遗传资源与进化国家重点实验室
State Key Laboratory of Genetic Resources and Evolution

2022年报
ANNUAL REPORT

中国科学院昆明动物研究所
KUNMING INSTITUTE OF ZOOLOGY ,CAS

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主任致辞

春风浩荡满目新，不负韶华万里程。2022 年是党和国家历史上具有里程碑意义的一年。这一年，党的二十大胜利召开，擘画了全面建成社会主义现代化强国、以中国式现代化全面推进中华民族伟大复兴的宏伟蓝图，明确了新时代新征程党和国家事业发展的目标任务。在这一年里，遗传资源与进化国家重点实验室在各级主管部门的领导与关怀下，立足于我国西南和东南亚丰富的生物多样性遗传资源，面向战略生物资源的国家需求和世界科技前沿以及国民经济主战场，在任务承担、科研成果、队伍建设、开放交流等各方面工作均取得了可喜进展。

在承担科研项目方面，实验室积极发挥集群优势，组织策划国家、国际重大科技任务，成效显著。2022 年，实验室新增科研项目 83 项，包括主持国家重点研发计划 2 项，参与 6 项；参与基金委基础科学中心项目 1 项；主持云南省重大科技专项 1 项；全年新增各类研究经费 14102.7 万元。

在科研成果产出方面，实验室围绕三大研究方向，2022 年共发表 SCI 论文 154 篇，其中以第一完成单位发表论文 51 篇，以论文第一单位或通讯作者 (含并列) 在 *Cell*、*Nature Methods*、*Nature Genetics*、*Molecular Biology and Evolution*、*National Science Review* 等国际高水平期刊发表论文 37 篇；授权发明专利 6 项，其中 1 项为美国授权专利；获北京市科学技术进步二等奖 1 项。

在人才队伍建设方面，实验室继续采用“引进加培养”的方式，创新人才机制，激发队伍活力，取得明显成效。2022 年，培养 1 人获得国家杰出青年基金资助，1 人获得国家优秀青年基金资助，晋升副高级职称 4 人；1 人获得谈家桢生命科学创新奖；1 人获得第十八届中国青年女科学家奖；3 人新入选中科院青年创新促进会会员；新增昆明市高层次创新创业团队和中科院西部交叉团队各 1 个；1 人入选科学家工作室；1 人入选“兴滇英才支持计划”科技领军人才；2 人入选“兴滇英才支持计划”云岭学者；9 人入选“兴滇英才支持计划”青年人才。培养输出博士研究生 14 人，硕士研究生 23 人，出站博士后 3 人。

实验室长期遵循“交流促进合作”的原则，在 2022 年开展了一系列合作交流活动。定期举办“遗传资源与进化青年学者论坛”共计 8 期，提升了室内青年学者学术表达能力并充分促进了室内外交流合作。不定期举办“遗传与进化前沿交叉论坛”，邀请 8 名国内外知名专家来室进行学术交流。同时，实验室继续参与《生物多样性公约》缔约方大会第十五次会议 (COP15) 第二阶段会议，杨君兴研究员和杨晓君研究员接受《COP15 七彩交响》系列人物访谈节目专访。此外，实验室还积极发挥国内相关研究领域的辐射和带动作用，对外设立开放课题 16 项，并将各科研平台开放共享。

笃志前行，虽远必达。2023 年是全面贯彻落实党的二十大精神的开局之年，也是研究所实施“十四五”规划承上启下的关键之年。新的一年里，我们在学术委员会指导下，戮力同心、奋楫向前，力争做出更大贡献。在此，我谨代表实验室向给予大力帮助的各级领导及社会各界朋友致以最诚挚的感谢，并期望能得到大家一如既往的关心和支持！

实验室主任：

实验室概况

一、实验室介绍

遗传资源与进化国家重点实验室依托于中国科学院昆明动物研究所，前身为中科院重点实验室“细胞与分子进化重点实验室”。2007 年 11 月经科技部批准筹建，2009 年 9 月通过验收。

实验室立足于我国西南和东南亚丰富的生物多样性遗传资源，面向战略生物资源的国家需求和世界科技前沿，围绕“遗传、发育与进化的统一”这一重大科学前沿问题，部署三个研究方向：遗传资源多样性的演化与保护、基因与基因组的进化、遗传发育与进化。

实验室积极发挥地域优势和资源特色，开展了大量动物和人类遗传资源收集工作，为生物多样性相关研究打下了坚实的基础。同时将资源优势与科学前沿有机结合，围绕遗传资源多样性的演变规律、自然 / 人工选择与生物适应的遗传机制等关键科学问题，在生物多样性演化的格局、过程与人工选择机制方面做出了具有影响力的代表性成果。近五年，实验室承担国家级、省部级、国际合作及横向项目共 360 项，到位研究经费共计 4.69 亿元。发表 SCI 论文共 891 篇，包括在 *Cell*、*Nature*、*Science*、*Nature Genetics*、*Cell Stem Cell*、*Cell Research*、*Molecular Biology and Evolution* 等国际高水平学术期刊上发表论文 236 篇。出版专著 9 部。授权专利 20 项。农业农村部认定水产新品种 2 项。荣获云南省自然科学一等奖 3 项、三等奖 1 项，云南省科技进步三等奖 2 项，云南省技术发明一等奖 1 项，云南省专利二等奖 1 项。

实验室共有研究组 21 个，支撑部门 1 个。实验室固定人员 157 人，正高级职称 26 人，副高级职称 32 人。其中中国科学院院士 1 人，欧洲科学院院士 1 人，发展中国家科学院院士 1 人，人社部百千万人才工程 5 人，科技部中青年科技创新领军人才 4 人，教育部长江学者奖励计划 1 人，国家高层次人才特殊支持计划科技创新领军人才 4 人，国家高层次人才特殊支持计划青年拔尖人才 1 人，国家海外高层次人才引进计划 2 人，国家杰出青年科学基金获得者 6 人，国家优秀青年科学基金获得者 5 人。拥有博士学位的固定人员共 95 人，占比总数的 60.5%；研究队伍年轻有活力，40 岁以下的青年研究人员和技术骨干占固定人员总数的 74.5%。目前在站博士后 7 人，在读博士研究生 119 人，硕士研究生 87 人。

实验室目前建设有 7 大平台：分子实验平台、显微影像与操作平台、生物信息学平台、功能基因发掘与分析平台、生物多样性考察平台、生命条形码平台、集成家猪平台。拥有 30 万元以上的大型仪器设备共计 105 台 / 套，设备总价值 8260 万元。这些设施除了满足实验室在后基因组时代对基因组进化与基因功能研究的需求以外，所有大型设备还依托于昆明大型仪器区域中心，并通过“仪器设备共享管理网”对实验室内外乃至研究所内外全面开放共享。

另外，实验室还拥有无量山黑长臂猿监测站、哀牢山国家级自然保护区野生动物研究基地双柏监测站等野外观察站 4 个，云南土著鱼类养殖基地 3 个，嵩明小耳猪分子育种基地 1 个，为实验室的创新发展提供了重要支撑。

实验室积极开展与国内外的交流与合作，提高实验室在国内、国际学术界的知名度和影响力，促进实验室发展。在运行管理方面，严格按照科技部及中科院对国家重点实验室的要求，进一步完善“开放、流动、联合、竞争”的运行机制，实行依托单位领导下的主任负责制，加强规范化管理，营造出团结协作、开放自主的科研氛围。

二、研究方向及内容

1. 遗传资源多样性的演化与保护

围绕我国西南及东南亚等生物多样性热点区域，建立世界一流的遗传资源库；研究遗传资源多样性形成和演变的规律，尤其是珍稀物种的濒危机制及其保护策略、野生和家养动物遗传资源的多样性和驯化演变关系，系统发掘农业动物基因，为我国农业可持续发展提供资源、理论和技术支撑，为遗传资源的保护和合理利用提供科学依据，为阐明基因和基因组进化的模式和规律、研究遗传、发育和进化的分子机制提供素材。

2. 基因与基因组的进化

以生命进化关键节点的物种和类群为研究对象，研究基因起源方式与进化规律、基因适应性进化与形态发生和环境适应的关系、基因互作网络形成的进化模式、基因组起源与多样化形成机制；探讨基因、基因互作网络和基因组的结构、功能多样性的起源与进化，阐明生命形态与功能多样化的基因组基础。

3. 遗传发育与进化

通过对不同进化地位和近缘物种的代表类群（如昆虫、头索动物、两栖类和哺乳类等）发育调控机制的研究与比较，从而解析进化中代表性和关键性性状的进化发育规律，进而在不同进化水平分析物种演化的发育生物学机制，如新基因、新的基因表达调控机制、表观遗传元件对物种形态演化与适应性的贡献等，阐明基因和基因组进化模式和规律的分子机制，最终实现遗传、发育与进化的统一。

