

# 中国农业大学生物学院建院 40 周年重要科研成果回顾

傅静雁, 傅缨, 郭岩, 韩建永, 李大伟, 毛同林, 任东涛, 田长富, 王超, 王毅\*, 杨淑华, 于静娟, 张华, 赵要风

中国农业大学生物学院, 北京 100193

\* 联系人, E-mail: [yiwang@cau.edu.cn](mailto:yiwang@cau.edu.cn)

2025-03-13 收稿, 2025-06-10 修回, 2025-07-02 接受, 2025-07-02 网络版发表

**摘要** 1984 年 12 月, 中国农业大学整合彼时农学系、植保系、兽医系、农业物理气象系、畜牧系的相关专业、教研组以及中心实验室, 成立生物学院, 这是我国最早组建的生物(生命科学)学院。到 2025 年, 生物学院已走过 40 载春秋, 迎来建院 40 周年。40 年来, 在国家各级部门的大力支持下, 中国农业大学生物学院广纳海内外优秀人才, 组建起一支兼具国际化视野与强大竞争力的教师队伍。生物学院聚焦科研创新团队建设, 凭借优良的科研条件和坚实的技术支撑平台开展科学研究, 积极拓展国际合作与交流, 在生命科学、农业生物学领域取得了一系列令人瞩目的科研成果, 在国际上产生了广泛影响。本文主要介绍生物学院成立 40 年来, 在植物生理学、动物生理学、微生物学与免疫学、细胞生物学、生物化学与生物技术等领域取得的重要原创性学术成果。这些成果不仅助力生物学院跻身生命科学学科国际领先行列, 也为农业科技创新和人类生命健康贡献了重要力量。

**关键词** 植物生理学, 动物生理学, 微生物学与免疫学, 细胞生物学, 生物化学与生物技术

1984 年 12 月, 中国农业大学将当时农学系的植物生理生化专业、植保系的农业微生物专业、兽医系的动物生理生化专业、农业物理气象系的农业生物物理专业, 农学系的植物教研组、细胞生物学教研组、分子遗传学教研组, 畜牧系的动物教研组, 农业物理气象系的数学、物理两个教研组以及中心实验室整合成立了生物学院, 成为我国最早组建成立的生物(生命科学)学院。历经 40 年的发展, 中国农业大学生物学院形成了一支具有国际化视野与竞争力的教师队伍和科研团队, 在植物生理学、动物生理学、微生物学与免疫学、细胞生物学、生物化学与生物技术等领域取得一批具有国际影响力的科研成果。本文将简要介绍生物学院近 40 年以来取得的代表性科研成果。

## 1 植物生理学

植物生理学是研究植物生命活动规律及其与环境

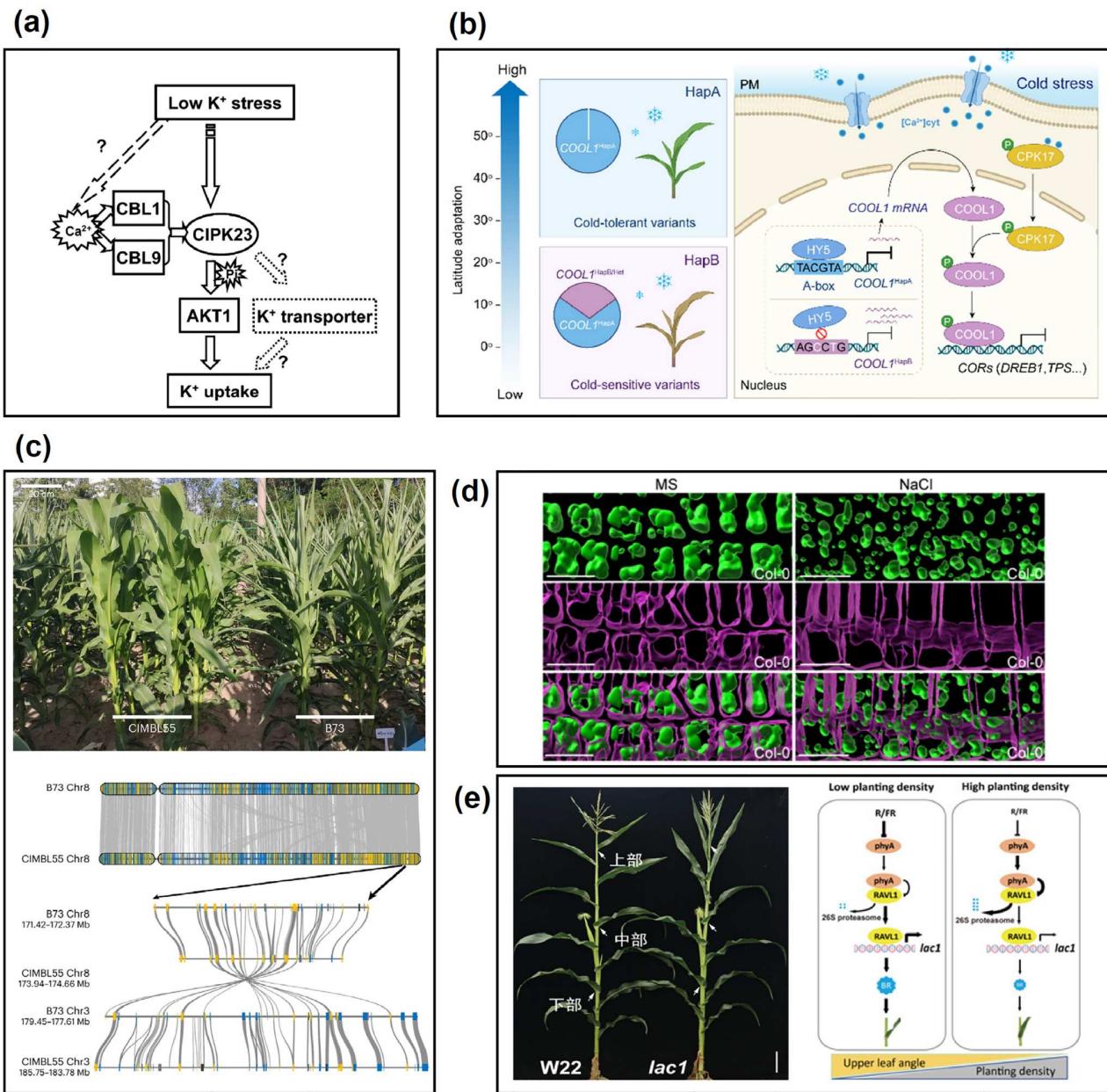
相互关系的科学。在农业生产中, 植物生理学理论在指导合理施肥、精准灌溉、密植管理、抗逆品种改良、作物产量和品质提升等方面发挥了重要作用。生物学院植物生理学的研究始于娄成后院士(1911~2009 年), 他长期从事高等植物细胞间物质运输及信息传递的研究, 为研究植物感应性和植物对环境变化的适应性开辟了新的思路。他对中国农业科学, 特别是植物生理学学科的发展作出了重大贡献, 也开启了生物学院植物抗逆高效研究的方向。生物学院一直致力于开展“植物/作物抗逆高效的生理生化及分子生物学基础”的创新性和前瞻性研究, 形成了鲜明的研究特色, 引领了该领域的国际学术研究方向。过去 40 年, 在植物响应干旱、盐碱、低温等非生物胁迫的分子调控机制, 植物养分和光能高效利用的基础理论研究, 以及作物环境适应机制解析和作物抗逆高效种质创新等方面取得了突破性进展。武维华院士团队首次报道了植物中较完整的

引用格式: 傅静雁, 傅缨, 郭岩, 等. 中国农业大学生物学院建院 40 周年重要科研成果回顾. 科学通报, 2025, 70: 4241~4258

Fu J, Fu Y, Guo Y, et al. Review of major scientific research achievements on the 40th anniversary of the establishment of the College of Biological Sciences, China Agricultural University (in Chinese). Chin Sci Bull, 2025, 70: 4241~4258, doi: [10.1360/CSB-2025-0277](https://doi.org/10.1360/CSB-2025-0277)

钾吸收分子调控通路CBL1/9-CIPK23-AKT1, 发表了国内植物领域第一篇*Cell*研究论文<sup>[1]</sup>(图1(a)), 成果入选教育部“2006年度中国高等学校十大科技进展”; 阐明了植物应答低钾胁迫的信号感受和转导通路<sup>[2]</sup>; 系统解

析了植物钾、磷吸收和转运的分子调控网络<sup>[3,4]</sup>, 为植物养分高效利用提供了理论支持。张静教授团队解析了铁氧还蛋白调控玉米氮代谢的分子机制<sup>[5]</sup>, 阐明了氮信号通过NRT2.1-PIN7及CIPK1-NAC075-WRKY53



**图 1** 植物生理学方向代表性研究成果. (a) 植物中的CBL1/9-CIPK23-AKT1钾吸收调控通路, Reproduced from Ref. [1]; (b) 玉米适应高纬度低温环境的分子机制, Reproduced from Ref. [11]; (c) 玉米抗旱优异材料CIMBL55基因组高质量组装, Reproduced from Ref. [19]; (d) 液泡动态变化调控植物耐盐性的分子机制, Reproduced from Ref. [29]; (e) 玉米“智慧株型”基因LAC1调控玉米株型适应密植的分子机制, Reproduced from Ref. [41]

**Figure 1** Representative research achievements in plant physiology. (a) Schematic model of the CBL1/9-CIPK23-mediated regulatory pathway of AKT1, Reproduced from Ref. [1]. (b) Proposed model for the cold tolerance and high-latitude adaptability of maize mediated by *COOL1*, Reproduced from Ref. [11]. (c) Drought-resistant phenotypes and genome assembly of maize inbred line CIMBL55, Reproduced from Ref. [19]. (d) Dynamics of multi-vesicular body trafficking and vacuolar regulation in response to salt stress, Reproduced from Ref. [29]. (e) Working model for the maize smart-canopy architecture gene *LAC1* in enhancing yield at high densities, Reproduced from Ref. [41]

模块介导根系适应性生长的分子机理<sup>[6~8]</sup>, 揭示了植物激素ABA和独脚金内脂与生长素互作调控植物生长的新机制<sup>[9,10]</sup>, 这些成果为揭示植物氮高效和根系可塑性发育的分子机制提供了重要理论基础。杨淑华教授团队率先揭示了玉米适应高纬度低温环境的分子机制, 发现玉米COOL1基因的自然变异通过增强低温耐受性, 促进其适应高纬度气候, 这一发现填补了关于玉米适应高纬度低温环境分子机制的研究空白, 并为高纬度地区玉米的种植提供了新的分子育种策略<sup>[11]</sup>(图1(b))。此外, 该团队还发现了调控植物耐低温胁迫的关键蛋白激酶OST1, 构建了以OST1为核心的植物响应和适应低温的分子调控网络<sup>[12~15]</sup>, 并揭示了植物激素、光温信号互作协同调控植物低温适应性机制, 为全面阐明低温和光及内源信号的互作机制提供了重要范式<sup>[16~18]</sup>。秦峰教授团队发现玉米抗旱优异种质资源材料CIMBL55, 并完成了该基因组高质量的从头组装(图1(c)), 构建了玉米转录因子家族及其靶基因的调控层级网络<sup>[19,20]</sup>; 开展了玉米抗旱基因的全基因组关联分析, 并克隆多个玉米抗旱关键基因<sup>[21,22]</sup>; 解析了抗旱基因ZmSRO1d的自然变异通过促进气孔关闭增强玉米抗旱性, 并调控抗旱性与产量之间的平衡<sup>[23]</sup>, 研究成果为玉米抗逆、高产的分子设计育种提供了理论支撑和关键的基因资源。巩志忠教授团队发现了干旱胁迫应答调控网络中GHR1、EAR1、PUB12/13、ZmCPK2等多个重要组分<sup>[24~27]</sup>, 从信号转导、蛋白稳定性、转录调节等不同层面, 解析了ABA和干旱胁迫信号调节气孔运动、影响植物抗旱性的分子机理。郭岩教授团队揭示了以SOS2为核心的植物耐盐信号调控网络<sup>[28,29]</sup>(图1(d)), 并解析了盐胁迫下植物调控根尖分生、根系生长、根毛发生的分子机制<sup>[30,31]</sup>, 阐明了磷脂信号分子和内源小分子在调控植物抗逆性和离子稳态中的作用机理<sup>[32,33]</sup>, 这些研究为理解植物应答盐碱胁迫的分子机制提供了重要理论依据。蒋才富教授团队定位并克隆了多个玉米耐盐碱QTL和关键基因; 阐明了盐碱胁迫下钙信号解码及其调控盐离子转运的新机制<sup>[34]</sup>, 发现HAK家族Na<sup>+</sup>转运蛋白介导木质部盐离子卸载从而增强耐盐性<sup>[35]</sup>, 解析了玉米通过调控凯氏带可塑性抑制盐离子向根中柱装载的重要耐盐机制<sup>[36]</sup>, 这些研究为培育耐盐碱玉米新品种奠定了重要基础。李继刚教授团队围绕光调控植物逆境响应的分子机制, 鉴定了植物远红光信号传递的新组分TZP, 并阐明其调控光受体phyA磷酸化的分子机制<sup>[37,38]</sup>; 揭示了光与

