做行政管理工作。
范思洁	2016 级	同济大学攻读博士学位	在校期间曾获优秀学生一等奖学金，优秀学生干部，国家级生物竞赛一等奖等。
郭桐	2016 级	北京航空航天大学攻读硕士学位	在校期间曾获得一次国家奖学金、一次优秀学生一等奖学金、两次优秀学生二等奖学金，被评为校三好学生三次、校优秀学生干部三次、优秀团员两次。积极参与学科竞赛并获得美国大学生数学建模大赛一等奖、亚太地区大学生数学建模大赛二等奖、中国大学生计算机设计大赛二等奖、Mathorcup 高校数学建模挑战赛三等奖、首都“挑战杯”二等奖、北京林业大学“梁希杯”二等奖等荣誉。拥有 1 项软件著作权，参与 1 项校级大创并优秀结题。
刘霏霏	2016 级	北京航空航天大学攻读硕士学位	在校期间参与北京市大创 1 项。研究项目获得 2019 “华为杯”全国大学生物联网竞赛全国一等奖、2019 “挑战杯”首都大学生课外学术科技作品竞赛二等奖、2018 “蓝桥杯”团队创业赛全国总决赛二等奖、2017 “TT”杯全国大学生物联网设计大赛华北赛区一等奖等；曾获 2017 全国大学生数学建模竞赛获得北京市一等奖，首都高校武术集体项目获得太极功夫扇第一名。
吴宇晴	2016 级	北京邮电大学攻读硕士学位	在校期间曾获美国大学生数学建模比赛 M 奖、北京动漫设计大赛三等奖、北京数字媒体设计大赛三等奖、国家励志奖学金、北京林业大学二等奖学金、校级三好学生、优秀学生干部、团干部、军训优秀标兵、院级职业生涯规划大赛一等奖等。
张晓璇	2016 级	北京师范大学攻读硕士学位	在校期间多次获得校三好学生、优秀学生干部、优秀团支部书记、优秀学生二、三等奖学金、社会实践先进个人等荣誉；积极参加科研项目，主持的国家级大创项目“基于深度学习的湿地自然保护区水鸟识别”获得全国大学生创新创业年会“最喜爱的项目”奖，结题优秀，项目成果获得全国数字媒体技术大赛一等奖等奖项。
张雨薇	2016 级	中国科学院大学攻读硕士学位	在校期间曾获 2020 届北京地区高等学校优秀毕业生；曾获评国家奖学金、优秀学生一等奖学金、陈谋询信息专业奖学金、校级三好学生等荣誉；积极参与科研竞赛，曾获蓝桥杯三等奖、亚太地区数学建模二等奖等，参与北京市级大学生创新训练项目，以第一作者身份发表

			期刊论文。
王福琳	2016 级	北京大学攻读硕士学位	在校期间曾三度获得国家奖学金、优秀学生一等奖学金、三好学生等荣誉。积极参与学科竞赛，曾获美国大学生数学建模竞赛二等奖、全国大学生数学建模竞赛北京二等奖、蓝桥杯全国软件和信息技术专业人才大赛北京二等奖等奖项；主持一项大学生创新创业项目并在结题验收中被评为优秀，此外在校内以及实习期间曾参与多项科研课题。
蔡高轅	2016 级	北京林业大学攻读硕士学位	在校期间曾获学业一等奖学金、优秀研究生干部、优秀研究生等奖励和荣誉称号；2020 级研究生会主席，院级校友联络员。毕业后在天津某国企任职。
许哲楠	2016 级	清华大学攻读硕士学位	在校期间获得三好学生、校优秀学生一等奖学金、学术优秀奖学金、社团活动奖学金等。曾获中国大学生数学建模竞赛国家级一等奖、ACM 国际大学生程序设计竞赛亚洲区域赛铜牌、中国大学生程序设计竞赛铜牌等。
王子谊	2015 级	清华大学攻读博士学位	现于清华大学入职博士后。在校期间曾获国家奖学金、优秀学生一等奖学金、三好学生、全国大学生生命科学创新创业大赛一等奖。
张书豪	2015 级	清华大学攻读博士学位	现于斯坦福大学入职博士后。在校期间曾获国家奖学金、优秀学生一等奖学金、三好学生等。
翟浩铭	2015 级	纽约大学攻读硕士学位	在校期间曾参与国家级大学生创新项目。现担任美国 Biointron 公司业务拓展经理。
黄逸凯	2015 级	加州大学尔湾分校攻读博士学位	主要研究方向为发育细胞生物学。在校期间曾任百奥生物协会主席，生物院足球队队长；多次主持并完成国家级，市级大创以及学生社会实践活动；曾获优秀学生干部优秀学生三等奖学金等。现从事生物企业战略咨询和初级研究员工作。
刘天禹	2015 级	清华大学攻读博士学位	在 ICML 等国际顶级会议发表多篇论文。在校期间曾获国家奖学金、宝钢奖学金、北京市优秀毕业生、优秀学生干部等荣誉；硕士期间获评西贝尔学者荣誉称号。曾获全国校园铁人三项邀请赛冠军、首都高校速滑比赛亚军，研究生阶段带队夺得全国大学生冰球联赛(CUHL)常规赛冠军。
滑蕊	2015 级	北京理工大学攻读硕士学位	在校期间连续三年获得校一等奖学金，多次获得三好学生、优秀学生干部、社团活动奖学金；曾任剧社 15 级社长，社团十佳人物。