三、组织结构

1. 现任实验室领导

主　任

施　鹏 研究员

副主任

文建凡 研究员

毛炳宇 研究员

焦保卫 研究员

2. 第三届学术委员会

主　任

张亚平 院　士，中国科学院

副主任

宿　兵 研究员，中国科学院昆明动物研究所

委 员

桂建芳　院　士，中国科学院水生生物学研究所

金　力　院　士，复旦大学

魏辅文　院　士，中国科学院动物研究所

吴仲义　院　士，中山大学

张克勤　院　士，云南大学

焦保卫　研究员，中国科学院昆明动物研究所

李德铢　研究员，中国科学院昆明植物研究所

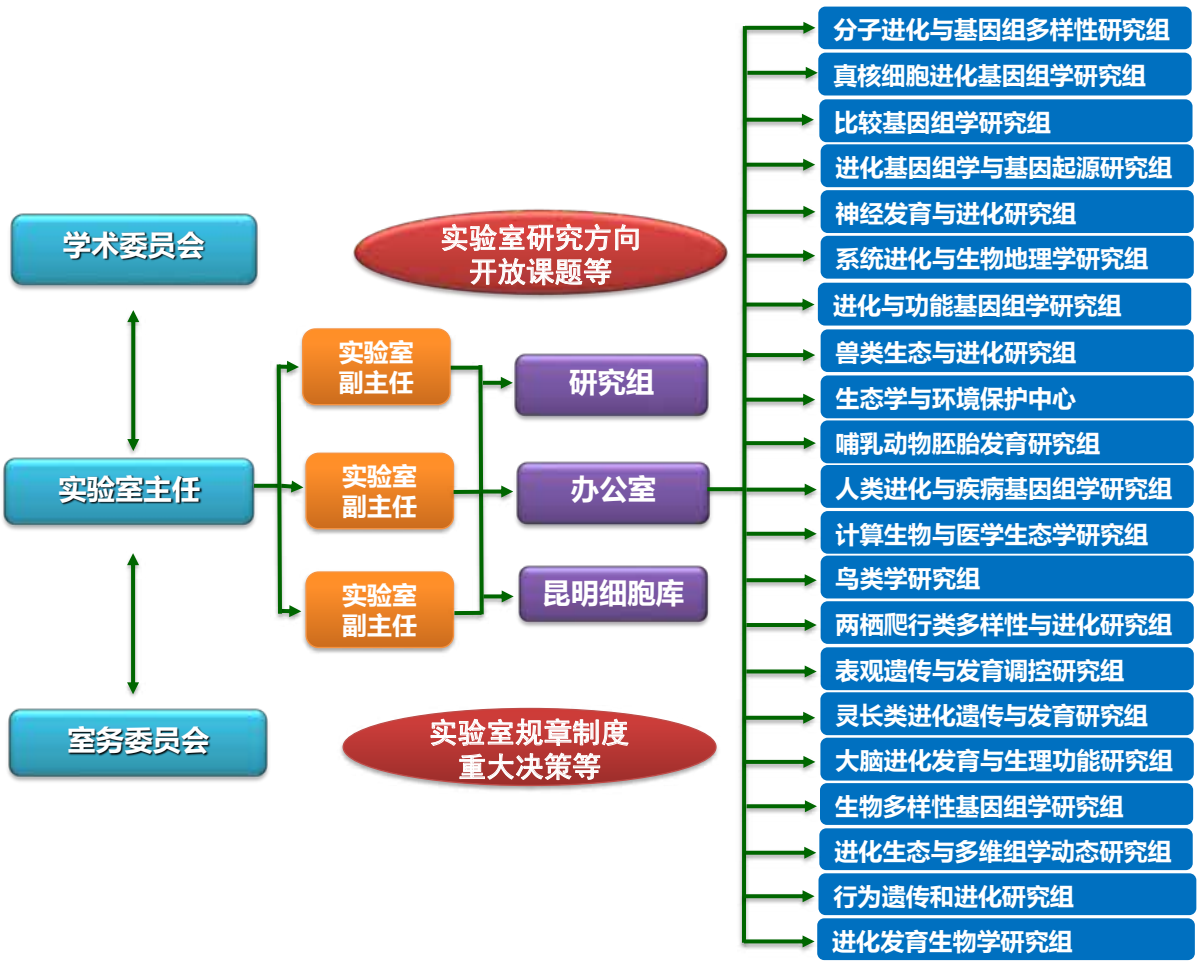
施　鹏　研究员，中国科学院昆明动物研究所

汪小全　研究员，中国科学院植物研究所

王　文　研究员，中国科学院昆明动物研究所

杨　光　教　授，南京师范大学

3. 研究队伍



大事记

实验室与云南大学张志刚研究员团队共同拍摄了反应卓乃湖生物多样性的自然纪录片，该纪录片为《我们的生物多样性》系列的首部作品，并作为“青藏高原第二次综合科学考察”任务五“生物多样性保护与可持续利用”的重要科普成果。该纪录片通过最先进的拍摄设备，向公众首次展示了可可西里无人区腹地的生态景观以及以藏羚羊迁徙产仔为主的生物多样性故事。纪录片发布后受到了来自央视、人民日报、新华社、中国日报等主流媒体的关注与报道。在 COP15 第二阶段会议期间，被生态环境部和国家林草局广泛宣传。

2022 年，实验室举办第五届“青年学者论坛”共计 8 场次，为青年学者们搭建了展示分享科研进展的平台。每场邀请室外专家及学术带头人、研究生或青年骨干进行学术报告和嘉宾评选，激发研究生以及青年骨干的科研创新思维，促进学术交流，并吸引了研究所内外广大师生积极参与。

2022 年，实验室不定期举办“遗传与进化前沿交叉论坛”，邀请到南方医科大学赵小阳教授、厦门大学袁晶教授和李光教授等国内外知名学者到实验室进行学术报告及课程讲授，共计 8 人次，并开展线上报告直播，追踪研究领域热点前沿，积极与国内外一流机构开展学术交流及合作研究。

科学传播与科教融合

7 月 25-29 日，研究生处与实验室联合举办了优秀大学生夏令营，70 余名来自全国高校的优秀学员来昆参会。通过学术讲座、师生座谈、实验室近距离感受科研生活、研究所园区及科研平台参观等丰富的活动环节，普及前沿热点科学知识的同时，也吸引了优质大学生生源。

2022 年 12 月，杨君兴研究员和杨晓君研究员分别接受了云南卫视《COP15 七彩交响》系列人物访谈节目专访，相关采访分别以“滇池金线鲃：从濒危到恢复”和“保护绿孔雀”为主题，在云南卫视《晚间新闻》同步播出，引起了广泛的社会关注。

李权副研究员受中央电视台纪录片频道之邀拍摄《荒野至上》第二季第 4 集《揭秘》，向公众介绍了鼯鼠的分类、演化以及保护的相关知识。记录片多次在中央电视台纪录片频道和网络客户端重播，社会反响良好。

实验室王文研究团队完成了一个较为全面的云南蝴蝶名录，报道云南蝴蝶 1300 种，该研究成果受到中央电视台、新华网、人民网、光明日报等多家媒体的关注和报道。

第一章　科研工作进展

研究方向一：遗传资源多样性的演化与保护　代表性成果一

揭示随机事件对物种演化的影响

Incomplete Lineage Sorting and Phenotypic Evolution in Marsupials

Feng SH[1], Bai M[1], Rivas-Gonzalez I, Li C, Liu S, Tong Y, Yang H, Chen G, Xie D, Sears KE, Franco LM, Gaitan-Espitia JD, Nespolo RF, Johnson WE, Yang H, Brandies PA, Hogg CJ, Belov K, Renfree MB, Helgen KM, Boomsma JJ, Schierup MH, **Zhang GJ***

Summary

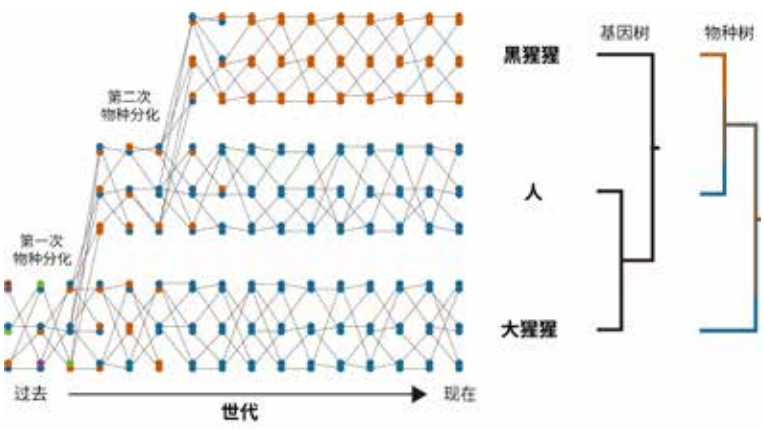
Incomplete lineage sorting (ILS) makes ancestral genetic polymorphisms persist during rapid speciation events, inducing incongruences between gene trees and species trees. ILS has complicated phylogenetic inference in many lineages, including hominids. However, we lack empirical evidence that ILS leads to incongruent phenotypic variation. Here, we performed phylogenomic analyses to show that the South American monito del monte is the sister lineage of all Australian marsupials, although over 31% of its genome is closer to the Diprotodontia than to other Australian groups due to ILS during ancient radiation. Pervasive conflicting phylogenetic signals across the whole genome are consistent with some of the morphological variation among extant marsupials. We detected hundreds of genes that experienced stochastic fixation during ILS, encoding the same amino acids in non-sister species. Using functional experiments, we confirm how ILS may have directly contributed to hemiplasy in morphological traits that were established during rapid marsupial speciation ca. 60 mya.