ABA信号拮抗、光促进植物耐盐以及光与低温信号互作的新机制<sup>[39,40]</sup>; 阐释了玉米“智慧株型”基因LAC1通过光信号途径动态调控玉米株型适应密植的分子机制<sup>[41]</sup>(图1(e)), 为进一步深入解析远红光信号途径以及光信号调控网络提供了新的见解, 也为玉米耐密高产分子设计育种提供了重要理论基础和技术支撑。王涛和董江丽教授团队以苜蓿为材料开展了系统性研究, 率先解析了高杂合高重复的紫花苜蓿基因组结构<sup>[42]</sup>; 发现胞质氧化还原感受器APT1, 并系统解析了膜锚定转录因子ATAF亚家族通过NAC-APT模块抵抗非生物胁迫的共性机制<sup>[43,44]</sup>, 发现豆科植物特有的能量感受器<sup>[45]</sup>; 建构了基于细胞核雄性不育系的三系快捷育种体系<sup>[46]</sup>, 这些成果为苜蓿抗逆高效研究和生物育种提供了重要基础。巩志忠和齐俊生团队通过工程菌发酵创制了蛋白干粉“VDAL-维大力”和“VIPR1L-禾敏素”, 相关成果已获中国、美国、俄罗斯等13国专利授权, 累计转让金额达5800万元。经50余种作物田间证明, 维大力和禾敏素能够显著提高作物产量、改善品质并增强作物免疫力和抗逆性, 已在小麦、玉米、水稻及果蔬等作物上推广超过1000万亩。这些研究成果不仅推动了植物抗逆和高效利用的理论进展, 还为农业生产中的作物育种和种植提供了重要的理论依据和技术支持。

## 2 动物生理学

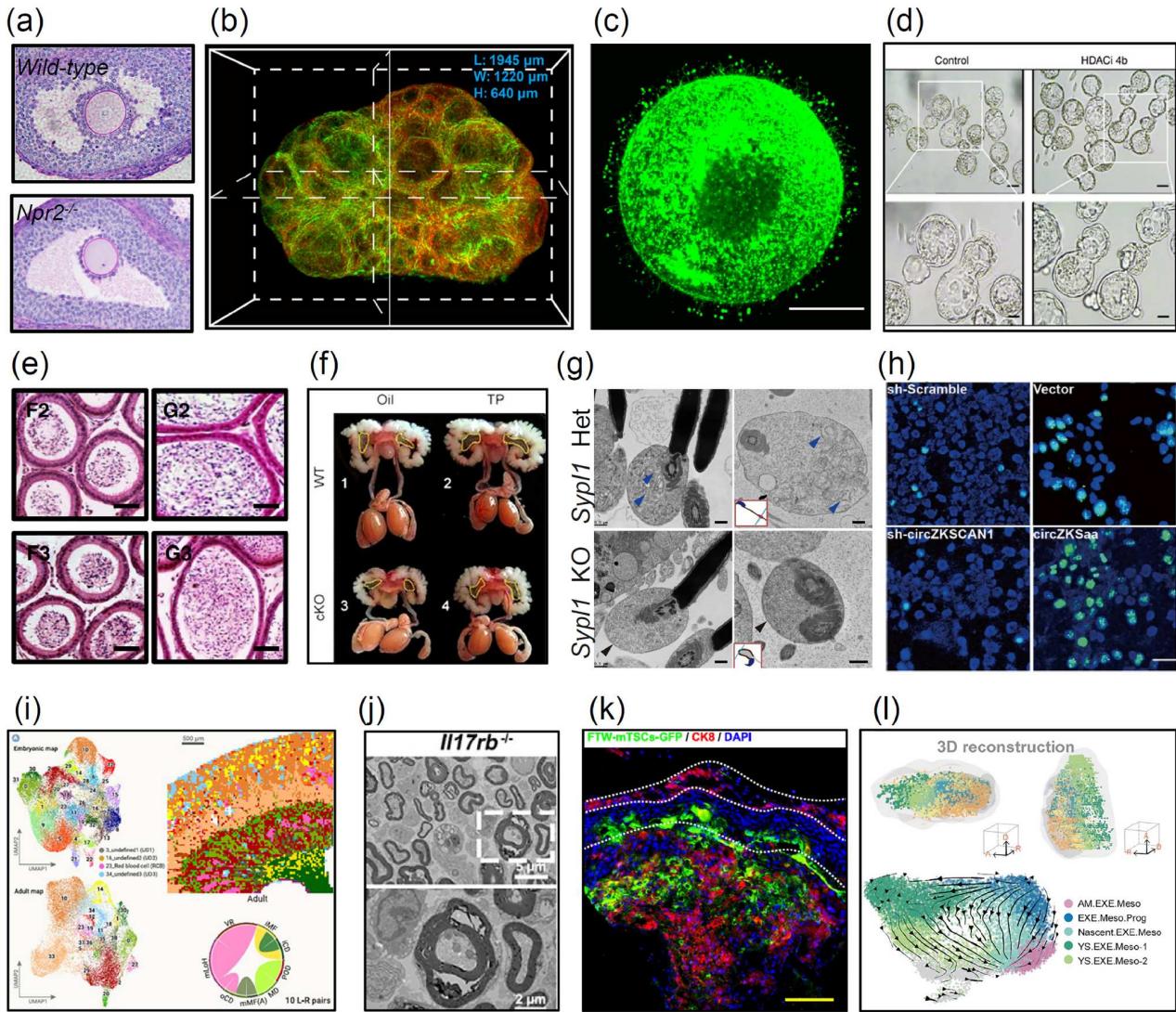
生理学是生命科学研究的基石学科, 也是认识生命宏观规律和微观规律的桥梁和纽带。自建院以来, 生物学院生理学工作者立足于农业畜牧生产的特点, 结合生理学研究对理、农、医的广泛辐射效应, 形成了以生殖繁育、营养代谢为主线, 以服务国家和社会需求为核心的研究模式, 为我国生理学研究的发展与进步作出了显著的贡献。建院伊始, 老一辈生理科学家们为学院的发展奠定了坚实的基础。杨传任教授带领刘敏雄、汪琳仙、郑行和乔惠理等教授围绕着生理生化常值开展研究, 协同其他17个农业院校一起填补了我国畜牧兽医学上的空白; 建立了包括羊催乳素等多个放射免疫测定方法, 为我国畜禽生理研究的定量化和规范化提出了范本, 并获1990年农业部科技进步奖。进入21世纪, 伴随着生命科学研究向着数字化、高通量和精细化模式的发展变化, 生物学院生理学研究工作者本着守正创新的理念, 围绕生理学解析宏观生命规律的本质目标, 积极引入多种前沿技术手段, 围绕生殖、营养、代谢等方向不断取得创新性突破。夏国良

教授和张美佳教授揭示了哺乳动物卵母细胞减数分裂抑制和恢复的生理性机制,明确了旁分泌因子C型钠肽及其受体是耦联内分泌上游激素信号和卵母细胞胞内信号通路作用的核心分子<sup>[47]</sup>(图2(a))。崔胜教授和刘佳利教授聚焦于生殖内分泌系统的上下游整合调节,揭示了褪黑素等节律和代谢相关激素的合成和分泌调控机制<sup>[48~50]</sup>(图2(f)),并解析了可变剪切以及细胞质内囊泡调控精子发生和成熟的过程机制<sup>[51,52]</sup>(图2(g))。李向东教授则致力于内分泌稳态和雄性生殖调控的分子机制研究,明确了寨卡病毒引起小鼠睾丸损伤导致雄性不育的分子机制<sup>[53]</sup>(图2(e)),发现了circRNA是新型癌症标志物及其在癌症治疗中的功能机制<sup>[54]</sup>(图2(h))。张华教授聚焦于雌性生育力的维持和质量决定,解析了卵母细胞在卵巢内激活和生长的调控机制,发现新的卵母细胞亚细胞通讯结构-卵源微绒毛<sup>[55]</sup>(图2(c)),阐明了成年卵巢血管持续性新生及重塑对生殖质量和卵巢衰老的生理调控作用<sup>[56,57]</sup>(图2(b))。王超教授系统阐释了表观遗传修饰协同内分泌调节卵泡生长发育及优势化选择的生理调控机制<sup>[58,59]</sup>(图2(d))。柯玉文教授通过建立高分辨率、高通量的单细胞空间转录组技术及相关数据算法,聚焦动物器官发育,明确了距离限定的细胞通讯调控了细胞类型分化、迁移以及器官结构建立<sup>[60]</sup>(图2(i))。英郑欣教授围绕着神经损伤修复相关机制,解析了神经损伤后髓鞘降解以及施旺细胞在神经修复早期炎症调控中的功能<sup>[61]</sup>(图2(j)),明确了脱髓鞘疾病关键致病蛋白的结构与功能<sup>[63]</sup>。魏育蕾教授解读了胚胎早期发育的3D时空结构,并证明胚胎尾部存在关键信号源调控发育,且原始生殖细胞起源为胚胎尾部<sup>[64,65]</sup>(图2(l));通过建立干细胞模型解析胚胎发育过程中胚外细胞对胚内细胞的互作关系,阐明了早期发育过程中细胞外基质对于胎儿的正常发育的关键调控作用<sup>[66,67]</sup>(图2(k))。

### 3 微生物学与免疫学

1959年,俞大绂院士带领李季伦等人创立农业微生物学专业,培育赤霉素高产稳产菌种,掀起了全国赤霉素研究热潮。1984年该专业并入生物学院,2004年更名为微生物学与免疫学系。在微生物代谢领域,李季伦院士团队开发了赤霉素、玉米赤霉烯酮和玉米赤霉醇、莫能菌素和马杜霉素、阿维菌素和伊维菌素等系列微生物发酵产品,获国家科技进步奖二等奖1项。李颖、文莹和姜伟教授团队揭示了阿维菌素、达托霉

素、非核糖体肽和DHA(二十二碳六烯酸)的合成调控机制,构建了系列高产工程菌株<sup>[68]</sup>;率先提出并实践了以磁螺菌为功能化纳米材料底盘生物的构想,在高密度培养、磁小体功能化修饰与晶体改造等方面保持国际领先水平<sup>[69,70]</sup>,在磁小体合成转录调控机制方面颠覆了趋磁细菌“被动趋磁”的假说<sup>[71]</sup>(图3(i))。在物质循环利用领域,袁红莉教授团队建立了微生物降解褐煤生产腐植酸和黄腐酸技术,创制了系列具有自主知识产权的黄腐酸、ALA类植物生长调节剂<sup>[72,73]</sup>,建立了基于微生物组的多项农业绿色生产技术,挖掘了多个新型高效生物质转化系统及酶资源<sup>[74]</sup>,获省部级奖励5项;姜伟教授团队开发了一系列高效生物质降解酶系用于益生元生产<sup>[75]</sup>(图3(h))。在生物固氮方向,陈文新院士团队建立了国际上菌株最多、宿主来源最广泛的根瘤菌种质资源库,系统揭示了根瘤菌生物地理学特征,是国际上发现命名根瘤菌新种最多的团队<sup>[76]</sup>(图3(a)),相关成果获国家自然科学二等奖及省部级一、二等奖6项;田长富教授团队系统挖掘了广宿主根瘤菌抗逆与共生基因模块<sup>[77,78]</sup>(图3(b)),揭示了共生匹配性快速演化机制<sup>[79,80]</sup>,解析了抗逆与共生功能在根瘤菌底盘适配的全局调控机理<sup>[81,82]</sup>,近3年与企业合作应用广宿主根瘤菌500余万亩;李季伦院士团队从20世纪80年代初开始研究固氮酶催化机理并提出固氮酶双位点放H<sub>2</sub>模型<sup>[83]</sup>;陈三凤教授团队建立了国内外最大的固氮类芽孢杆菌资源库,发现已知最小固氮基因簇并实现其在大肠杆菌的功能性表达,揭示了GlnR对该基因簇的正负调控机制及丙氨酸促进高铵条件下固氮的机理<sup>[84]</sup>,在水稻中实现固氮基因表达与固氮酶NifDK四聚体的形成并解决了NifH蛋白被切割的问题,为探索植物自主固氮提供了重要参考<sup>[85]</sup>(图3(c));选育系列“生防促生”固氮类芽孢杆菌并实现产业化,获省部级二、三等奖3项。真核微生物学的食用菌学研究始于娄隆后教授,1978年他提交给国务院的报告显著推动了我国食用菌产业发展。王贺祥教授担任国家食用菌产业技术体系岗位专家和加工研究室主任,并带领团队在真菌凝集素、食用菌多糖、草菇保鲜及HIV逆转录酶抑制剂的研究中取得了系列进展。何群教授团队从事模式真菌生物钟运行机制、染色质结构影响基因表达调控的研究,发现粗糙脉孢菌不依赖转录激活因子的生物钟蛋白转录<sup>[86]</sup>,确定蛋白激酶参与调控组蛋白修饰在异染色质建成中的作用<sup>[87]</sup>(图3(f)),发现异染色质建成缺陷影响近端基因转录的激活或抑制机制<sup>[88~90]</sup>。楼慧强教