唐瑶	2015 级	北京航空航天大学攻读硕士学位	在校期间参与国家级大创 1 个, 校级大创 2 个, 发表论文一篇。国家励志奖学金 2 次; 优秀学生一等奖学金 1 次; 优秀学生二等奖学金 2 次; 优干三好学干之星等荣誉称号 6 次。
卜郁	2015 级	北京林业大学攻读硕士学位	在校期间曾担任班级团支书, 获一等奖学金、优秀研究生干部等荣誉。毕业后担任北京林业大学水保学院辅导员一职。
莫丽红	2014 级	广西大学攻读硕士学位	主要研究方向为环境中重金属与有机物的交互作用机理; 发表学术论文 1 篇, 参与科研项目 3 项, 完成 20 余个环境评价项目。现担任广西工程职业学院教师一职。
吕卿毓	2014 级	中国人民大学攻读硕士学位	主要研究方向为生命健康产业发展、企业培育等。在校期间曾获得优秀学生二等奖学金、全国大学生英语竞赛二等奖, 并完成北京大学经济学双学位学习获得毕业证书。现担任武汉东湖新技术开发区管理委员会副科级干部。
纳静	2012 级	北京航空航天大学攻读硕士学位	主要研究方向为骨科力学生物学、干细胞与组织再生; 在 Biomaterials 、 Bioactive Materials 等高水平期刊发表 SCI 论文 14 篇; 主持国家自然科学基金青年项目和天津市自然科学基金青年项目各 1 项; 参与南开大学医学院眼视光研究院开放基金项目和天津市卫生健康科技项目青年项目各 1 项; 曾获北京航空航天大学优秀博士学位论文。现担任南开大学讲师一职。
张硕	2012 级	中国农业大学攻读博士学位	主要研究方向为生理学和警犬技术; 发表 SCI 论文 9 篇。在校期间曾任生科 12 班团支书, 院学生会文艺部副部长, 获校级优秀团支书。现担任北京警察学院讲师。
刘佳琪	2011 级	北京林业大学攻读硕士学位	主要研究方向为污水除磷与资源回收研究; 发表 SCI 论文 3 篇, 申请专利 1 项。现担任瑞士 MDPI 出版集团期刊编辑一职。
郑倩雯	2011 级	北京林业大学攻读博士学位	主要研究方向为 CO2 捕集与资源化利用技术及机制研究; 中科院生态环境研究中心博士后, 发表 SCI 论文 15 篇, 申请专利 2 项; 主持国家自然科学基金青年基金和中国博士后科学基金面上项目等。在校期间曾获国家奖学金、先后两次获北京市优秀毕业生、国家公派留学奖学金等荣誉。
杨文	2011 级	北京师范大学攻读博士学位	主要研究方向为水污染资源化治理与多功能传感器件开发等; 共发表 SCI 及 EI 论文 20 余篇; 承担或参研多项军委或陆军科研项目。现担任中国人民解放军陆军防化学院讲师一职。
张亦蓁	2011 级	浙江大学攻读硕士学位	主要研究方向为污水收集系统碳排放监测与评估; 发表学术论文 4 篇, 参与团体标准编制

			1 项，申请软件著作权 1 项。曾作为骨干参与 14 项污水处理工程设计，参与科研项目 7 项。所参与项目曾获上海市水务海洋科技进步一等奖、南京市优秀工程设计一等奖、江苏省优秀勘察设计三等奖。现担任上海市环境科学研究院工程师一职。
席丽琴	2011 级	北京林业大学攻读硕士学位	主要研究方向为肉类加工的应用技术研究、工程化开发、食品质量和安全检测；发表 SCI 论文 4 篇。在校期间曾获得学术创新奖，校级优秀毕业生等荣誉。毕业后就职于中国肉类食品综合研究中心。
徐小牧	2011 级	英国曼彻斯特大学攻读硕士学位	发表学术论文 3 篇。现担任中国科学院文献情报中心馆员，文献传递与馆际互借团队负责人。参与中国科学院、文献情报中心、国家科技图书文献中心(NSTL)等相关任务十余项。
孙中恩	2009 级	北京林业大学攻读硕士学位	现担任北京市公安局环食药旅总队机动支队三级警长一职；负责知识产权和烟草领域违法犯罪打击工作，曾荣立个人三等功 2 次、个人嘉奖 5 次，获评环食药旅总队“优秀共产党员”荣誉称号。
崔雁翔	2008 级	香港科技大学攻读博士学位	主要研究方向为硫基自养反硝化脱氮在移动床式生物膜反应器（MBBR）上的应用；发表 SCI 论文 15 篇，申请专利 2 项，出版著作 1 本。现担任中国建筑工程助理设计经理。参与香港环保署和澳门环保局的大型基建项目的招投标和工程项目管理工作，包括香港有机资源回收中心第二期（合约额约 36 亿港元），澳门有机资源回收中心（合约额约 20 亿澳门币），香港新界西填埋场扩展工程（合约额约 611 亿港元），香港综合废物管理设施第二期（预计合约额超 300 亿）。
高艳珊	2008 级	北京林业大学攻读博士学位	主要研究方向为大气污染控制；在 Chemosphere、Journal of Materials Chemistry B 等高水平期刊发表 SCI 论文 40 余篇。入选北京市科协青年人才托举工程，获北京市科学技术三等奖、教育部优秀成果二等奖、中国科技产业化促进会科学技术二等奖。现担任北京林业大学环境科学与工程学院教授一职。