Cell, 2022, 185(10): 1646-1660.e18

早在 19 世纪，达尔文就在他的旷世著作《物种起源》中提出现在地球上的所有物种最初都是从同一种原始生命演化而来，即共同祖先理论。由这个共同祖先不断分叉演化形成现在物种类群的历程即构成了生命之树，从简单的单细胞生物到复杂的生命体，每个物种都可以找到它的最近缘物种和最近共同祖先。重构正确的物种关系树是演化生物学研究和开展跨物种比较研究的基础，对我们推理各种生物学现象的起源过程至关重要。

张国捷研究团队联合深圳华大生命科学研究院、动物研究所、哥本哈根大学等中外多个课题组，公布了对有袋类哺乳动物的物种辐射性大爆发过程的研究结果。该结果重建了有袋类物种的演化关系，并揭示了物种快速分化过程中，一些随机事件有可能会导致远缘物种具有相似表型的现象，解释了利用形态和分子数据在构建物种树经常出现冲突的发生机制。

物种性状的演化被认为是物种长期适应环境的结果：突变产生新的基因与新的性状，新基因通过繁殖扩散开来，有利于生存与繁殖的性状及其基因会被自然选择保留下来。在远缘物种中出现相同的性状，过去往往会用趋同演化来解释这样现象。然而，本研究则揭示不同类群间相同性状的出现也可能是随机遗传了祖先性状引起的。同时，这一研究还证明，仅依靠部分基因、部分性状的溯源来构建物种关系树是不可靠的，全基因组数据才是重构物种发生历程的金标准。通过全基因组数据可以充分揭示不完全的谱系分流作为一种可能的机制来解释基因组物种树和表型变异之间冲突的现象。此外，本研究还综合了古气候地理，物种分化、形态、DNA 等多方面证据来佐证有袋类物种演化进程。



不完全的谱系分流示意图（每组两个圆点代表一个个体，每个圆点代表一个基因）

该研究成果发表于国际顶级学术期刊 ***Cell***。

研究方向一：遗传资源多样性的演化与保护

代表性成果二

非洲野生猪科动物遗传资源挖掘

African suid genomes provide insights into the local adaptation to diverse African environments

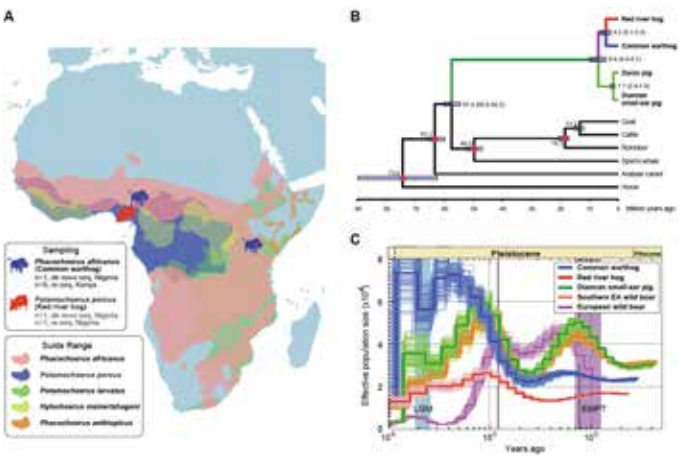
Xie HB[1], Yan C[1], Adeola AC[1], Wang K[1], **Huang CP[1], Xu MM**, Qiu Q, Yin X, Fan CY, **Ma YF, Yin TT, Gao Y, Deng JK**, Okeyoyin AO, Oluwole OO, Omotosho O, Okoro VMO, Omitogun OG, Dawuda PM, Olaogun SC, **Nneji LM, Ayoola AO**, Sanke OJ, Luka PD, Okoth E, Lekolool I, Mijele D, Bishop RP, Han JL*, **Wang W*, Peng MS*, Zhang YP***

Abstract

African wild suids consist of several endemic species that represent ancient members of the family Suidae and have colonized diverse habitats on the African continent. However, limited genomic resources for African wild suids hinder our understanding of their evolution and genetic diversity. In this study, we assembled high-quality genomes of a common warthog (*Phacochoerus africanus*), a red river hog (*Potamochoerus porcus*), as well as an East Asian Diannan small-ear pig (*Sus scrofa*). Phylogenetic analysis showed that common warthog and red river hog diverged from their common ancestor around the Miocene/Pliocene boundary, putatively predating their entry into Africa. We detected species-specific selective signals associated with sensory perception and interferon signaling pathways in common warthog and red river hog, respectively, which contributed to their local adaptation to savannah and tropical rainforest environments, respectively. The structural variation and evolving signals in genes involved in T-cell immunity, viral infection, and lymphoid development were identified in their ancestral lineage. Our results provide new insights into the evolutionary histories and divergent genetic adaptations of African suids.

Molecular Biology and Evolution, 2022, 39(12): msac256

非洲猪瘟（African Swine Fever, ASF）是由非洲猪瘟病毒（ASFV）感染引起的猪的一种急性、烈性、高度接触性传染病。经过长期的共进化，非洲的野生猪科动物对 ASFV 产生了天然抗性，表现为宿主可携带 ASFV，但不表现临床征状，是研究非洲猪瘟抗性形成的宝贵遗传资源。



非洲猪科动物的地理分布、系统发育关系与群体历史动态

张亚平院士研究团队发挥对非合作优势，联合国际家畜研究所和尼日利亚国家公园管理局等研究力量，运用三代长片段测序技术，构建了普通疣猪和红河猪的高质量基因组。通过系统比较非洲野生猪科动物与欧亚家猪基因组的精细结构，发现非洲猪科动物共同祖先支系上产生的结构变异和选择信号与 T 细胞免疫、病毒感染和淋巴组织发育相关。其中，体细胞重排后参与编码 T 细胞受体的 *TRBV27* 基因在非洲猪科动物中存在 284 bp 缺失，导致相关 T 细胞受体缺乏 CDR1 编码区，影响其 T 细胞受体对抗原呈递细胞的识别，这可能与对非洲大陆上古老病原的免疫应答相关。研究人员对此前报道的与 ASFV 抗性相关的 *CD163* 和 *RELA* 基因进行了深入分析，与对 ASFV 易感的欧亚家猪相比，非洲猪科动物的这两个基因并未受到选择或表现出快速进化的信号。本研究表明非洲猪科动物的基因组资源有助于筛选家猪受 ASFV 感染和致病的关键基因，为家猪抗病育种提供关键理论依据和技术支撑。

该研究成果发表于 ***Molecular Biology and Evolution***。

MOLECULAR BIOLOGY AND EVOLUTION

研究方向一：遗传资源多样性的演化与保护

代表性成果三

利用蚂蝗 iDNA 来评估自然保护区的管理成效

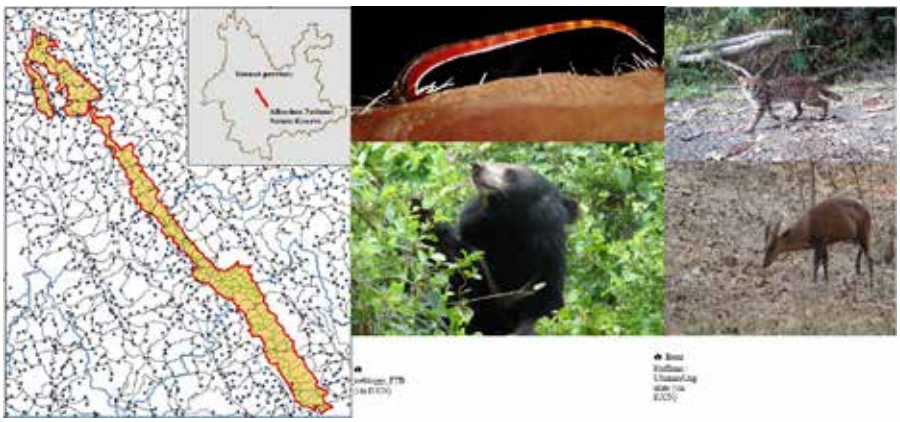
Measuring Protected-area Effectiveness Using Vertebrate Distributions from Leech iDNA

Ji YQ[1], Baker CCM[1*], Popescu VD, **Wang JX**, **Wu CY**, Wang Z, **Li YH**, Wang L, Hua C, Yang Z, **Yang CY**, Xu CCY, Diana A, Wen Q, Pierce NE[*], **Yu DW**[*]

Abstract

Protected areas are key to meeting biodiversity conservation goals, but direct measures of effectiveness have proven difficult to obtain. We address this challenge by using environmental DNA from leech-ingested bloodmeals to estimate spatially-resolved vertebrate occupancies across the 677 km2 Ailaoshan reserve in Yunnan, China. From 30,468 leeches collected by 163 park rangers across 172 patrol areas, we identify 86 vertebrate species, including amphibians, mammals, birds and squamates. Multi-species occupancy modelling shows that species richness increases with elevation and distance to reserve edge. Most large mammals (e.g. sambar, black bear, serow, tufted deer) follow this pattern; the exceptions are the three domestic mammal species (cows, sheep, goats) and muntjak deer, which are more common at lower elevations. Vertebrate occupancies are a direct measure of conservation outcomes that can help guide protected-area management and improve the contributions that protected areas make towards global biodiversity goals. Here, we show the feasibility of using invertebrate-derived DNA to estimate spatially-resolved vertebrate occupancies across entire protected areas.