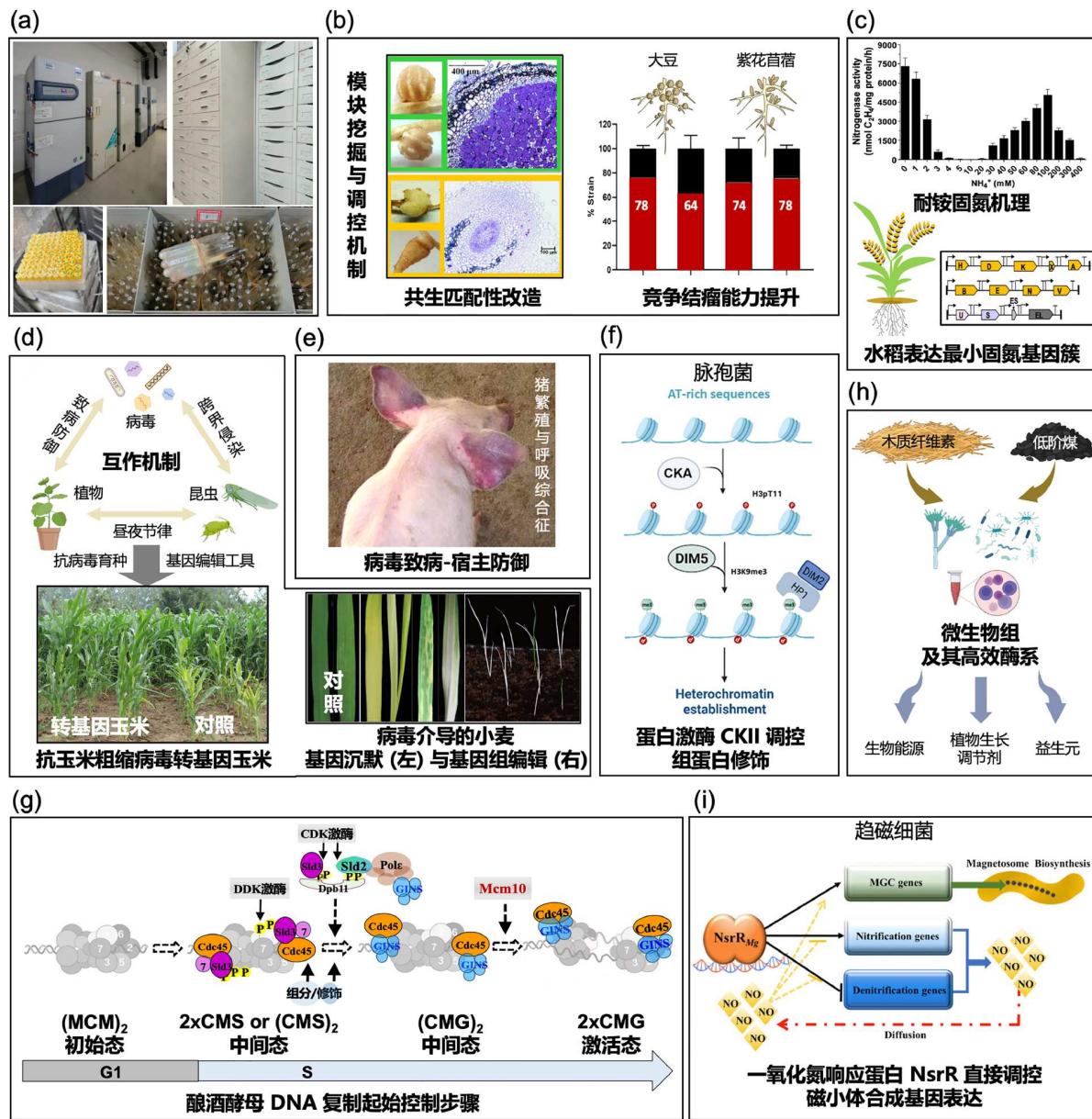


**图 2** 动物生理方向代表性研究成果。(a) 卵母细胞减数分裂抑制和恢复机制, Reproduced from Ref. [47]。(b) 成年卵巢血管持续性新生及重塑特征, Reproduced from Ref. [56]。(c) 卵母细胞微绒毛亚细胞通讯结构, Reproduced from Ref. [55]。(d) 表观遗传修饰调控卵母细胞成熟与质量机制, Reproduced from Ref. [58]。(e) 塞卡病毒导致小鼠睾丸损伤机制, Reproduced from Ref. [53]。(f) 酪蛋白激酶调控睾丸发育机制, Reproduced from Ref. [48]。(g) 囊泡促进精子生成, Reproduced from Ref. [51]。(h) circRNA是新型癌症标志物, Reproduced from Ref. [54]。(i) 单细胞空间转录组技术解析肾脏发育, Reproduced from Ref. [60]。(j) 施旺细胞在神经修复早期炎症调控中的功能, Reproduced from Ref. [61]。(k) 小鼠类胚胎干细胞模型, Reproduced from Ref. [66]。(l) 3D人类原肠胚“数字胚胎”, Reproduced from Ref. [64]

**Figure 2** Representative research findings in the field of animal physiology. (a) Mechanism of oocyte meiosis inhibition and restoration, Reproduced from Ref. [47]. (b) Continuous angiogenesis and remodeling features in adult ovaries [56]. (c) Subcellular communication structure of oocyte microvilli, Reproduced from Ref. [55]. (d) Epigenetic modification regulating oocyte maturation and quality mechanisms, Reproduced from Ref. [58]. (e) Mechanism of Zika virus-induced testicular injury in mice, Reproduced from Ref. [53]. (f) Casein kinase 1 $\alpha$  regulation of testicular development, Reproduced from Ref. [48]. (g) A vesicular pathway essential for spermatogenesis, Reproduced from Ref. [51]. (h) A novel circZKSCAN1-encoded peptide acts as a tumor suppressor, Reproduced from Ref. [54]. (i) Single-cell spatial transcriptomics for kidney development analysis, Reproduced from Ref. [60]. (j) Schwann cell autocrine signaling improving demyelinating disease., Reproduced from Ref. [61]. (k) Mouse embryonic stem cell-like model, Reproduced from Ref. [66]. (l) 3D human gastruloid “digital embryo”, Reproduced from Ref. [64]

授团队揭示了酵母复制解旋酶激活必需中间态Pre-IC的生化性质及Mcm10的功能<sup>[91]</sup>, 阐述了DNA复制时空程序控制机制<sup>[25]</sup>, 解析了姐妹染色单体黏连建立与

DNA复制的偶联机制及其对称性<sup>[92-94]</sup>, 阐明了糖代谢重塑可激活DNA复制检验点、从而维持基因组稳定性的机制<sup>[95]</sup>(图3(g))。动物病毒免疫方向, 王宾教授团队



**图 3** 微生物学与免疫学方向代表性研究成果. (a) 建立了国际最大的根瘤菌种质资源库, Reproduced from Ref. [76]. (b) 根瘤菌共生功能模块挖掘与调控机制及菌种改造, Reproduced from Refs. [77~82]. (c) 最小固氮基因簇的发现与调控机制及异源表达, Reproduced from Refs. [84,85]. (d) “病毒-植物-昆虫介体”互作机制及病毒载体的开发利用与抗病毒转基因作物, Reproduced from Refs. [101~116]. (e) 猪繁殖与呼吸综合征(俗称“蓝耳病”)的病毒与宿主互作机制及疫苗开发, Reproduced from Refs. [96,97]. (f) 脉孢菌蛋白激酶CKII参与调控组蛋白修饰在异染色质建成中的作用, Reproduced from Ref. [87]. (g) 酿酒酵母DNA复制起始控制机理, Reproduced from Ref. [91~95]. (h) 基于微生物组及其高效酶系的物质循环利用, Reproduced from Ref. [72~75]. (i) 趋磁细菌一氧化氮响应蛋白NsrR直接调控磁小体合成基因转录, Reproduced from Ref. [71]

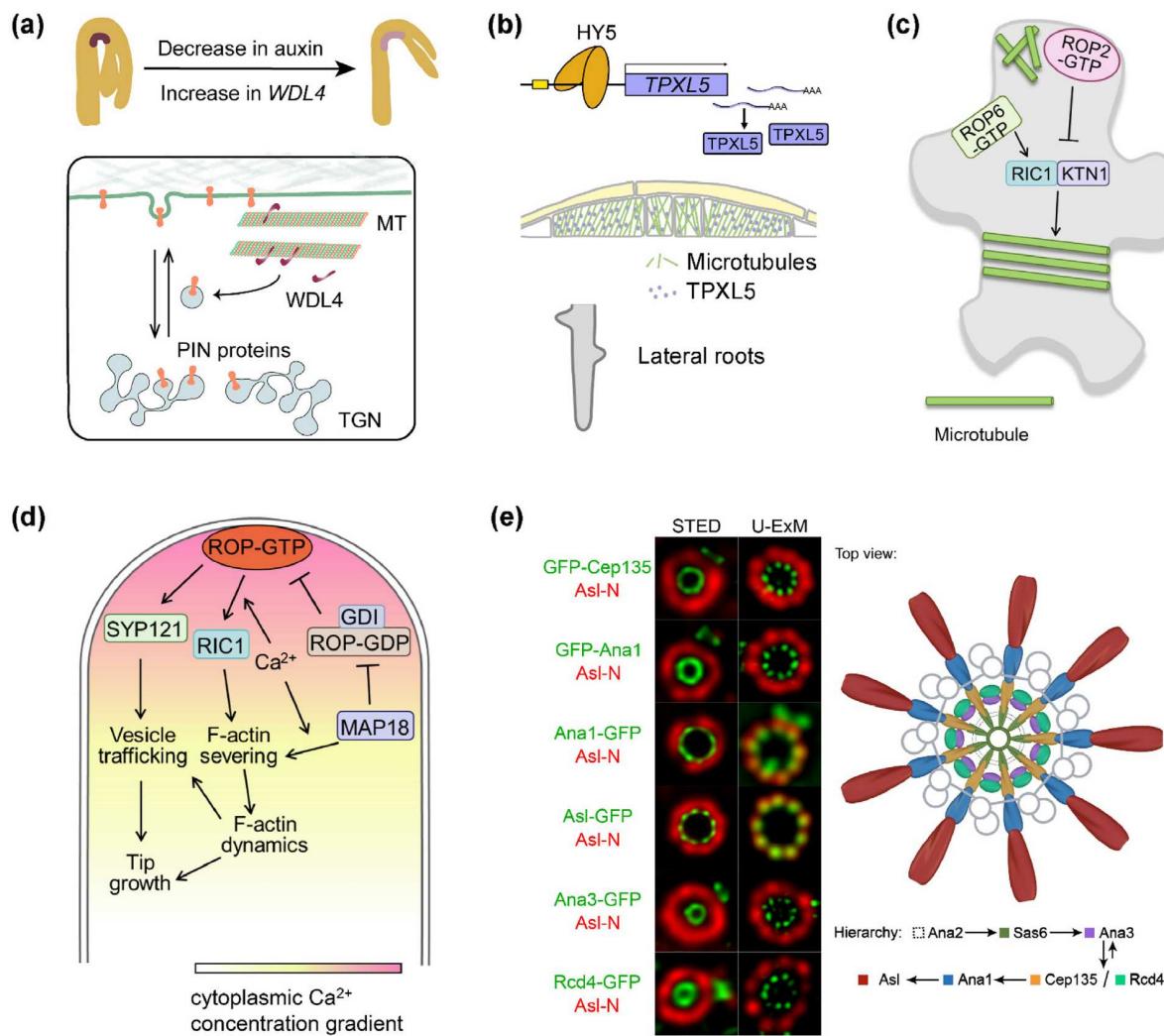
**Figure 3** Representative research achievements in microbiology and immunology. (a) Established the world's largest germplasm resource bank of rhizobia, Reproduced from Ref. [76]. (b) Mining and regulatory mechanisms of symbiotic functional modules of rhizobia, as well as strain modification, Reproduced from Refs. [77~82]. (c) Discovery and regulatory mechanisms of the minimal nitrogen-fixing gene cluster, as well as its heterologous expression, Reproduced from Refs. [84,85]. (d) Interaction mechanisms among “virus-plant-insect vector”, development and utilization of viral vectors, and transgenic crops with antiviral properties, Reproduced from Refs. [101~116]. (e) Interaction mechanisms between the virus causing porcine reproductive and respiratory syndrome (commonly known as “blue ear disease”) and the host, as well as vaccine development, Reproduced from Refs. [96,97]. (f) The role of protein kinase CKII in *Neurospora crassa* in regulating histone modification during heterochromatin formation, Reproduced from Ref. [87]. (g) The mechanism of DNA replication initiation control in *Saccharomyces cerevisiae*, Reproduced from Refs. [91~95]. (h) Material recycles based on the microbiome and its highly efficient enzyme system, Reproduced from Refs. [72~75]. (i) The nitric oxide response protein NsrR in magnetotactic bacteria directly regulates the transcription of magnetosome synthesis genes, Reproduced from Ref. [71].

发现DNA与蛋白“共免疫”可抑制自身免疫病，并实现成果转化。封文海教授团队系统揭示了高致病性猪繁殖与呼吸综合征病毒致病分子机制以及microRNA调控该病毒感染与复制的机制<sup>[96,97]</sup>(图3(e)), 创制了具备开发潜力的系列致弱毒株, 荣获省部级奖1项。生物学院是国内最早开展分子植物病毒学的单位之一, 从分子水平首次鉴定了小麦花叶病、玉米粗缩病的病原, 澄清了真菌传小麦病毒和玉米粗缩病研究中的一些长期混淆不清的问题<sup>[98,99]</sup>; 发现甜菜黑色焦枯病毒(beet black scorch virus, BBSV), 并深入研究了该病毒及其卫星RNA的生物学和分子特征<sup>[100]</sup>。“甜菜丛根病基础研究”荣获原国家教委科技进步奖一等奖。近年来, 李大伟、王献兵和张永亮教授团队重点研究植物病毒与寄主及昆虫介体互作机制, 解析了病毒蛋白 $\gamma b$ 在大麦条纹花叶病毒barley stripe mosaic virus, BSMV)复制、运动和病毒粒子装配中的新功能, 首次发现病毒编码的细胞自噬的抑制子<sup>[101]</sup>, 发现 $\gamma b$ 蛋白的翻译后修饰(磷酸化、泛素化、棕榈酰化)在侵染过程中的不同功能<sup>[102]</sup>; 率先在禾本科作物和传毒昆虫介体上建立了负链RNA病毒的反向遗传学体系, 解析了大麦黄条点花叶病毒(barley yellow striate mosaic virus, BYSMV)复制中心的形成和调控机制<sup>[103]</sup>, 阐明了多种寄主蛋白与BSMV、BBSV和BYSMV病毒蛋白互作的分子机制<sup>[104~109]</sup>(图3(d))。发现病毒诱导小肽VISP1是新型选择性自噬受体, 靶标植物和病毒蛋白降解<sup>[110,111]</sup>。系统解析了植物病毒复制复合体的三维结构, 克隆了第一例单子叶植物NLR类抗病毒基因 $BSR1$ , 发现了多个植物抗病毒免疫功能模块<sup>[112~114]</sup>; 开发了用于植物互作蛋白鉴定的邻近标记技术<sup>[115]</sup>和麦类作物基因沉默与基因编辑载体<sup>[116]</sup>, 被广泛使用。

## 4 细胞生物学

细胞是植物结构、代谢、功能和遗传的基本单位, 细胞的分裂、生长和分化是植物生长发育及适应环境的基础。过去40年中国农业大学生物学院在植物细胞生物学研究方向, 尤其是在细胞骨架相关研究领域取得了多项重要的创新性科研成果。阎隆飞院士(1921~2001年)是国际上植物细胞骨架微丝系统研究的奠基人之一。1963年在国际上首次发现植物中的肌动球蛋白<sup>[117]</sup>, 揭示了高等植物细胞微丝骨架系统的存在, 这一发现对于理解植物细胞运动的分子机制至关重要, 成为国际上植物细胞骨架研究的里程碑。1988年, Gor-

don Research Conference的植物细胞骨架细胞生物学学术讨论会主席Palevitz指出: 阎隆飞的这一发现是高等植物中存在细胞骨架微丝系统的第一个证据。此后的近40年时间里, 阎先生团队在植物细胞微丝微管骨架蛋白及其马达蛋白的生化特性、功能及基因克隆等方面进行了大量研究, 相关成果早在20世纪80年代末90年代初就已发表于*Plant Physiology*等国际期刊<sup>[118,119]</sup>。王学臣教授自1988年以来, 主要从事植物细胞对逆境信息的感受、传递和信号转导的机理以及气孔运动机制的研究, 对细胞骨架、水孔蛋白和乙酰胆碱在信号转导和气孔运动中的作用机制有重要发现。袁明教授团队致力于解析植物细胞骨架的生理功能, 指出微管骨架的动态变化是植物细胞适应盐胁迫所必需的生理学过程, 开创了细胞骨架参与调控植物逆境适应性的新领域<sup>[120]</sup>; 另外, 阐明了微管骨架和微丝骨架调控植物细胞各向异性生长以及胞间连丝通透性的重要机制<sup>[121,122]</sup>。毛同林教授团队从多角度、多层次揭示了微管骨架响应生长发育和环境/逆境信号, 介导植物细胞生长和保卫细胞运动的分子机制<sup>[123~127]</sup>, 发现了微管结合蛋白WDL4通过调控生长素转运蛋白在质膜上的定位, 改变下胚轴顶端弯钩内外两侧生长素的分布特征, 介导植物不对称性生长的新机制(图4(a)); 此外, 还揭示了微管结合蛋白TPXL5通过调控微管骨架的成束能力, 控制建成细胞边缘区的扩张, 参与调控侧根发育的新功能<sup>[128,129]</sup>(图4(b))。傅缨教授团队系统解析了响应激素和盐胁迫信号调控微丝、微管骨架动态和囊泡运输以控制不同类型植物细胞极性生长和逆境响应的ROP GTPases信号转导网络, 并阐明了相关分子机制。研究证明了ROPs信号途径中的RIC1与MAP18均为多功能蛋白, 在进行极性扩张性生长的下胚轴和叶片表皮细胞中结合微管并调控微管组织动态, 而在进行顶端生长的根毛和花粉管中则行使Ca<sup>2+</sup>依赖的微丝调节功能(图4(c, d)); 此外, 还发现驱动膜融合的SNARE蛋白SYP121是ROP2的下游效应子, 揭示了ROP信号途径与囊泡运输间的直接联系<sup>[130~137]</sup>; 该团队最近的研究阐释了微管与囊泡运输协同参与光诱导气孔开放的新调控机制, 并进一步解析了光诱导胞质类受体激酶LKS4磷酸化调控SYP121促进胞吐作用的分子机制<sup>[138,139]</sup>; 还探究了微管组织动态在玉米株型调控中的重要功能<sup>[140]</sup>。这些创新性成果系统性地阐明细胞骨架的生理学功能、组织动态调控、信号转导调控等机制, 极大地促进、拓展了我国植物细胞骨架领域的发展,



**图 4** 细胞生物学方向代表性研究成果. (a) 微管结合蛋白通过调控生长素分布介导植物不对称生长的作用机制, Reproduced from Ref. [128]; (b) 周质微管参与侧根发育的作用机制, Reproduced from Ref. [129]; (c) 叶片铺板细胞中调控横向周质微管的ROP信号途径; (d) 顶端生长细胞中调控微丝和囊泡运输的ROP信号途径; (e) 超高分辨显微技术解析中心粒九轴对称结构的装配机制, Reproduced from Ref. [142]

**Figure 4** Representative research achievements in the field of cell biology. (a) Mechanism of microtubule associated protein regulating auxin distribution and differential cell growth during apical hook opening, Reproduced from Ref. [128]; (b) mechanism of cortical microtubules regulating lateral root development, Reproduced from Ref. [129]; (c) ROP signaling pathways regulating cortical transverse microtubules in leaf pavement cells undergo polarized diffuse growth; (d) ROP signaling pathways regulating F-actin dynamics and vesicle trafficking in cells undergoing tip growth. (e) Centrosome biogenesis under Sub-Diffraction Resolution, Reproduced from Ref. [142]

丰富了人们对相关基础理论的认识, 为阐明植物环境适应性的细胞学机制作出了重要贡献. 傅静雁教授团队通过优化多种超高分辨显微技术对动物细胞的中心体细胞器进行解析, 在120 nm分辨率水平揭示了中心体蛋白的层叠式分布, 提出了分区的概念, 由此建立了中心体的分层装配模型; 在25 nm分辨率水平上揭示了中心粒九轴对称装配的分子模型, 诠释了如此高精度、高对称性的结构在细胞内是如何自发组建的这一基础

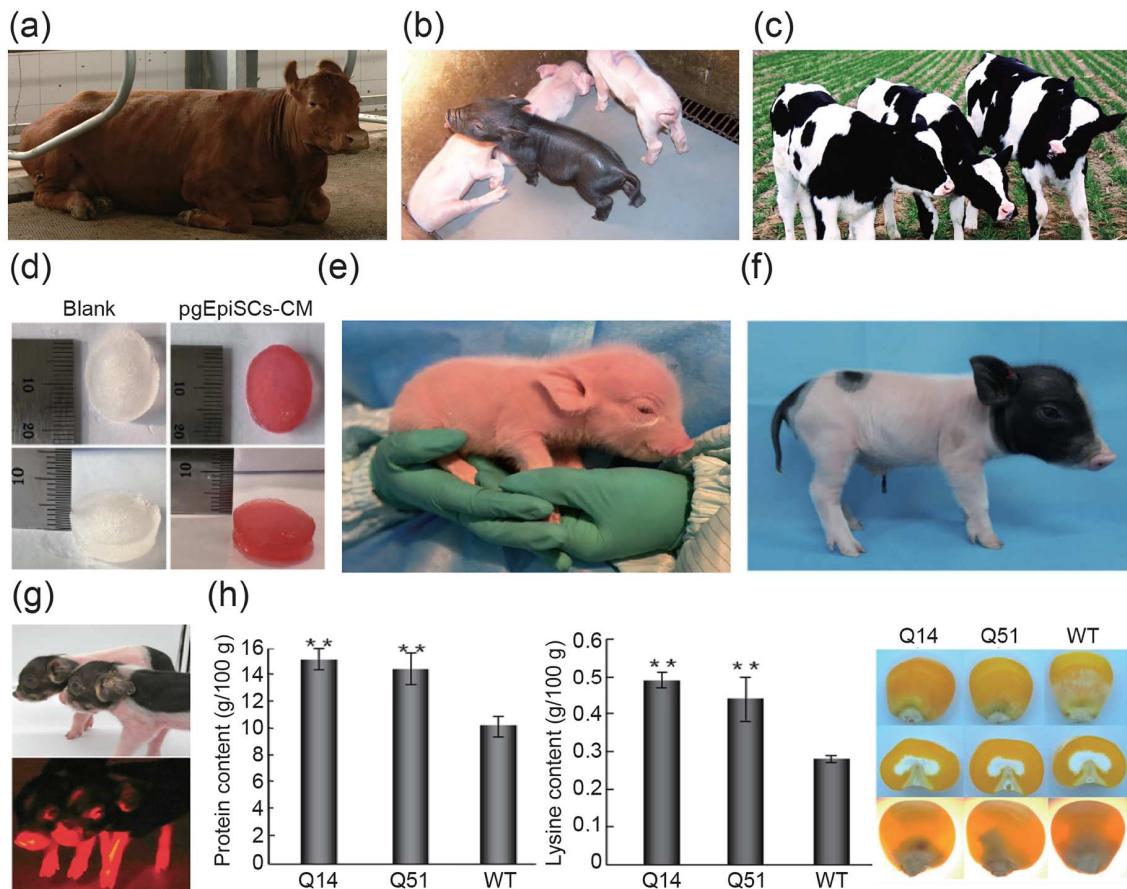
科学问题; 揭示了三元蛋白复合体Cep135-Ana1-Asl及其上游调控蛋白Ana3和Rcd4调控新生的子中心粒转变为成熟母中心粒, 从而获得繁衍后代中心粒的能力的机制, 为研究如何限制中心体过度复制和寻找抑制肿瘤的新靶标提供了新的角度<sup>[141~143]</sup>(图4(e)).