Nature Communications, 2022, 13(1): 1555



哀牢山地图、吸血蚂蝗和本研究检测到的部分保护动物

生物多样性的灾难性丧失是目前全球面临的重大问题之一，而建立自然保护区是公认的保护生物多样性的最重要措施。截至 2015 年，全球已经有大约 15% 的陆地面积被划为自然保护区，但是由于缺乏野生动物（尤其是脊椎动物）的多样性信息，如何判断这些保护区是否真正有效地保护了当地的生物多样性，成为了一个全球性的难题。为了解决这一难题， Douglas 研究团队首次利用蚂蝗吸食的脊椎动物血液中的 DNA（iDNA，invertebrate-derived DNA）进行了一次大规模的尝试，对占地 677 平方公里的哀牢山国家级自然保护区进行了一个全局的脊椎动物多样性的调查。

本研究证明了基于蚂蝗 iDNA 的高通量条形码技术可以实际应用于大规模、高空间分辨率的野生脊椎动物多样性评估调查。本研究是迄今为止基于 iDNA 进行的空间分辨度最高、规模最广的野生脊椎动物多样性调查。研究结果表明，哀牢山自然保护区（主要在其核心区域）为具有高保护价值的脊椎动物提供了保护空间。研究结果还展示了保护区由于人类活动（如农业、畜牧和偷猎）而引发退化的脆弱性。本研究为哀牢山自然保护区建立了基于 iDNA 的脊椎动物多样性基线，未来的 iDNA 调查可以基于这个基线检测各个物种分布的变化，作为评估自然保护区的效率指标。

该研究成果发表于 ***Nature Communications***。

研究方向一：遗传资源多样性的演化与保护

代表性成果四

揭示数千年以来的人类干扰导致中国南方鸟类普遍种群衰退

Potential Millennial-scale Avian Declines by Humans in Southern China

Dong F*, Zhang Q, **Chen YL**, Lei FM, Li SH, **Wu F**, **Yang XJ***

Abstract

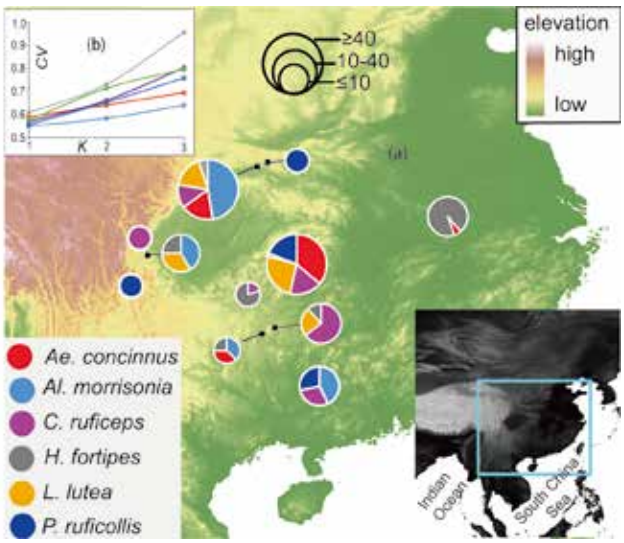
Mounting observational records demonstrate human-caused faunal decline in recent decades, while accumulating archaeological evidence suggests an early biodiversity impact of human activities during the Holocene. A fundamental question arises concerning whether modern wildlife population declines began during early human disturbance. Here, we performed a population genomic analysis of six common forest birds in East Asia to address this question. For five of them, demographic history inference based on 25-33 genomes of each species revealed dramatic population declines by 4- to 48-fold over millennia (e.g. 2000-5000 thousand years ago). Nevertheless, summary statistics detected nonsignificant correlations between these population size trajectories and Holocene temperature variations, and ecological niche models explicitly predicted extensive range persistence during the Holocene, implying limited demographic consequence of Holocene climate change. Further analyses suggest high negative correlations between the reconstructed population declines and human disturbance intensities and indicate a potential driver of human activities. These findings provide a deep-time and large-scale insight into the recently recognized avifaunal decline and support an early origin hypothesis of human effects on biodiversity. Overall, our study sheds light on the current biodiversity crisis in the context of long-term human-environment interactions and offers a multi-evidential framework for quantitatively assessing the ecological consequences of human disturbance.

Global Change Biology, 2022, 28(18): 5505-5513

当前生物多样性正以空前的速度流失，人类干扰无疑是背后的主因，但目前对于人类影响的时间尺度尚存争议。主流观点认为这些影响主要发生于工业革命以来的 200 余年间，而日益积累的考古证据提示该时间轴可能早至新石器时代（距今 10000-2000 年前）。针对上述假说，尚未有系统检验。

杨晓君研究团队以中国南方广泛分布的 6 种常见鸟类为研究对象，综合利用多种信息（种群基因组学、生态位模型、历史气候和人类活动数据等）以检验人类干扰对于野生动物种群数量的影响历史。结果显示，其中 5 种鸟类经历了距今 5000-2000 年以来的显著种群衰退过程，种群缩减幅度达 4-48 倍。进一步的统计分析显示历史气候变化的影响不显著，而人类活动可能是背后的主因。本研究首次以定量方式揭示当前的生物多样性危机可能根植于数千年以来的人类干扰，强调生物多样性的有效保护需要同时关注“常见物种”。研究同时提出了一套以物种历史种群动态为窗口检验人类活动生物效应的分析框架，该方法在其它地区和类群中的扩展应用有望为保护生物学提供新的思路。

该研究成果发表于 ***Global Change Biology***。



研究涉及的 6 种中国南方常见鸟类的采样信息

Global Change Biology

研究方向二：基因与基因组进化

代表性成果一

揭示青藏高原沙蜥属物种杂交带生殖隔离维持的基因组学机制

Species Persistence with Hybridization in Toad-headed Lizards Driven by Divergent Selection and Low Recombination

Gao W[1], Yu CX[1], Zhou WW[1], Zhang BL, Chambers EA, Dahn HA, **Jin JQ, Murphy RW, Zhang YP[*], Che J***

Abstract

Speciation plays a central role in evolutionary studies, and particularly how reproductive isolation (RI) evolves. The origins and persistence of RI are distinct processes that require separate evaluations. Treating them separately clarifies the drivers of speciation and then it is possible to link the processes to understand large-scale patterns of diversity. Recent genomic studies have focused predominantly on how species or RI originate. However, we know little about how species persist in face of gene flow. Here, we evaluate a contact zone of two closely related toad-headed lizards (*Phrynocephalus*) using a chromosome-level genome assembly and population genomics. To some extent, recent asymmetric introgression from *Phrynocephalus putjatai* to *P. vlangalii* reduces their genomic differences. However, their highly divergent regions (HDRs) have heterogeneous distributions across the genomes. Functional gene annotation indicates that many genes within HDRs are involved in reproduction and RI. Compared with allopatric populations, contact areas exhibit recent divergent selection on the HDRs and a lower population recombination rate. Taken together, this implies that divergent selection and low genetic recombination help maintain RI. This study provides insights into the genomic mechanisms that drive RI and two species persistence in the face of gene flow during the late stage of speciation.

Molecular Biology and Evolution, 2022, 39(4): msac064

物种形成是进化生物学中一个基础而又重要的问题，生殖隔离的建立和维持是物种形成过程中不同的阶段，目前大多数全基因组水平的研究关注在生殖隔离的建立方面，而对于生殖隔离维持的分子机制并不清楚。

车静研究团队从全基因组水平对发生基因渐渗时生殖隔离是如何维持的进行了探讨。基于三代高质量染色体水平的青海沙蜥基因组，对青海沙蜥 (*Phrynocephalus vlangalii*) 和贵德沙蜥 (*P. putjatai*) 共 86 个个体进行了全基因组重测序。群体基因组学分析显示，两物种的基因组高分化区在染色体上呈现异质性分布，高分化区中包含多个与生殖相关的基因，提示可能与两物种的生殖隔离有关。而接触区两物种的群体基因组分析显示，两物种间存在偏向性的基因流，进一步提示二者可能已经形成了一定的生殖隔离；分析发现基因流主要由重组介导，它虽然在一定程度上减少了接触区两物种的遗传分化，但分析提示，在高分化区基因流受到限制。更重要的，在基因组高分化区检测到明显的歧化选择信号，且具有较低的重组水平，表明歧化选择和低重组在物种间生殖隔离的维持中发挥了重要作用。综上，该研究利用群体基因组学的技术方法，系统解析了面对基因流时生殖隔离得以维持的分子基础，为物种多样性形成和维持的基因组学机制研究开拓了思路。

该研究成果发表于 ***Molecular Biology and Evolution***。

青海沙蜥和贵德沙蜥的生态照（接触区）

MOLECULAR BIOLOGY AND EVOLUTION

研究方向二：基因与基因组进化

代表性成果二

揭示中亚人群迁徙和混合历史

The Genetic Echo of the Tarim Mummies in Modern Central Asians

Dai SS[1], Sulaiman X[1], Isakova J[1], Xu WF[1], Abdulloevich NT, Afanasevna ME, Ibrohimovich KB, Chen X, Yang WK, Wang MS, Shen QK, Yang XY, Yao YG, Aldashev AA, Saidov A, Chen W, Cheng LF[*], **Peng MS[*], Zhang YP[*]**

Abstract

The diversity of Central Asians has been shaped by multiple migrations and cultural diffusion. Although ancient DNA studies have revealed the demographic changes of the Central Asian since the Bronze Age, the contribution of the ancient populations to the modern Central Asian remains opaque. Herein, we performed high-coverage sequencing of 131 whole genomes of Indo-European-speaking Tajik and Turkic-speaking Kyrgyz populations to explore their genomic diversity and admixture history. By integrating the ancient DNA data, we revealed more details of the origins and admixture history of Central Asians. We found that the major ancestry of present-day Tajik populations can be traced back to the admixture of the Bronze Age Bactria-Margiana Archaeological Complex and Andronovo-related populations. Highland Tajik populations further received additional gene flow from the Tarim mummies, an isolated ancient North Eurasian-related population. The West Eurasian ancestry of Kyrgyz is mainly derived from Historical Era populations in Xinjiang of China. Furthermore, the recent admixture signals detected in both Tajik and Kyrgyz are ascribed to the expansions of Eastern Steppe nomadic pastoralists during the Historical Era.