## 5 生物化学与生物技术

生物学院自成立以来, 在生物化学与生物技术领

域已经走过了四十年的光辉历程，取得了众多具有里程碑意义的重大科研成果。在建院之初，老一辈科学家们就为学院的发展奠定了坚实的基础。阎隆飞院士最早发现了植物中的碳酸酐酶<sup>[144]</sup>，并推测其参与光合作用中CO<sub>2</sub>的吸收过程，此研究被多个国际知名出版物引用，展现了植物碳酸酐酶在未来太空探索中的潜在应用价值。齐顺章教授是动物生物技术领域的杰出代表，他在猪的代谢、同工酶和基因工程<sup>[145]</sup>方面进行了开创性的研究，成功研制了重组猪生长激素<sup>[146]</sup>，获得了农业部科技进步二等奖。陈永福教授担任生物学院院长期间，领导团队承担了国家高技术研究发展计划

(“863”计划)中的“动物乳腺生物反应器研究”课题，成功实现了外源基因在乳腺中的表达<sup>[147]</sup>，为后续转基因动物的研究开辟了新的道路，也预示着利用生物反应器大规模生产药用蛋白的可能性。敖光明教授领导的团队专注于玉米品质的生物技术改良，领导团队承担植物转基因与产业化专项和“863”计划，通过基因工程技术解决了赖氨酸和蛋白质不能同时提高的问题<sup>[148]</sup>，成功培育出高赖氨酸、高蛋白质的优质转基因玉米品种，研究成果获得北京市科学技术奖三等奖。进入新世纪后，生物学院在大动物克隆领域的研究取得了显著进展，中国首例体细胞克隆冀南黄牛<sup>[149]</sup>和首例体细胞克隆



**图 5** 生物化学与生物技术方向代表性研究成果。 (a) 中国首例体细胞克隆冀南黄牛, Reproduced from Ref. [149]. (b) 中国首例体细胞克隆猪, Reproduced from Ref. [150]. (c) 转乳铁蛋白克隆牛, Reproduced from Refs. [155,156]. (d) 家畜干细胞来源细胞培养肉, Reproduced from Ref. [161]. (e) 猪胚胎干细胞来源多基因编辑克隆猪, Reproduced from Ref. [160]. (f) 人类新冠肺炎(COVID-19)猪模型, Reproduced from Ref. [164]. (g) 人类妊娠早期流产猪模型, Reproduced from Ref. [165]. (h) 转基因玉米Q14和Q51 T2代种子蛋白质、赖氨酸含量显著提高, 粟粒正常, Reproduced from Ref. [171]

**Figure 5** Representative research achievements in biochemistry and biotechnology. (a) The first somatic cell cloning of Jinan yellow cattle in China, Reproduced from Ref. [149]. (b) China's first somatic cell cloned pig, Reproduced from Ref. [150]. (c) Cloned human-lactoferrin transgenic cattle, Reproduced from Refs. [155,156]. (d) Cultured meat from domestic animal stem cells-derived cells, Reproduced from Ref. [161]. (e) Porcine embryonic stem cells derived from polygene editing cloned porcine, Reproduced from Ref. [160]. (f) Swine model of COVID-19, Reproduced from Ref. [164]. (g) Pig model of human early pregnancy abortion, Reproduced from Ref. [165]. (h) The protein and lysine contents of T2 seeds of transgenic corn Q14 and Q51 were significantly increased, and the grain was normal, Reproduced from Ref. [171]

猪<sup>[150]</sup>相继产生(图5(a, b)), 同时在乳腺生物反应器领域的研究也取得重大突破, 利用转基因技术高效表达了多种药用重组蛋白和抗体, 如人溶菌酶<sup>[151~153]</sup>、CD20 单克隆抗体<sup>[154]</sup>和人乳铁蛋白(图5(c))<sup>[155,156]</sup>等, 为医药产业带来了新的契机。赵要风教授团队深入开展了动物免疫球蛋白基因的比较和进化研究<sup>[157]</sup>, 建立了非驼科动物来源纳米抗体的生产平台<sup>[158]</sup>, 有助于小分子纳米抗体的广泛应用; 与吴森教授团队一起建立了病毒感染相关宿主基因的高通量筛选平台<sup>[159]</sup>, 为基因编辑抗病育种奠定了基础。韩建永教授团队在大家畜多能干细胞研究方面取得重大突破, 创建了稳定的猪上胚层干细胞分离与培养技术体系<sup>[160]</sup>、干细胞培养肉技术体系(图5(d))<sup>[161]</sup>等, 获得了无外源基因整合的猪诱导多能性干细胞(iPSCs)<sup>[162]</sup>, 获得了连续三次基因编辑的干细胞克隆猪(图5(e))<sup>[160]</sup>, 进一步在建立了牛稳定胚胎干细胞系<sup>[163]</sup>, 为细胞工厂、家畜生物育种以及人类疾病模型建立提供种子细胞等关键技术支撑。吴森教授团队致力于基因编辑克隆猪模型的研究, 开发了高度敏感的人SARS-CoV-2感染人源化猪模型(图5(f))<sup>[164]</sup>及早期流产猪模型(图5(g))<sup>[165]</sup>, 为传染病防控和家畜繁殖提供了宝贵的资源。胡晓湘教授团队在畜禽基因组选择育种<sup>[166,167]</sup>方法学上有突出贡献, 而于政权教授团队

则在肠道及乳腺疾病建模和药物筛选方面表现优异<sup>[168,169]</sup>。于静娟教授团队聚焦改善玉米籽粒胚乳中的赖氨酸和蛋白质含量(图5(h))<sup>[170,171]</sup>和谷子抗旱功能基因组学研究。提出能够利用细胞骨架相关蛋白在玉米籽粒胚乳中的积累, 同时提高籽粒胚乳中蛋白质和赖氨酸含量, 以改良玉米籽粒的营养品质。在国内率先建立了农杆菌介导的谷子遗传转化体系<sup>[172]</sup>, 构建了谷子在干旱条件下的转录组、降解组和小RNA组平台<sup>[173,174]</sup>, 绘制了高时间分辨率的谷子苗期干旱转录组图谱<sup>[175]</sup>, 揭示类转录因子SiARDP和m6A“阅读器”SiYTH1调控谷子抗旱的机制<sup>[176,177]</sup>。任东涛教授团队的研究工作集中于阐释蛋白质磷酸化在调控植物发育及逆境响应中的功能。揭示了丝裂原激活的蛋白激酶级联如何调控植物鞘脂和植保素的合成<sup>[178,179]</sup>, 发现了植保素生物合成途径上的关键酶<sup>[180]</sup>, 为植物病理学提供了新的视角。

中国农业大学生物学院在过去四十年间, 从生命科学基础理论到实际应用, 从传统农业到现代农业生物技术, 始终走在科学的研究的前沿, 为我国生命科学学科发展和农业科技创新提供了重要的科技支持。未来, 学院将继续秉承创新精神, 致力于解决更多关乎国计民生的重大问题, 为实现中华民族伟大复兴贡献力量。

**致谢** 感谢中国农业大学生物学院巩志忠、杨永青、施怡婷、王涛、董江丽、陈其军、王瑜、张焱、刘佳利、文莹、袁红莉、陈三凤、王贺祥、何群、楼慧强、封文海、康友敏、张永亮等老师参与撰写本文或提供材料。

## 参考文献

- Xu J, Li H D, Chen L Q, et al. A Protein kinase, interacting with two calcineurin B-like proteins, regulates K<sup>+</sup> transporter AKT1 in *Arabidopsis*. *Cell*, 2006, 125: 1347–1360
- Wang F L, Tan Y L, Wallrad L, et al. A potassium-sensing niche in *Arabidopsis* roots orchestrates signaling and adaptation responses to maintain nutrient homeostasis. *Dev Cell*, 2021, 56: 781–794.e6
- Wang Y, Wu W H. Potassium transport and signaling in higher plants. *Annu Rev Plant Biol*, 2013, 64: 451–476
- Wang Y, Chen Y, Wu W. Potassium and phosphorus transport and signaling in plants. *J Integr Plant Biol*, 2021, 63: 34–52
- Jia G, Chen G, Zhang Z, et al. Ferredoxin-mediated mechanism for efficient nitrogen utilization in maize. *Nat Plants*, 2025, 11: 643–659
- Wang Y, Yuan Z, Wang J, et al. The nitrate transporter NRT2.1 directly antagonizes PIN7-mediated auxin transport for root growth adaptation. *Proc Natl Acad Sci USA*, 2023, 120: e2221313120
- Xiao H, Hu Y, Wang Y, et al. Nitrate availability controls translocation of the transcription factor NAC075 for cell-type-specific reprogramming of root growth. *Dev Cell*, 2022, 57: 2638–2651.e6
- Wang Y, Gong Z, Friml J, et al. Nitrate modulates the differentiation of root distal stem cells. *Plant Physiol*, 2019, 180: 22–25
- Li Y, Wang Y, Tan S, et al. Root growth adaptation is mediated by PYLs ABA receptor-PP2A protein phosphatase complex. *Adv Sci*, 2020, 7: 1901455
- Zhang J, Mazur E, Balla J, et al. Strigolactones inhibit auxin feedback on PIN-dependent auxin transport canalization. *Nat Commun*, 2020, 11: 3508

- 11 Zeng R, Shi Y, Guo L, et al. A natural variant of *COOL1* gene enhances cold tolerance for high-latitude adaptation in maize. *Cell*, 2025, 188: 1315–1329.e13
- 12 Ding Y, Jia Y, Shi Y, et al. OST1-mediated BTF3L phosphorylation positively regulates CBF s during plant cold responses. *EMBO J*, 2018, 37: e98228
- 13 Ding Y, Li H, Zhang X, et al. OST1 kinase modulates freezing tolerance by enhancing ICE1 stability in *Arabidopsis*. *Dev Cell*, 2015, 32: 278–289
- 14 Ding Y, Lv J, Shi Y, et al. EGR2 phosphatase regulates OST1 kinase activity and freezing tolerance in *Arabidopsis*. *EMBO J*, 2019, 38: e99819
- 15 Liu Q, Ding Y, Shi Y, et al. The calcium transporter ANNEXIN1 mediates cold-induced calcium signaling and freezing tolerance in plants. *EMBO J*, 2021, 40: e104559
- 16 Jiang B, Shi Y, Zhang X, et al. PIF3 is a negative regulator of the *CBF* pathway and freezing tolerance in *Arabidopsis*. *Proc Natl Acad Sci USA*, 2017, 114: E6695–E6702
- 17 Jiang B, Shi Y, Peng Y, et al. Cold-induced CBF–PIF3 interaction enhances freezing tolerance by stabilizing the phyB thermosensor in *Arabidopsis*. *Mol Plant*, 2020, 13: 894–906
- 18 Li Y, Shi Y, Li M, et al. The CRY2–COP1–HY5–BBX7/8 module regulates blue light-dependent cold acclimation in *Arabidopsis*. *Plant Cell*, 2021, 33: 3555–3573
- 19 Tian T, Wang S, Yang S, et al. Genome assembly and genetic dissection of a prominent drought-resistant maize germplasm. *Nat Genet*, 2023, 55: 496–506
- 20 Liu S, Li C, Wang H, et al. Mapping regulatory variants controlling gene expression in drought response and tolerance in maize. *Genome Biol*, 2020, 21: 163
- 21 Liu B, Zhang B, Yang Z, et al. Manipulating *ZmEXP44* expression ameliorates the drought-induced prolonged anthesis and silking interval in maize. *Plant Cell*, 2021, 33: 2058–2071
- 22 Wang X, Wang H, Liu S, et al. Genetic variation in *ZmVPP1* contributes to drought tolerance in maize seedlings. *Nat Genet*, 2016, 48: 1233–1241
- 23 Gao H, Cui J, Liu S, et al. Natural variations of *ZmSRO1d* modulate the trade-off between drought resistance and yield by affecting *ZmRBOHC*-mediated stomatal ROS production in maize. *Mol Plant*, 2022, 15: 1558–1574
- 24 Hua D, Wang C, He J, et al. A plasma membrane receptor kinase, GHR1, mediates abscisic acid- and hydrogen peroxide-regulated stomatal movement in *Arabidopsis*. *Plant Cell*, 2012, 24: 2546–2561
- 25 Wang K, He J, Zhao Y, et al. EAR1 Negatively regulates ABA signaling by enhancing 2C protein phosphatase activity. *Plant Cell*, 2018, 30: 815–834
- 26 Kong L, Cheng J, Zhu Y, et al. Degradation of the ABA co-receptor ABI1 by PUB12/13 U-box E3 ligases. *Nat Commun*, 2015, 6: 8630
- 27 Hu X, Cheng J, Lu M, et al. Ca<sup>2+</sup>-independent *ZmCPK2* is inhibited by Ca<sup>2+</sup>-dependent *ZmCPK17* during drought response in maize. *J Integr Plant Biol*, 2024, 66: 1313–1333
- 28 Ma L, Ye J, Yang Y, et al. The SOS2-SCaBP8 complex generates and fine-tunes an AtANN4-dependent calcium signature under salt stress. *Dev Cell*, 2019, 48: 697–709.e6
- 29 Liu G, Zeng Y, Li B, et al. SOS2 phosphorylates FREE1 to regulate multi-vesicular body trafficking and vacuolar dynamics under salt stress. *Plant Cell*, 2025, 37: koaf012
- 30 Li J, Zhou H, Zhang Y, et al. The GSK3-like kinase BIN2 is a molecular switch between the salt stress response and growth recovery in *Arabidopsis thaliana*. *Dev Cell*, 2020, 55: 367–380.e6
- 31 Hao R, Zhou W, Li J, et al. On salt stress, PLETHORA signaling maintains root meristems. *Dev Cell*, 2023, 58: 1657–1669.e5
- 32 Li J, Shen L, Han X, et al. Phosphatidic acid-regulated SOS2 controls sodium and potassium homeostasis in *Arabidopsis* under salt stress. *EMBO J*, 2023, 42: e112401
- 33 Liu X, Yu X, Shi Y, et al. Phosphorylation of RhoGDI1, a Rho GDP dissociation inhibitor, regulates root hair development in *Arabidopsis* under salt stress. *Proc Natl Acad Sci USA*, 2023, 120: e2217957120
- 34 Cao Y, Zhang M, Liang X, et al. Natural variation of an EF-hand Ca<sup>2+</sup>-binding-protein coding gene confers saline-alkaline tolerance in maize. *Nat Commun*, 2020, 11: 186
- 35 Zhang M, Liang X, Wang L, et al. A HAK family Na<sup>+</sup> transporter confers natural variation of salt tolerance in maize. *Nat Plants*, 2019, 5: 1297–1308
- 36 Wang Y, Cao Y, Liang X, et al. A dirigent family protein confers variation of Caspary strip thickness and salt tolerance in maize. *Nat Commun*, 2022, 13: 2222
- 37 Feng Z, Wang M, Liu Y, et al. Liquid–liquid phase separation of TZP promotes PPK-mediated phosphorylation of the phytochrome A photoreceptor. *Nat Plants*, 2024, 10: 798–814
- 38 Han R, Ma L, Lv Y, et al. SALT OVERLY SENSITIVE2 stabilizes phytochrome-interacting factors PIF4 and PIF5 to promote *Arabidopsis* shade avoidance. *Plant Cell*, 2023, 35: 2972–2996

- 39 Dong X, Yan Y, Jiang B, et al. The cold response regulator CBF1 promotes *Arabidopsis* hypocotyl growth at ambient temperatures. *EMBO J*, 2020, 39: e103630
- 40 Qi L, Liu S, Li C, et al. PHYTOCHROME-INTERACTING FACTORS interact with the ABA receptors PYL8 and PYL9 to orchestrate ABA signaling in darkness. *Mol Plant*, 2020, 13: 414–430
- 41 Tian J, Wang C, Chen F, et al. Maize smart-canopy architecture enhances yield at high densities. *Nature*, 2024, 632: 576–584
- 42 Shen C, Du H, Chen Z, et al. The chromosome-level genome sequence of the autotetraploid alfalfa and resequencing of core germplasms provide genomic resources for alfalfa research. *Mol Plant*, 2020, 13: 1250–1261
- 43 Ji T, Zheng L, Wu J, et al. The thioesterase APT1 is a bidirectional-adjustment redox sensor. *Nat Commun*, 2023, 14: 2807
- 44 Ye Q, Zheng L, Liu P, et al. The S-acylation cycle of transcription factor MtNAC80 influences cold stress responses in *Medicago truncatula*. *Plant Cell*, 2024, 36: 2629–2651
- 45 Guo D, Liu P, Liu Q, et al. Legume-specific SnRK1 promotes malate supply to bacteroids for symbiotic nitrogen fixation. *Mol Plant*, 2023, 16: 1396–1412
- 46 Ye Q, Meng X, Chen H, et al. Construction of genic male sterility system by CRISPR/Cas9 editing from model legume to alfalfa. *Plant Biotechnol J*, 2022, 20: 613–615
- 47 Zhang M, Su Y Q, Sugiura K, et al. Granulosa cell ligand NPPC and its receptor NPR2 maintain meiotic arrest in mouse oocytes. *Science*, 2010, 330: 366–369
- 48 Guo H, Zhang D, Zhou Y, et al. Casein kinase 1 $\alpha$  regulates testosterone synthesis and testis development in adult mice. *Endocrinology*, 2023, 164: bquad042
- 49 Qiu J, Zhang J, Zhou Y, et al. MicroRNA-7 inhibits melatonin synthesis by acting as a linking molecule between leptin and norepinephrine signaling pathways in pig pineal gland. *J Pineal Res*, 2019, 66: e12552
- 50 Xie X, Chen X, Wang C, et al. PARN maintains RNA stability to regulate insulin maturation and GSIS in pancreatic  $\beta$  cells. *Adv Sci*, 2024, 11: 2407774
- 51 Liu J, Hermo L, Ding D, et al. SYPL1 defines a vesicular pathway essential for sperm cytoplasmic droplet formation and male fertility. *Nat Commun*, 2023, 14: 5113
- 52 Sun L, Lv Z, Chen X, et al. Splicing factor SRSF1 is essential for homing of precursor spermatogonial stem cells in mice. *eLife*, 2024, 12: RP89316
- 53 Ma W, Li S, Ma S, et al. Zika virus causes testis damage and leads to male infertility in mice. *Cell*, 2016, 167: 1511–1524.e10
- 54 Song R, Ma S, Xu J, et al. A novel polypeptide encoded by the circular RNA ZKSCAN1 suppresses HCC via degradation of mTOR. *Mol Cancer*, 2023, 22: 16
- 55 Zhang Y, Wang Y, Feng X, et al. Oocyte-derived microvilli control female fertility by optimizing ovarian follicle selection in mice. *Nat Commun*, 2021, 12: 2523
- 56 Xu X, Mu L, Li L, et al. Imaging and tracing the pattern of adult ovarian angiogenesis implies a strategy against female reproductive aging. *Sci Adv*, 2022, 8: eabi8683
- 57 Mu L, Wang G, Yang X, et al. Physiological premature aging of ovarian blood vessels leads to decline in fertility in middle-aged mice. *Nat Commun*, 2025, 16: 72
- 58 Wang H, Cai H, Wang X, et al. HDAC3 maintains oocyte meiosis arrest by repressing amphiregulin expression before the LH surge. *Nat Commun*, 2019, 10: 5719
- 59 Zhu Z, He M, Zhang T, et al. LSD1 promotes the FSH responsive follicle formation by regulating autophagy and repressing Wt1 in the granulosa cells. *Sci Bull*, 2024, 69: 1122–1136
- 60 Jiang S, Yu H, Zhao T, et al. A high-definition spatiotemporal transcriptomic atlas of mammalian kidney development. *Innovation*, 2025, 6: 100767
- 61 Huang Y, Wu L, Zhao Y, et al. Schwann cell promotes macrophage recruitment through IL-17B/IL-17RB pathway in injured peripheral nerves. *Cell Rep*, 2024, 43: 113753
- 62 Guo J, Guo Z, Huang Y, et al. Blockage of MLKL prevents myelin damage in experimental diabetic neuropathy. *Proc Natl Acad Sci USA*, 2022, 119: e2121552119
- 63 Jia Y, Zhang Y, Wang W, et al. Structural and functional insights of the human peroxisomal ABC transporter ALDP. *eLife*, 2022, 11: e75039
- 64 Xiao Z, Cui L, Yuan Y, et al. 3D reconstruction of a gastrulating human embryo. *Cell*, 2024, 187: 2855–2874.e19
- 65 Cui L, Lin S, Yang X, et al. Spatial transcriptomic characterization of a Carnegie stage 7 human embryo. *Nat Cell Biol*, 2025, 27: 360–369
- 66 Wei Y, Zhang E, Yu L, et al. Dissecting embryonic and extraembryonic lineage crosstalk with stem cell co-culture. *Cell*, 2023, 186: 5859–5875.e24
- 67 Pinzón-Arteaga C A, Wang Y, Wei Y, et al. Bovine blastocyst-like structures derived from stem cell cultures. *Cell Stem Cell*, 2023, 30: 611–616.e7

- 68 Yan H, Xin Z, Sang Z, et al. A rational multi-target combination strategy for synergistic improvement of non-ribosomal peptide production. *Nat Commun*, 2025, 16: 1883
- 69 Wu S, Ma F, He J, et al. Fusion expression of nanobodies specific for the insecticide fipronil on magnetosomes in *Magnetospirillum gryphiswaldense* MSR-1. *J Nanobiotechnol*, 2021, 19: 27
- 70 Xu J, Ma S, Zhang W, et al. *In vitro* magnetosome remineralization for silver-magnetite hybrid magnetosome biosynthesis and used for healing of the infected wound. *J Nanobiotechnol*, 2022, 20: 364
- 71 Pang B, Zheng H, Ma S, et al. Nitric oxide sensor NsrR is the key direct regulator of magnetosome formation and nitrogen metabolism in *Magnetospirillum*. *Nucleic Acids Res*, 2024, 52: 2924–2941
- 72 Luo Y, Liu L, Yang J, et al. Efficient biosynthesis of 5-aminolevulinic acid from glutamate via whole-cell biocatalyst in immobilized engineered *Escherichia coli*. *Catal Sci Technol*, 2023, 13: 2810–2819
- 73 Li D, Wang W, Peng Y, et al. Soluble humic acid suppresses plant immunity and ethylene to promote soybean nodulation. *Plant Cell Environ*, 2024, 47: 871–884
- 74 Liu L, Zhang Y, Huang Y, et al. Characterization of a multifunctional enzyme from *Trichoderma harzianum* and its application in enhanced enzymatic hydrolysis. *Bioresource Tech*, 2025, 415: 131701
- 75 Basit A, Miao T, Liu J, et al. Highly efficient degradation of xylan into xylose by a single enzyme. *ACS Sustain Chem Eng*, 2019, 7: 11360–11368
- 76 Wang E T, Chen W F, Tian C F, et al. Ecology and Evolution of Rhizobia. In: Wang E T, Tian C F, Chen W F, et al., eds. *Ecology and Evolution of Rhizobia: Principles and Applications*. Singapore: Springer Nature, 2019
- 77 Tian C F, Zhou Y J, Zhang Y M, et al. Comparative genomics of rhizobia nodulating soybean suggests extensive recruitment of lineage-specific genes in adaptations. *Proc Natl Acad Sci USA*, 2012, 109: 8629–8634
- 78 Ji Y Y, Zhang B, Zhang P, et al. Rhizobial migration toward roots mediated by FadL-ExoFQP modulation of extracellular long-chain AHLs. *ISME J*, 2023, 17: 417–431
- 79 Zhao R, Liu L X, Zhang Y Z, et al. Adaptive evolution of rhizobial symbiotic compatibility mediated by co-evolved insertion sequences. *ISME J*, 2018, 12: 101–111
- 80 Guo H, Shi W T, Zhang B, et al. Intracellular common gardens reveal niche differentiation in transposable element community during bacterial adaptive evolution. *ISME J*, 2023, 17: 297–308
- 81 Jiao J, Zhang B, Li M L, et al. The zinc-finger bearing xenogeneic silencer MucR in  $\alpha$ -proteobacteria balances adaptation and regulatory integrity. *ISME J*, 2022, 16: 738–749
- 82 Shi W T, Zhang B, Li M L, et al. The convergent xenogeneic silencer MucR predisposes  $\alpha$ -proteobacteria to integrate AT-rich symbiosis genes. *Nucleic Acids Res*, 2022, 50: 8580–8598
- 83 Li J, Burris R H. Influence of pN<sub>2</sub> and pD<sub>2</sub> on HD formation by various nitrogenases. *Biochemistry*, 1983, 22: 4472–4480
- 84 Li Q, Zhang H, Song Y, et al. Alanine synthesized by alanine dehydrogenase enables ammonium-tolerant nitrogen fixation in *Paenibacillus sabinae* T27. *Proc Natl Acad Sci USA*, 2022, 119: e2215855119
- 85 Shang Y, Shi H, Liu M, et al. Using synthetic biology to express nitrogenase biosynthesis pathway in rice and to overcome barriers of nitrogenase instability in plant cytosol. *Trends Biotechnol*, 2025, 43: 946–968
- 86 Zhou Z, Liu X, Hu Q, et al. Suppression of WC-independent frequency transcription by RCO-1 is essential for *Neurospora* circadian clock. *Proc Natl Acad Sci USA*, 2013, 110
- 87 Tian Y, Zhang C, Tian X, et al. H3T11 phosphorylation by CKII is required for heterochromatin formation in *Neurospora*. *Nucleic Acids Res*, 2024, 52: 9536–9550
- 88 Yang S, Li W, Qi S, et al. The highly expressed methionine synthase gene of *Neurospora crassa* is positively regulated by its proximal heterochromatic region. *Nucleic Acids Res*, 2014, 42: 6183–6195
- 89 Cui G, Dong Q, Duan J, et al. NC2 complex is a key factor for the activation of catalase-3 transcription by regulating H2A.Z deposition. *Nucleic Acids Res*, 2020, 48: 8332–8348
- 90 Zhang C, Tian Y, Song S, et al. H3K56 deacetylation and H2A.Z deposition are required for aberrant heterochromatin spreading. *Nucleic Acids Res*, 2022, 50: 3852–3866
- 91 Quan Y, Xia Y, Liu L, et al. Cell-cycle-regulated interaction between Mcm10 and double hexameric Mcm2-7 is required for helicase splitting and activation during S phase. *Cell Rep*, 2015, 13: 2576–2586
- 92 Fang D, Lengronne A, Shi D, et al. Dbf4 recruitment by fork head transcription factors defines an upstream rate-limiting step in determining origin firing timing. *Genes Dev*, 2017, 31: 2405–2415
- 93 Zhang J, Shi D, Li X, et al. Rtt101-Mms1-Mms22 coordinates replication-coupled sister chromatid cohesion and nucleosome assembly. *EMBO Rep*, 2017, 18: 1294–1305
- 94 Zhang J, Li L, Miao Y, et al. Symmetric control of sister chromatid cohesion establishment. *Nucleic Acids Res*, 2023, 51: 4760–4773