Molecular Biology and Evolution, 2022, 39(9): msac179

生活在帕米尔高原的塔吉克人

中亚位于欧亚大陆的交界处，一直是研究人类生物多样性与文化多样性的热点地区。在过去的二十年内，关于中亚民族人群的群体历史开展了大量研究。但是由于所采用遗传标记的限制以及缺乏周边古代人群的遗传学数据，难以剖析中亚人群真正的祖先。

张亚平研究员团队联合新疆医科大学、吉尔吉斯斯坦的分子生物学与医学研究所以及塔吉克斯坦科学院动物与寄生虫研究所等科研力量，组织开展了中亚民族人群典型代表塔吉克人和吉尔吉斯人多个群体的样本收集，并进行了高深度的基因组重测序。通过整合大量已发表的古代人群和当代人群的基因组测序数据，研究发现，生活在帕米尔和周边瓦罕走廊的高原塔吉克人群基因组中含有小河人群的 ANE 遗传组分；在平原塔吉克以及吉尔吉斯人群体中，以及其他中亚人群中则没有能检出这一组分。研究团队进一步构建了高原塔吉克人群体的混合历史，提出一个可能的情景：小河人群并没有完全湮灭，在放弃塔里木盆地的定居点后，向西迁徙到帕米尔高原，并与印欧语系人群发生了通婚融合。帕米尔高原成为了小河人群最后的庇护所。本研究加深了当前对于中亚人群的起源、迁徙以及混合历史的认识，对于阐明中华民族、中华文明多元一体的形成过程、探究欧亚大陆早期文化、文明的交流互鉴都具有重要意义。

该研究成果发表于 ***Molecular Biology and Evolution***。

MOLECULAR BIOLOGY AND EVOLUTION

研究方向二：基因与基因组进化

代表性成果三

发现藏族人群适应高原强紫外线的遗传机制

Genetic Adaptation of Skin Pigmentation in Highland Tibetans

Yang ZH[1*], Bai C[1], Pu Y[1], Kong Q[1], **Guo YB**[1], Ouzhuluobu, Gengdeng, Liu X, Zhao Q, Qiu Z, **Zheng WS, He YX,** Lin Y, Deng L, Zhang C, Xu S, **Peng Y, Xiang K**, Zhang X, Baimayangji, Cirenyangji, Cui C, Baimakangzhuo, Gonggalanzi, Bianba, Pan Y, Xin J, Wang Y, Liu S, Wang L, Guo H, Feng Z, Wang S, Shi H, Jiang B, Wu T, **Qi XB**[*], **Su B**[*]

Abstract

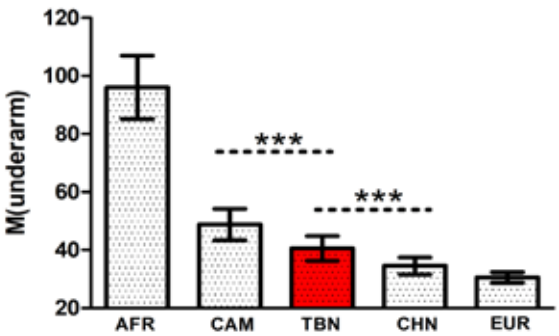
Strong ultraviolet (UV) radiation at high altitude imposes a serious selective pressure, which may induce skin pigmentation adaptation of indigenous populations. We conducted skin pigmentation phenotyping and genome-wide analysis of Tibetans in order to understand the underlying mechanism of adaptation to UV radiation. We observe that Tibetans have darker baseline skin color compared with lowland Han Chinese, as well as an improved tanning ability, suggesting a two-level adaptation to boost their melanin production. A genome-wide search for the responsible genes identifies GNPAT showing strong signals of positive selection in Tibetans. An enhancer mutation (rs75356281) located in GNPAT intron 2 is enriched in Tibetans (58%) but rare in other world populations (0 to 18%). The adaptive allele of rs75356281 is associated with darker skin in Tibetans and, under UVB treatment, it displays higher enhancer activities compared with the wild-type allele in in vitro luciferase assays. Transcriptome analyses of gene-edited cells clearly show that with UVB treatment, the adaptive variant of GNPAT promotes melanin synthesis, likely through the interactions of CAT and ACAA1 in peroxisomes with other pigmentation genes, and they act synergistically, leading to an improved tanning ability in Tibetans for UV protection.

PNAS, 2022, 119(40): e2200421119

世居高原的藏族人群是研究人类如何适应极端环境的理想人群。过去对藏族高原适应遗传机制的研究主要聚焦人体对高原低压低氧环境的适应，并发现了多个低氧适应基因。然而，在高原环境中，除了低压低氧这个胁迫因素外，高原紫外辐射是另一个重要的环境胁迫因素，对高原紫外辐射这一重要的环境胁迫的适应性机制鲜有研究。世居高原的藏族人群拥有较深的原肤色以及继发性肤色，但强紫外刺激下的深肤色是否可以遗传及其适应的遗传机制仍然是未解之谜。

宿兵研究团队与西藏大学医学院和郑州大学等单位合作，通过对藏族群体全基因组数据的分析，发现了参与机体黑色素合成的基因 *GNPAT* 在藏族人群中存在很强的达尔文正选择信号。位于该基因上游的一个增强子调控元件发生了点突变（rs75356281），其衍生等位基因频率在藏族人群中达 58%，而在世界其他人群中的比例仅为 0-18%，说明长期的自然选择导致了这个突变在藏族人群中的富集。综合遗传学和细胞生物学的实验证据，他们认为在自然选择的作用下，*GNPAT* 基因在藏族人群中发生了适应性突变的富集。这个适应性突变导致藏族人群黑色素合成能力的增强和肤色变深（包括原肤色和继发肤色）。特别是在紫外照射条件下，藏族人群的晒黑能力显著增强，以适应高原上的强紫外辐射。

该研究成果发表于 ***PNAS***。



世界人群肤色比较（AFR- 非洲，CAM- 柬埔寨，TBN- 藏族，CHN- 汉族，EUR- 欧洲）

研究方向二：基因与基因组进化

代表性成果四

揭示蜂猴适应性进化的遗传机制和群体历史

Functional Genomics Analysis Reveals the Evolutionary Adaptation and Demographic History of Pygmy Lorises

Li ML[1], **Wang S**[1], Xu P[1], **Tian HY**[1], Bai M, **Zhang YP, Shao Y, Xiong ZJ**, Qi XG, Cooper DN, **Zhang GJ**, Zhu HH, **Wu DD**[*]

Abstract

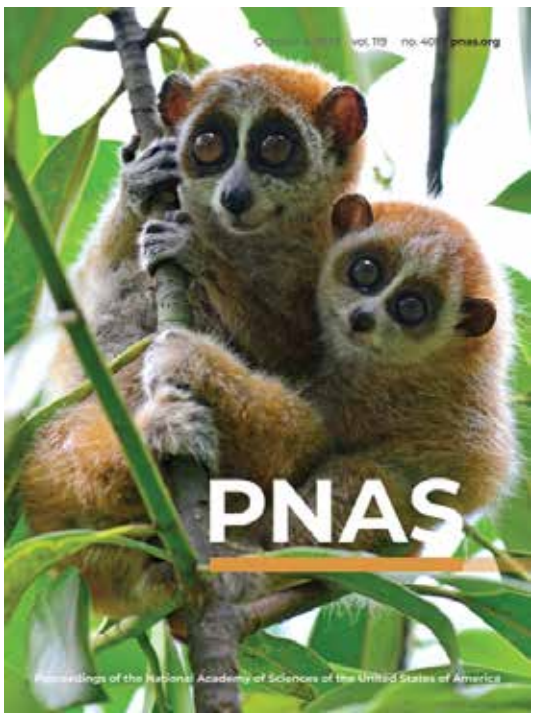
Lorises are a group of globally threatened strepsirrhine primates that exhibit many unusual physiological and behavioral features, including a low metabolic rate, slow movement, and hibernation. Here, we assembled a chromosome-level genome sequence of the pygmy loris (*Xanthonycticebus pygmaeus*) and resequenced whole genomes from 50 pygmy lorises and 6 Bengal slow lorises (*Nycticebus bengalensis*). We found that many gene families involved in detoxification have been specifically expanded in the pygmy loris, including the GSTA gene family, with many newly derived copies functioning specifically in the liver. We detected many genes displaying evolutionary convergence between pygmy loris and koala, including PITRM1. Significant decreases in PITRM1 enzymatic activity in these two species may have contributed to their characteristic low rate of metabolism. We also detected many evolutionarily convergent genes and positively selected genes in the pygmy loris that are involved in muscle development. Functional assays demonstrated the decreased ability of one positively selected gene, MYOF, to up-regulate the fast-type muscle fiber, consistent with the lower proportion of fast-twitch muscle fibers in the pygmy loris. The protein product of another positively selected gene in the pygmy loris, PER2, exhibited weaker binding to the key circadian core protein CRY, a finding that may be related to this species' unusual circadian rhythm. Finally, population genomics analysis revealed that these two extant loris species, which coexist in the same habitat, have exhibited an inverse relationship in terms of their demography over the past 1 million years, implying strong interspecies competition after speciation.

PNAS, 2022, 119(40): e2123030119

蜂猴是一类濒危的灵长类动物，在进化过程中表现出许多不寻常的生理和行为特征，包括低代谢率、行动缓慢和夜行性等。蜂猴为杂食动物，主要以野果为食，也能以有毒昆虫和树胶为食物。

为探究蜂猴适应性进化的遗传机制，吴东东团队从头组装了倭蜂猴（*Xanthonycticebus pygmaeus*）染色体水平的基因组序列，并对50 只倭蜂猴和 6 只孟加拉蜂猴 (*Nycticebus bengalensis*) 进行全基因组重测序。研究发现，与解毒有关的 GSTA 基因家族在蜂猴中特异性扩张，其在蜂猴肝脏中表现出特异性高表达。此外，研究人员发现 *PITRM1* 基因在蜂猴和考拉之间表现出趋同进化。功能实验证明蜂猴 *PITRM1* 酶活性显著降低，这可能导致了倭蜂猴低代谢率的特征。他们还在倭蜂猴中鉴定到与肌肉发育有关的正选择基因 *MYOF*，可能与其行动缓慢相关。相比较其它物种，倭蜂猴中正选择基因 *PER2* 与昼夜节律核心蛋白 CRY 的结合能力更弱，这一发现可能与该物种不寻常的昼夜节律有关。最后，群体基因组学分析显示，生活在同一地区的倭蜂猴和孟加拉蜂猴在过去 100 万年的时间里，在有效群体大小动态变化上表现出了一种逆相关关系，这意味着两个物种分化后存在物种间的竞争关系。

该研究成果发表于 ***PNAS***。



研究方向三： 遗传发育与进化

代表性成果一

构建家犬海马单细胞图谱并揭示各细胞类型与驯化的关系

A single-nucleus transcriptomic atlas of the dog hippocampus reveals the potential relationship between specific cell types and domestication

Zhou QJ[1], Liu X[1], **Zhang L**[1], **Wang R**, **Yin T**, Li X, **Li GM**, He Y, Ding Z, **Ma PC**, **Wang SZ**, **Mao BY**[*], Zhang SH[*], **Wang GD**[*]

Abstract

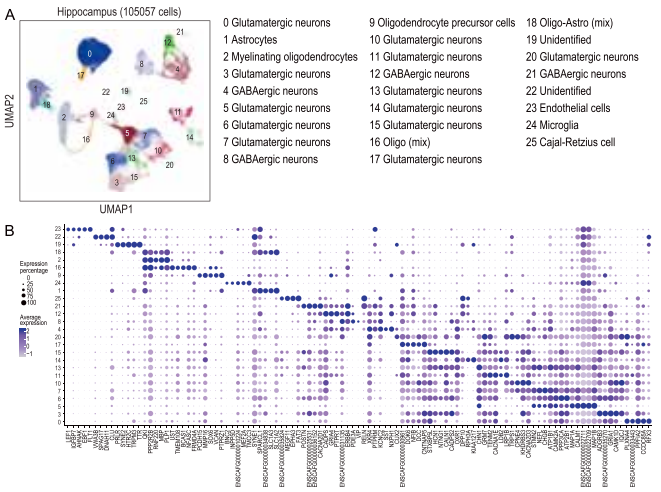
The process of domestication has led to dramatic differences in behavioral traits between domestic dogs and gray wolves. Whole-genome research found that a class of putative positively selected genes were related to various aspects of learning and memory, such as long-term potentiation and long-term depression. In this study, we constructed a single-nucleus transcriptomic atlas of the dog hippocampus to illustrate its cell types, cell lineage and molecular features. Using the transcriptomes of 105 057 nuclei from the hippocampus of a Beagle dog, we identified 26 cell clusters and a putative trajectory of oligodendrocyte development. Comparative analysis revealed a significant convergence between dog differentially expressed genes (DEGs) and putative positively selected genes (PSGs). Forty putative PSGs were DEGs in glutamatergic neurons, especially in Cluster 14, which is related to the regulation of nervous system development. In summary, this study provides a blueprint to understand the cellular mechanism of dog domestication.

National Science Review, 2022, 9(11): nwac147

海马是大脑边缘系统的重要组成部分，参与情景记忆，空间认知等过程。在驯化过程中海马同样发挥着重要的作用，比如参与了家鸡的恐惧记忆改变、家兔恐惧反应降低和信鸽认知功能增强。全基因组研究发现与海马突触功能相关的基因在家犬的驯化过程中受到了强烈的选择。

王国栋研究员团队联合毛炳宇研究员团队和中国科学院数学与系统科学研究院张世华研究员团队，使用 SPLiT-seq 单细胞核转录组测序技术，绘制了首张家犬海马单细胞图谱。该图谱定义了家犬海马中的 8 种细胞类型并推测其空间分布情况。与已发表的人类海马数据（Zhong et al. 2020）联合分析，发现人类和家犬之间细胞类型较为保守。拟时序分析结果显示家犬海马中存在少突胶质细胞祖细胞的分化过程，该过程同样存在于人类和小鼠海马中 (Zhong et al. 2020, Rosenberg et al. 2018)。超几何分布检验以及信息熵分析结果显示家犬驯化过程中受选择的基因在海马差异表达基因中显著富集，尤其是在谷氨酸能神经元中。基因调控网络结果显示谷氨酸能神经元可能通过改变突触传递进而影响家犬适应性进化中的行为改变。

该研究成果发表于 ***National Science Review***。



家犬海马细胞图谱

研究方向三： 遗传发育与进化

代表性成果二

揭示 ETS1 调控的核糖体功能降低是人类健康老化的新型机制

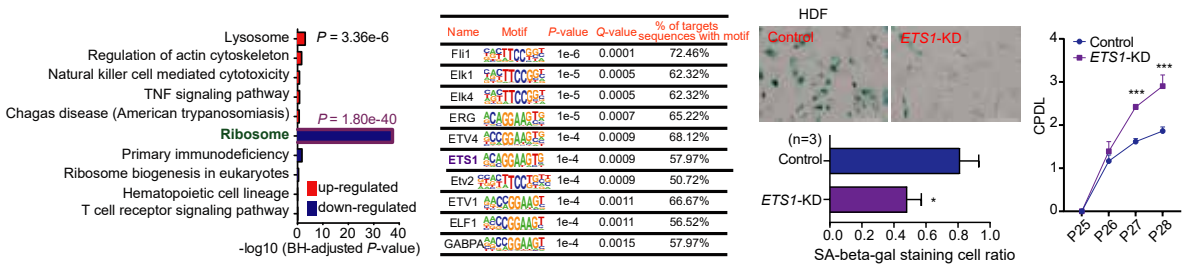
ETS1 Acts as a Regulator of Human Healthy Aging via Decreasing Ribosomal Activity

Xiao FH[1], Yu Q[1], Deng ZL[1], Yang K, Ye Y, **Ge MX**, Yan D, **Wang HT**, **Chen XQ, Yang LQ**, **Yang BY**, Lin R, Zhang W, **Yang XL, Dong L, He Y**, Zhou J, Cai WW[*], Li J[*], **Kong QP[*]**

Abstract

Adaptation to reduced energy production during aging is a fundamental issue for maintaining healthspan or prolonging life span. Currently, however, the underlying mechanism in long-lived people remains poorly understood. Here, we analyzed transcriptomes of 185 long-lived individuals (LLIs) and 86 spouses of their children from two independent Chinese longevity cohorts and found that the ribosome pathway was significantly down-regulated in LLIs. We found that the down-regulation is likely controlled by ETS1 (ETS proto-oncogene 1), a transcription factor down-regulated in LLIs and positively coexpressed with most ribosomal protein genes (RPGs). Functional assays showed that ETS1 can bind to RPG promoters, while ETS1 knockdown reduces RPG expression and alleviates cellular senescence in human dermal fibroblast (HDF) and embryonic lung fibroblast (IMR-90) cells. As protein synthesis/turnover in ribosomes is an energy-intensive cellular process, the decline in ribosomal biogenesis governed by ETS1 in certain female LLIs may serve as an alternative mechanism to achieve energy-saving and healthy aging.

Science Advances, 2022, 8(17): eabf2017



长寿人群转录组揭示 ETS1 调控的核糖体功能降低是人类健康老化的新型机制

中国人口老龄化程度自 2000 年以来持续加剧，推进健康老龄化战略关乎国家经济发展和民生福祉。长寿老人，寿命长且无重大老年疾病，正是人类健康老化的典范。因此，以健康长寿人群为研究对象，解析其健康老化分子机制，相关研究成果有较大潜力应用于老年健康干预，为我国实现“健康老龄化”提供新的路径和策略。

孔庆鹏研究团队联合中南大学湘雅医院李吉教授团队及海南医学院蔡望伟教授团队，新获得并分析海南省陵水县和临高县长寿人群 271 例（185 例长寿老人，86 例老年对照）外周血白细胞转录组数据（RNA-seq）。信息学分析发现，长寿老人自噬 - 溶酶体通路基因显著高表达，这与团队早期基于海南省澄迈、万宁地区长寿人群的研究结果一致（*Genome Research*, 2018）。有趣的是，研究人员于两批长寿人群中均发现一新的且极其显著的信号，即核糖体通路基因显著低表达（陵水：P=1.80e-40；临高：P=2.77e-52）；进一步分析发现，长寿老人核糖体编码基因低表达的转录调控因子很可能是 ETS Proto-Oncogene 1（*ETS1*）。进而，研究人员利用人真皮成纤维细胞（HDF）和 IMR-90 等复制衰老细胞模型进行功能验证，发现敲降 ETS1 可降低核糖体编码基因表达，并延缓细胞衰老。因此，该研究表明，降低核糖体参与的蛋白质翻译功能对延缓衰老 / 健康老化具有重要作用，转录调控因子 *ETS1* 参与该过程调控。

该研究成果发表于 ***Science Advances***。

研究方向三：遗传发育与进化

代表性成果三

发现 AMPA 受体泛素化在兴奋性突触功能调控中的新机制

RNF220 is an E3 Ubiquitin Ligase for AMPA Receptors to Regulate Synaptic Transmission