- 95 Li L, Wang J, Yang Z, et al. Metabolic remodeling maintains a reducing environment for rapid activation of the yeast DNA replication checkpoint. *EMBO J*, 2022, 41: e108290
- 96 Li S, Guo S, Liu F, et al. miR-451-targeted PSMB8 promotes PRRSV infection by degrading IRF3. *J Virol*, 2024, 98: e00784-24
- 97 Wang H, Du L, Liu F, et al. Highly pathogenic porcine reproductive and respiratory syndrome virus induces interleukin-17 production via activation of the IRAK1-PI3K-p38MAPK-C/EBP $\beta$ /CREB pathways. *J Virol*, 2019, 93: e01100-19
- 98 Fang S, Yu J, Feng J, et al. Identification of rice black-streaked dwarf fijivirus in maize with rough dwarf disease in China. *Arch Virol*, 2001, 146: 167–170
- 99 Yu J, Yan L, Su N, et al. Analysis of nucleotide sequence of wheat yellow mosaic virus genomic RNAs. *Sci China Ser C-Life Sci*, 1999, 42: 554–560
- 100 Cao Y, Cai Z, Ding Q, et al. The complete nucleotide sequence of Beet black scorch virus (BBSV), a new member of the genus Necrovirus. *Arch Virol*, 2002, 147: 2431–2435
- 101 Yang M, Zhang Y, Xie X, et al. *Barley stripe mosaic virus*  $\gamma b$  protein subverts autophagy to promote viral infection by disrupting the ATG7-ATG8 interaction. *Plant Cell*, 2018, 30: 1582–1595
- 102 Yue N, Jiang Z, Zhang X, et al. Palmitoylation of  $\gamma b$  protein directs a dynamic switch between *Barley stripe mosaic virus* replication and movement. *EMBO J*, 2022, 41: e110060
- 103 Gao Q, Xu W, Yan T, et al. Rescue of a plant cytorhabdovirus as versatile expression platforms for planthopper and cereal genomic studies. *New Phytol*, 2019, 223: 2120–2133
- 104 Ding Z H, Gao Q, Tong X, et al. MAPKs trigger antiviral immunity by directly phosphorylating a rhabdovirus nucleoprotein in plants and insect vectors. *Plant Cell*, 2022, 34: 3110–3127
- 105 Gao D M, Qiao J H, Gao Q, et al. A plant cytorhabdovirus modulates locomotor activity of insect vectors to enhance virus transmission. *Nat Commun*, 2023, 14: 5754
- 106 Gao Q, Yan T, Zhang Z J, et al. Casein kinase 1 regulates cytorhabdovirus replication and transcription by phosphorylating a phosphoprotein serine-rich motif. *Plant Cell*, 2020, 32: 2878–2897
- 107 Gao Q, Zang Y, Qiao J H, et al. The plant rhabdovirus viroporin P9 facilitates insect-mediated virus transmission in barley. *Plant Cell*, 2024, 36: 3483–3497
- 108 Wang X, Jiang Z, Yue N, et al. *Barley stripe mosaic virus*  $\gamma b$  protein disrupts chloroplast antioxidant defenses to optimize viral replication. *EMBO J*, 2021, 40: e107660
- 109 Zhang Q, Wen Z, Zhang X, et al. RETICULON-LIKE PROTEIN B2 is a proviral factor co-opted for the biogenesis of viral replication organelles in plants. *Plant Cell*, 2023, 35: 3127–3151
- 110 Tong X, Liu S, Zou J, et al. A small peptide inhibits siRNA amplification in plants by mediating autophagic degradation of SGS3/RDR6 bodies. *EMBO J*, 2021, 40: e108050
- 111 Tong X, Zhao J J, Feng Y L, et al. A selective autophagy receptor VISP1 induces symptom recovery by targeting viral silencing suppressors. *Nat Commun*, 2023, 14: 3852
- 112 Gao Z, Zhang D, Wang X, et al. Coat proteins of necroviruses target 14-3-3a to subvert MAPKK $\alpha$ -mediated antiviral immunity in plants. *Nat Commun*, 2022, 13: 716
- 113 Zhang D, Gao Z, Zhang H, et al. The MAPK-Alfin-like 7 module negatively regulates ROS scavenging genes to promote NLR-mediated immunity. *Proc Natl Acad Sci USA*, 2023, 120: e2214750120
- 114 Zhang D, Yang X, Wen Z, et al. Proxitome profiling reveals a conserved SGT1-NSL1 signaling module that activates NLR-mediated immunity. *Mol Plant*, 2024, 17: 1369–1391
- 115 Zhang Y, Song G, Lal N K, et al. TurboID-based proximity labeling reveals that UBR7 is a regulator of N NLR immune receptor-mediated immunity. *Nat Commun*, 2019, 10: 3252
- 116 Li T, Hu J, Sun Y, et al. Highly efficient heritable genome editing in wheat using an RNA virus and bypassing tissue culture. *Mol Plant*, 2021, 14: 1787–1798
- 117 Yan L, Shi D. Contraction proteins in higher plants (in Chinese). *Acta Biochim Biophys Sin*, 1963, 3: 490–495 [阎隆飞, 石德全. 高等植物中的收缩蛋白. 生物化学与生物物理学报, 1963, 3: 490–495]
- 118 Ma Y Z, Yen L F. Actin and myosin in pea tendrils. *Plant Physiol*, 1989, 89: 586–589
- 119 Liu X, Yen L F. Purification and characterization of actin from maize pollen. *Plant Physiol*, 1992, 99: 1151–1155
- 120 Wang C, Li J, Yuan M. Salt tolerance requires cortical microtubule reorganization in *Arabidopsis*. *Plant Cell Physiol*, 2007, 48: 1534–1547
- 121 Wang X, Zhu L, Liu B, et al. *Arabidopsis* MICROTUBULE-ASSOCIATED PROTEIN18 functions in directional cell growth by destabilizing cortical microtubules. *Plant Cell*, 2007, 19: 877–889
- 122 Su S, Liu Z, Chen C, et al. *Cucumber Mosaic Virus* movement protein severs actin filaments to increase the plasmodesmal size exclusion limit in

- tobacco. *Plant Cell*, 2010, 22: 1373–1387
- 123 Zhou D, Wang X, Wang X, et al. PHYTOCHROME INTERACTING FACTOR 4 regulates microtubule organization to mediate high temperature-induced hypocotyl elongation in *Arabidopsis*. *Plant Cell*, 2023, 35: 2044–2061
- 124 Dou L, He K, Peng J, et al. The E3 ligase MREL57 modulates microtubule stability and stomatal closure in response to ABA. *Nat Commun*, 2021, 12: 2181
- 125 Wang X, Mao T. Understanding the functions and mechanisms of plant cytoskeleton in response to environmental signals. *Curr Opin Plant Biol*, 2019, 52: 86–96
- 126 Lian N, Liu X, Wang X, et al. COP1 mediates dark-specific degradation of microtubule-associated protein WDL3 in regulating *Arabidopsis* hypocotyl elongation. *Proc Natl Acad Sci USA*, 2017, 114: 12321–12326
- 127 Wang X, Zhang J, Yuan M, et al. *Arabidopsis* MICROTUBULE DESTABILIZING PROTEIN40 is involved in brassinosteroid regulation of hypocotyl elongation. *Plant Cell*, 2012, 24: 4012–4025
- 128 Deng J, Wang X, Liu Z, et al. The microtubule-associated protein WDL4 modulates auxin distribution to promote apical hook opening in *Arabidopsis*. *Plant Cell*, 2021, 33: 1927–1944
- 129 Qian Y, Wang X, Liu Y, et al. HY5 inhibits lateral root initiation in *Arabidopsis* through negative regulation of the microtubule-stabilizing protein TPXL5. *Plant Cell*, 2023, 35: 1092–1109
- 130 Fu Y, Xu T, Zhu L, et al. A ROP GTPase signaling pathway controls cortical microtubule ordering and cell expansion in *Arabidopsis*. *Curr Biol*, 2009, 19: 1827–1832
- 131 Lin D, Cao L, Zhou Z, et al. Rho GTPase signaling activates microtubule severing to promote microtubule ordering in *Arabidopsis*. *Curr Biol*, 2013, 23: 290–297
- 132 Zhu L, Zhang Y, Kang E, et al. MAP18 regulates the direction of pollen tube growth in *Arabidopsis* by modulating F-actin organization. *Plant Cell*, 2013, 25: 851–867
- 133 Zhou Z, Shi H, Chen B, et al. *Arabidopsis* RIC1 severs actin filaments at the Apex to regulate pollen tube growth. *Plant Cell*, 2015, 27: 1140–1161
- 134 Li C, Lu H, Li W, et al. A ROP2-RIC1 pathway fine-tunes microtubule reorganization for salt tolerance in *Arabidopsis*. *Plant Cell Environ*, 2017, 40: 1127–1142
- 135 Kang E, Zheng M, Zhang Y, et al. The microtubule-associated protein MAP18 Affects ROP2 GTPase activity during root hair growth. *Plant Physiol*, 2017, 174: 202–222
- 136 Cui X, Wang S, Huang Y, et al. *Arabidopsis* SYP121 acts as an ROP2 effector in the regulation of root hair tip growth. *Mol Plant*, 2022, 15: 1008–1023
- 137 Zhao H, Wang Y, Zhao S, et al. HOMEobox PROTEIN 24 mediates the conversion of indole-3-butyric acid to indole-3-acetic acid to promote root hair elongation. *New Phytol*, 2021, 232: 2057–2070
- 138 Ding X, Wang S, Cui X, et al. LKS4-mediated SYP121 phosphorylation participates in light-induced stomatal opening in *Arabidopsis*. *Curr Biol*, 2024, 34: 3102–3115.e6
- 139 Zhong H, Wang S, Huang Y, et al. Endomembrane trafficking driven by microtubule growth regulates stomatal movement in *Arabidopsis*. *Nat Commun*, 2024, 15: 7967
- 140 Li W, Ge F, Qiang Z, et al. Maize *ZmRPH1* encodes a microtubule-associated protein that controls plant and ear height. *Plant Biotechnol J*, 2020, 18: 1345–1347
- 141 Fu J, Zhang C. Super-resolution microscopy: successful applications in centrosome study and beyond. *Biophys Rep*, 2019, 5: 235–243
- 142 Tian Y, Yan Y, Fu J. Nine-fold symmetry of centriole: the joint efforts of its core proteins. *BioEssays*, 2022, 44: 2100262
- 143 Tian Y, Wei C, He J, et al. Superresolution characterization of core centriole architecture. *J Cell Biol*, 2021, 220: e202005103
- 144 Yan L F, Han Y S, Shi D Q. Purification of plant contractile proteins and properties of adenotriphosphatase (in Chinese). *Chin Sci Bull*, 1966, 17: 88–90 [阎龙飞, 韩雅珊, 石德权. 植物收缩蛋白的提纯及其腺三磷酶的性质. 科学通报, 1966, 17: 88–90]
- 145 Shou S, Zhu B, Cui Z, et al. Study on the expression of human insulin gene with site directed mutation in CHO cells (in Chinese). *Chin J Diabetes*, 1999, 7: 269–272 [寿思明, 朱宝利, 崔振中, 等. 定点突变的人胰岛素基因在CHO细胞表达的研究. 中国糖尿病杂志, 1999, 7: 269–272]
- 146 Zhou F, Li X, Wang X, et al. Adenovirus mediated *pGH* gene expression and its growth-stimulating function in rats (in Chinese). *Chin J Virol*, 2003, 19: 133–137 [仲飞, 李秀锦, 王辛中, 等. 腺病毒介导的猪生长激素cDNA在大鼠体内的诱导表达及其促生长作用的研究. 病毒学报, 2003, 19: 133–137]
- 147 Gou K, An X, Tian J, et al. Transgenic animals bioreactors (in Chinese). *Chin J Biotechnol*, 2002, 18: 144–148 [苟克勉, 安晓荣, 田见晖, 等. 动物乳腺生物反应器的现状和趋势. 生物工程学报, 2002, 18: 144–148]
- 148 Yu J, Peng P, Zhang X, et al. Seed-specific expression of a lysine rich protein sb401 gene significantly increases both lysine and total protein content in maize seeds. *Mol Breeding*, 2004, 14: 1–7
- 149 People's Daily. China has made important progress in animal somatic cell cloning: the first high-quality Chinese yellow cattle has been