Ma P[1], Wan LP[1], Li Y[1], He CH[1], Song NN, **Zhao S, Wang H,** Ding YQ[*], **Mao BY[*], Sheng NY[*]**

Abstract

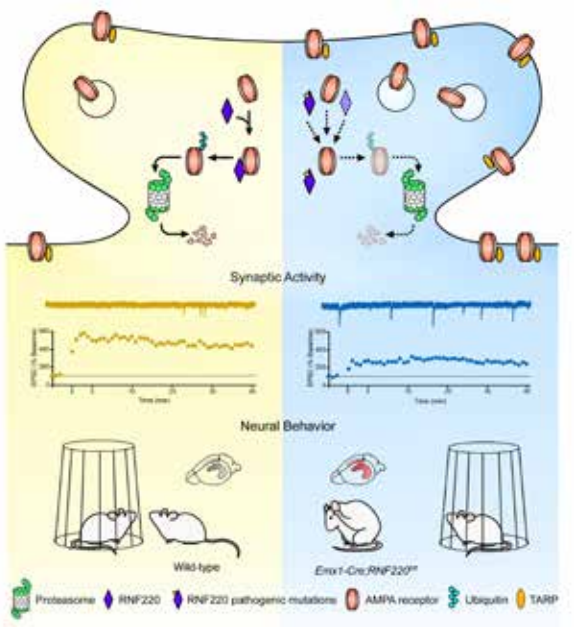
The accurate expression of postsynaptic AMPA receptors (AMPARs) is critical for information processing in the brain, and ubiquitination is a key regulator for this biological process. However, the roles of E3 ubiquitin ligases in the regulation of AMPARs are poorly understood. Here, we find that RNF220 directly interacts with AMPARs to meditate their polyubiquitination, and RNF220 knockout specifically increases AMPAR protein levels, thereby enhancing basal synaptic activity while impairing synaptic plasticity. Moreover, depending on its E3 ubiquitin ligase activity, RNF220 represses AMPAR-mediated excitatory synaptic responses and their neuronal surface expression. Furthermore, learning and memory are altered in forebrain RNF220-deficient mice. In addition, two neuropathology-related RNF220 variants fail to repress excitatory synaptic activity because of the incapability to regulate AMPAR ubiquitination due to their attenuated interaction. Together, we identify RNF220 as an E3 ubiquitin ligase for AMPARs and establish its substantial role in excitatory synaptic transmission and brain function.

Science Advances, 2022, 8(39): eabq4736

泛素化 - 溶酶体降解系统介导的突触分子蛋白稳定性在突触功能调控中发挥重要作用，其 E3 泛素连接酶 RNF220 突变导致的该调控紊乱被认为是神经精神疾病的重要发病因素。但对于 RNF220 在成熟神经元中的泛素化底物和生物学功能仍一无所知，特别是该分子调控是否参与突触调控及大脑生理功能和病理过程。

盛能印研究团队、毛炳宇研究研究团队与复旦大学的丁玉强教授课题组通力合作，揭示了 RNF220 在突触传递活性调控中的功能和分子机制。携带 RNF220 突变的病人会表现出智力障碍等症状，利用前脑敲除小鼠动物模型，他们发现 RNF220 是兴奋性突触关键分子 AMPA 受体的特异性 E3 泛素连接酶，通过调控 AMPA 受体的蛋白稳定性和突触转运，参与调控突触传递活性和可塑性 LTP 的产生。RNF220 前脑缺失会造成小鼠多种神经行为活动异常，包括认知能力、空间学习和社交记忆。RNF220 分子的神经疾病相关突变则导致其调控 AMPAR 泛素化和降解能力下降，从而影响其调控兴奋性突触活性的能力。该研究阐明了 AMPA 受体蛋白稳定性调控在突触活性和大脑生理功能调控中的作用机制，有助于进一步深入研究突触分子蛋白稳定性调控在大脑生理和病理过程中的作用机理。

该研究成果发表于 ***Science Advances***。



RNF220 作为新型 AMPA 受体泛素化连接酶调控突触活性和神经行为示意图

Science Advances

研究方向三： 遗传发育与进化

代表性成果四

阐明多能干细胞基因组稳态维持新机理

Lnc956-TRIM28-HSP90B1 Complex on Replication Forks Promotes CMG Helicase Retention to Ensure Stem Cell Genomic Stability and Embryogenesis

Zhang W[1], **Tang M**[1], **Wang L**, Zhou H, Gao J, Chen Z, Zhao B[*], **Zheng P**[*]

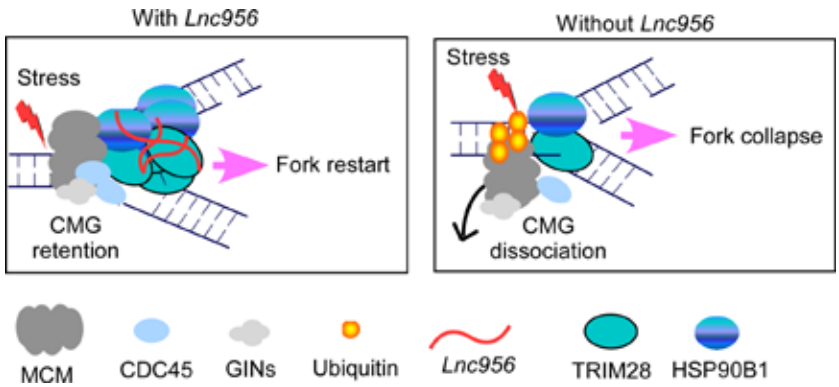
Abstract

Replication stress is a major source of endogenous DNA damage. Despite the identification of numerous proteins on replication forks to modulate fork or replication machinery activities, it remains unexplored whether noncoding RNAs can localize on stalled forks and play critical regulatory roles. Here, we identify an uncharacterized long noncoding RNA NONMMUT028956 (Lnc956 for short) predominantly expressed in mouse embryonic stem cells. Lnc956 is accumulated on replication forks to prevent fork collapse and preserve genomic stability and is essential for mouse embryogenesis. Mechanistically, it drives assembly of the Lnc956-TRIM28-HSP90B1 complex on stalled forks in an interdependent manner downstream of ataxia telangiectasia and Rad3-related (ATR) signaling. Lnc956-TRIM28-HSP90B1 complex physically associates with minichromosome maintenance proteins 2 (MCM2) to minichromosome maintenance proteins 7 (MCM7) hexamer via TRIM28 and directly regulates the CDC45-MCM-GINS (CMG) helicase retention on chromatin. The regulation of Lnc956-TRIM28-HSP90B1 on CMG retention is mediated by HSP90B1's chaperoning function. These findings reveal a player that actively regulates replisome retention to prevent fork collapse.

Science Advances, 2022, doi: 0.1126/sciadv.adf6277

多能干细胞（Pluripotent stem cells, PSCs）因其在体外具有无限增殖和分化为不同类型细胞的潜能，在再生医学领域中具有广泛应用前景，也成为目前临床上最具潜能的成药细胞。但人 PSCs 在体外扩增培养过程中，易出现遗传和表观遗传的变异，严重阻碍了 PSCs 的临床应用。因此研究 PSCs 遗传物质稳定性维持机理，是寻找改善策略、突破应用瓶颈的关键。

长非编码 RNA 在多种生物学功能中起重要作用。由于技术手段的限制，目前还没有发现复制叉上具有功能性长非编码 RNA 的报道。郑萍研究团队利用前期研发的一个新技术 - 分离新生 DNA 链上 (即复制叉)RNA 技术首次鉴定了 ESCs 复制叉上特异的新的功能性 LncRNA-*Lnc956*。对该 LncRNA 的研究发现，当复制压力发生时，Lnc956 能有效聚集到复制叉上，并大量招募 Trim28 和 Hsp90b1 聚集于复制叉形成复合体。Trim28 能直接与 DNA 复制解旋酶复合体 MCM2-7 相互作用，直接拉近了 Lnc956-Trim28-Hsp90b1 复合体与 MCM2-7 复合体之间的物理距离，使得分子伴侣 Hsp90b1 通过其 GTP 水解活性作用于 MCM7，阻碍 MCM7 进行 K48 和 K63 泛素化，从而使得复制小体能在一定程度复制压力情况下得以稳定，保持了基因组的完整性。他们也发现 Lnc956 缺失会导致小鼠胚胎部分致死，致死原因主要是胚胎细胞大量扩增过程中，细胞出现明显基因组不稳定现象，并导致胞质 DNA 水平显著增加，引起较严重的炎症反应。总之，该研究结果首次发现了小鼠多能干细胞复制叉上特异性功能性长非编码 RNA-*Lnc956*，并揭示了 Lnc956 维持多能干细胞基因组稳定和促进胚胎发育的分子机制。



Lnc956 维持复制叉稳定促进多能干细胞基因组稳定的分子机制

该研究成果发表于 ***Science Advances***。

系统进化与生物地理学研究

杨君兴，博士，研究员，博士生导师。现任农业部濒危水生野生动植物物种科学委员会委员、世界自然保护联盟（IUCN/WI）淡水鱼类专家组（FFSG）中国区主席、中国动物学会第十八届理事会理事、云南省水产学会顾问、第五届云南省省级自然保护区评审委员会委员、云南省中青年学术和技术带头人、蓝色粮仓科技创新咨询专家等。研究方向包括：生物多样性的考察监测及评价、系统分类、系统发育与生物地理学；珍稀特有物种的生态学研究和保育；湿地生态系统的恢复研究。至今已主持项目 40 余项。2022 年获得水产新品种 1 个，发表 SCI 论文 2 篇，国家授权专利 4 项，国外发明专利 1 项，新申请专利 8 项。获云南省科学技术奖 1 项（三等奖）。