- successfully cloned (in Chinese). 2002, <https://data.people.com.cn/rmrb/20020529/6> [人民日报. 我国动物体细胞克隆再获重要进展: 第一头优质中国黄牛克隆成功. 2002, <https://data.people.com.cn/rmrb/20020529/6>]
- 150 Pan D, Zhang Y, Sun X, et al. Cloned pigs derived from somatic cell nuclear transfer embryos cultured *in vitro* at low oxygen tension. *Sci Bull*, 2006, 51: 839–844
- 151 Lu D, Liu S, Shang S, et al. Production of transgenic-cloned pigs expressing large quantities of recombinant human lysozyme in milk. *PLoS One*, 2015, 10: e0123551
- 152 Lu D, Liu S, Ding F, et al. Large-scale production of functional human lysozyme from marker-free transgenic cloned cows. *Sci Rep*, 2016, 6: 22947
- 153 Wu H, Cao D, Liu T, et al. Purification and characterization of recombinant human lysozyme from eggs of transgenic chickens. *PLoS One*, 2015, 10: e0146032
- 154 Zhang R, Tang C, Guo H, et al. A novel glycosylated anti-CD20 monoclonal antibody from transgenic cattle. *Sci Rep*, 2018, 8: 13208
- 155 Cui D, Li J, Zhang L, et al. Generation of bi-transgenic pigs overexpressing human lactoferrin and lysozyme in milk. *Transgenic Res*, 2015, 24: 365–373
- 156 Liu S, Li X, Lu D, et al. High-level expression of bioactive recombinant human lysozyme in the milk of transgenic mice using a modified human lactoferrin BAC. *Transgenic Res*, 2012, 21: 407–414
- 157 Sun Y, Huang T, Hammarström L, et al. The immunoglobulins: new insights, implications, and applications. *Annu Rev Anim Biosci*, 2020, 8: 145–169
- 158 Zhang T, Cheng X, Yu D, et al. Genetic removal of the CH1 exon enables the production of heavy chain-only IgG in mice. *Front Immunol*, 2018, 9: 2202
- 159 Peng G, Liu T, Qi X, et al. A genome-wide CRISPR screening uncovers that TOB1 acts as a key host factor for FMDV infection via both IFN and EGFR mediated pathways. *PLoS Pathog*, 2024, 20: e1012104
- 160 Zhi M, Zhang J, Tang Q, et al. Generation and characterization of stable pig pregastrulation epiblast stem cell lines. *Cell Res*, 2022, 32: 383–400
- 161 Zhu G, Gao D, Li L, et al. Generation of three-dimensional meat-like tissue from stable pig epiblast stem cells. *Nat Commun*, 2023, 14: 8163
- 162 Zhu Q, Wang F, Gao D, et al. Generation of stable integration-free pig induced pluripotent stem cells under chemically defined culture condition. *Cell Prolif*, 2023, 56: e13487
- 163 Zhi M, Gao D, Yao Y, et al. Elucidation of the pluripotent potential of bovine embryonic lineages facilitates the establishment of formative stem cell lines. *Cell Mol Life Sci*, 2024, 81: 427
- 164 Du X, Guo Z, Fan W, et al. Establishment of a humanized swine model for COVID-19. *Cell Discov*, 2021, 7: 70
- 165 Yu D, Wang J, Zou H, et al. Silencing of retrotransposon-derived imprinted gene RTL1 is the main cause for postimplantational failures in mammalian cloning. *Proc Natl Acad Sci USA*, 2018, 115: 70
- 166 Chen J, Wang H, Bai J, et al. Generation of pigs resistant to highly pathogenic-porcine reproductive and respiratory syndrome virus through gene editing of *CD163*. *Int J Biol Sci*, 2019, 15: 481–492
- 167 Wang Y, Cao X, Luo C, et al. Multiple ancestral haplotypes harboring regulatory mutations cumulatively contribute to a QTL affecting chicken growth traits. *Commun Biol*, 2020, 3: 472
- 168 Song Y, Guerrero-Juarez C F, Chen Z, et al. The Ms1-mTOR pathway drives the pathogenesis of mammary and extramammary Paget's disease. *Cell Res*, 2020, 30: 854–872
- 169 Tian Y, Xu J, Li Y, et al. MicroRNA-31 reduces inflammatory signaling and promotes regeneration in colon epithelium, and delivery of mimics in microspheres reduces colitis in mice. *Gastroenterology*, 2019, 156: 2281–2296.e6
- 170 Yue J, Li C, Zhao Q, et al. Seed-specific expression of a lysine-rich protein gene, GhLRP, from cotton significantly increases the lysine content in maize seeds. *Int J Mol Sci*, 2014, 15: 5350–5365
- 171 Liu C, Li S, Yue J, et al. Microtubule-associated protein SBgLR facilitates storage protein deposition and its expression leads to lysine content increase in transgenic maize endosperm. *Int J Mol Sci*, 2015, 16: 29772–29786
- 172 Wang M Z. Culturing of immature inflorescences and *Agrobacterium*-mediated transformation of foxtail millet (*Setaria italica*). *Afr J Biotechnol*, 2011, 10: 5350–5350
- 173 Qi X, Xie S, Liu Y, et al. Genome-wide annotation of genes and noncoding RNAs of foxtail millet in response to simulated drought stress by deep sequencing. *Plant Mol Biol*, 2013, 83: 459–473
- 174 Yi F, Xie S, Liu Y, et al. Genome-wide characterization of microRNA in foxtail millet (*Setaria italica*). *BMC Plant Biol*, 2013, 13: 212
- 175 Yi F, Huo M, Li J, et al. Time-series transcriptomics reveals a drought-responsive temporal network and crosstalk between drought stress and the circadian clock in foxtail millet. *Plant J*, 2022, 110: 1213–1228
- 176 Li C, Yue J, Wu X, et al. An ABA-responsive DRE-binding protein gene from *Setaria italica*, SiARDP, the target gene of SiAREB, plays a critical role under drought stress. *J Exp Bot*, 2014, 65: 5415–5427

- 177 Luo W, Tang Y, Li S, et al. The m<sup>6</sup>A reader SiYTH1 enhances drought tolerance by affecting the messenger RNA stability of genes related to stomatal closure and reactive oxygen species scavenging in *Setaria italica*. *J Integr Plant Biol*, 2023, 65: 2569–2586
- 178 Xu J, Li Y, Wang Y, et al. Activation of MAPK kinase 9 induces ethylene and camalexin biosynthesis and enhances sensitivity to salt stress in *Arabidopsis*. *J Biol Chem*, 2008, 283: 26996–27006
- 179 Li Y, Cao H, Dong T, et al. Phosphorylation of the LCB1 subunit of *Arabidopsis* serine palmitoyltransferase stimulates its activity and modulates sphingolipid biosynthesis. *J Integr Plant Biol*, 2023, 65: 1585–1601
- 180 Su T, Xu J, Li Y, et al. Glutathione-indole-3-acetonitrile is required for camalexin biosynthesis in *Arabidopsis thaliana*. *Plant Cell*, 2011, 23: 364–380

Summary for “中国农业大学生物学院建院40周年重要科研成果回顾”

## Review of major scientific research achievements on the 40th anniversary of the establishment of the College of Biological Sciences, China Agricultural University

Jingyan Fu, Ying Fu, Yan Guo, Jianyong Han, Dawei Li, Tonglin Mao, Dongtao Ren, Changfu Tian, Chao Wang, Yi Wang\*, Shuhua Yang, Jingjuan Yu, Hua Zhang & Yaofeng Zhao

College of Biological Sciences, China Agricultural University, Beijing 100193, China

\* Corresponding author, E-mail: [yiwang@cau.edu.cn](mailto:yiwang@cau.edu.cn)

In December 1984, China Agricultural University integrated the relevant majors, teaching and research groups, and central laboratories from the then Department of Agronomy, Department of Plant Protection, Department of Veterinary Medicine, Department of Agricultural Physics and Meteorology, and Department of Animal Husbandry to establish the College of Biological Sciences, which was the earliest college of biology (life sciences) established in China. By 2025, the College of Biological Sciences has gone through 40 years and is celebrated its 40th anniversary since its establishment. Over the past 40 years, with the strong support of various national departments at all levels, the College of Biological Sciences of China Agricultural University has widely recruited outstanding talents from both home and abroad and established a teaching faculty with both an international perspective as well as strong competitiveness. The College of Biological Sciences focuses on the construction of scientific research innovation teams, conducts scientific research relying on excellent scientific research conditions and a solid technical support platform, actively expands international cooperation and exchanges, has achieved a series of remarkable scientific research achievements in the fields of life sciences and agricultural biology, exerting a wide influence internationally. The college has two state key laboratories, one ministerial key laboratory, and one Frontier Science Center for Molecular Design Breeding of the Ministry of Education. The college has three national key disciplines (Botany, Biochemistry and Molecular Biology, Microbiology) and one key discipline of Beijing Municipality (Zoology). The biological discipline has been included in the “Double First-Class” Disciplines (Class A), and selected into the “Basic Discipline Top-Notch Student Training Program 2.0” and the basic discipline enrollment reform pilot major (Strong Foundation Plan) of the Ministry of Education. The majors of Biological Sciences and Biotechnology have been selected into the national “Ten Thousand First-Class Undergraduate Programs Construction Plan”. The college’s disciplines, such as Biology and Biochemistry, Microbiology, Molecular Biology and Genetics, and Plant and Animal Sciences, rank among the top 1% in the world, among which Plant and Animal Sciences have entered the top 0.01% globally. This article mainly introduces the important original academic achievements made by the College of Biological Sciences in the fields of plant physiology, animal physiology, microbiology and immunology, cell biology, biochemistry, and biotechnology over the past 40 years since its establishment. These achievements not only have helped the College of Biological Sciences to rank among the international leaders in the discipline of life sciences but also have made important contributions to agricultural, scientific, and technological innovation and human life and health.

**plant physiology, animal physiology, microbiology and immunology, cell biology, biochemistry and biotechnology**

doi: [10.1360/CSB-2025-0277](https://doi.org/10.1360/CSB-2025-0277)