重要成果及产出：

1. Yang SY[1],Leng SH[1], Li YK,**Wang XA, Zhang YW,Wu AL,**Gao YF,Wu JY,Zeng XY,Du XG,**Pan XF*.**Identification and functional characteristics of two TLR5 subtypes in *S. grahami.2022.* ***Fish and Shellfish Immunology.*** 131:707-717. IF 4.622
2. Min R, Zhao YH, Shi JS ,**Yang JX*.**A new species of Homatula (Teleostei, Cobitoidea, Nemacheilidae) from the Pearl River drainage, Yunnan, China.2022. ***ZooKeys.***1089:109-124. IF 1.492
3. **Yin YH[1], Zhang YW[1],** Hua ZX, **Wu AL, Pan XF, Yang JX*, Wang XA*.**Muscle transcriptome analysis provides new insights into the growth gap between fast_x0002_and slow-growing *Sinocyclocheilus grahami.2022.****Aquaculture Reports.*** (submitted) IF3.385
4. **潘晓赋，王晓爱，杨君兴，张源伟等．水产新品种 —— 软鳍新光唇鱼“墨龙 1 号”．品种登记号：GS-01-004-2022.**
5. **张源伟，王晓爱，潘晓赋，杨君兴**．一种滇池金线鲃和鲫鱼杂交方法．专利号：ZL 2021 1 0154107.1
6. **潘晓赋，王晓爱，张源伟，杨君兴，范伟，王云峰**．一种软鳍新光唇鱼人工繁殖方法．专利号：ZL 2020 1 1411971.2
7. **王晓爱，张源伟，潘晓赋，杨君兴，**卢泊霖．一种犀角金线鲃人工繁殖方法．专利号：ZL 2020 1 1410487.2.
8. **张源伟，王晓爱，潘晓赋，杨君兴**．一种滇池金线鲃和鲤鱼杂交方法．专利号：ZL 2020 1 1410270.1.
9. **Yuanwei Zhang, Xiaoai Wang, Xiaofu Pan, Junxing.** HYBRIDIZATION METHOD OF SINOCYCLOCHEILUS GRAHAMI AND CARP. Application Number:17204302
10. **张源伟，王晓爱，杨君兴，潘晓赋，吴安丽**．一种滇池金线鲃和犀角金线鲃杂交方法．专利受理号：202211532602.2
11. **王晓爱，张源伟，杨君兴，潘晓赋，吴安丽**．一种软鳍新光唇鱼和中国结鱼杂交方法．专利受理号：202211531854.3
12. **潘晓赋，王晓爱，杨君兴，张源伟，邓涛**．一种软鳍新光唇鱼和保山新光唇鱼的杂交方法．专利受理号：202211532621.5
13. **潘晓赋**，艾祖军，范伟，刘兴，王云峰，程乐，**杨君兴**．云南省科学技术奖，三等奖，暗色唇鱼人工繁殖与产业推广，2022.05.17.

1. 国审水产新品种 —— 软鳍新光唇鱼“墨龙 1 号”

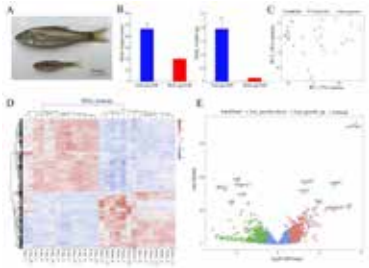
软鳍新光唇鱼是云南元江流域特有珍稀名贵大型鱼类，野生最大个体可达 20 公斤，且外观绚丽、耐力强，具有高端食用、高端观赏、高端垂钓等多重价值，市场需求大，但缺乏软鳍新光唇鱼良种。团队自 2007 年开始，先后开展了软鳍新光唇鱼野外引种、人工驯养、人工繁殖、苗种培育、疾病防治等一系列研究，构建了软鳍新光唇鱼“保 - 育 - 繁”技术体系。并以此为基础，以生长和肌间刺为主要选育指标，采用群体选育，经连续 4 代，成功培育出生长快、肌间刺弱化、抗病力强的水产新品种 —“墨龙 1 号”。在相同养殖条件下，与未经选育的软鳍新光唇鱼相比，“墨龙 1 号”体重平均提高 30.27%，肌间刺弱化 16.4%，适宜在我国南部及东南亚等水温 8-26℃ 人工可控的淡水水体中养殖。品种登记号：GS-01-004-2022。

【潘晓赋等 . 2022 国家农业农村部】

2. 滇池金线鲃生长相关候选基因识别

滇池金线鲃位列“云南四大名鱼”之首，因其肉质鲜美而著称，是滇池流域特有经济鱼类。但其生长缓慢，且个体间生长差异较大，严重制约了其水产养殖业的发展。因此，我们对生长快速（n=14）和生长缓慢（n=14）群体开展肌肉转录组学研究，发现能量物质的摄取可能是影响生长的根本原因，而胶原蛋白的合成差异可能是个体间生长差异的直接原因。同时，我们也发现一些调节食欲（如 *adipoq*）和胶原蛋白合成的基因（如 *col1a1*、*col1a2*、*col5a1*、*col6a2*、*col10a1*、*col26a1*）可能是滇池金线鲃生长的关键基因，值得后续更加深入的研究。本研究结果为指导滇池金线鲃的育种提供了重要的理论依据。

【**Yin YH** et al. 2022 ***Aquaculture Reports,*** (submitted) IF= 3.385】



3. 云南珍稀特有鱼类的人工繁殖、养殖推广和野外种群复壮

目前，保存土著鱼类活体 102 种，60 余万尾，无重大鱼病出现。单位养殖水体的养殖密度逐年提高。对西畴、曲靖、宜良等养殖基地定期进行技术指导。

2022 年度累计生产土著鱼类 500 余万尾，在滇池、牛栏江流域、李仙江流域放流滇池金线鲃 20 万余尾，短须裂腹鱼 20 万尾，昆明裂腹鱼 10 万尾，云南光唇鱼 10 万尾，软鳍新光唇鱼 20 万尾。

Phylogenetics and Biogeography

Dr. Junxing Yang, Professor. Current agriculture endangered aquatic wildlife species science committee, the world conservation union (IUCN/WI) freshwater fish expert group (FFSG), chairman of China, China institute of zoology, the 18th session of board of directors, yunnan province, aquatic consultant in yunnan province, the fifth in yunnan province, yunnan provincial nature reserve review committee members Provincial young and middle-aged academic and technical leaders, blue Granary science and technology innovation consulting experts, etc. The research team is mainly interested in biodiversity monitoring survey and evaluation, fauna taxonomic, phylogenetic and biogeographic; ecology and conservation research to rare and native species; especially focuses on the restoration of wetland ecosystem and application. So far, presided over more than 40 projects, in 2022,1 new aquatic product was obtained, 2 SCI papers were published, 4 national authorized patents, 1 foreign invention patent and 8 new patents were applied. Yunnan Province Science and Technology Award 1 (third prize).

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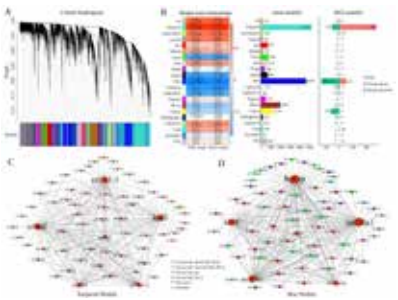
1. A new aquatic product -- Neolissochilus benasi “Molong No.1”

Neolissochilus benasi, a uniquely, rarely and preciously large fish in Yuanjiang basin on the Yunnan Province, which the maximum body weight is up to 20 kg for wild individuals. Further, it possesses huge value for edible, ornamental and angling due to its beautiful appearance and strong endurance. However, superior varieties are lack for breeding market. Therefore, we has successively carried out a series of studies for introduction, artificial domestication and propagation, seedling cultivation and disease prevention since 2007, and a technical system were constructed for “conservation-breeding-breeding” of *N. benasi*. Moreover, a new variety “Molong No.1” with accelerated growth rate (accelerated by 30.27%), weakened inter-muscular bones (weakened by 16.4%) and improved resistance to disease were selected based on four generation of artificial selection of the farmed populations, which suitable for breeding in the south of China and Southeast Asia, where the water temperature is 8-26 ℃. Variety registration number:GS-01-004-2022.

【**Pan XF et al**. 2022 Ministry of Agriculture and Rural Affairs of the People’s Republic of China】

2. Muscle transcriptome analysis provides new insights into the growth gap between fast- and slow-growing Sinocyclocheilus grahami

Sinocyclocheilus grahami, an economically valuable species known for its excellent quality , and possess huge breeding potential, especially in freshwater aquaculture. However, the new breed (“*S. grahami*, Bayou No. 1”, hereafter *S.grahami*) still faces some challenges, such as slow growth and large growth differences among individuals.Therefore,To promote the selective breeding of new breeds with a faster and more stable growing, in this study, we conducted muscle transcriptomic analysis in 14 fast and 14 slow-growth individuals to investigate the growth gaps among individuals and the mechanism underlying growth in *S.grahami*.Based on the gene expression profiles, the uptake of energy substances was considered as the root cause, while collagen synthesis was considered as the direct reason for the growth gap between fast- and slow-growth *S.grahami*. Furthermore, several genes regulate appetite, food intake (e.g., *adipoq*), and collagen synthesis (e.g., *col1a1*, *col1a2*, *col5a1*, *col6a2*, *col10a1*, *col26a1*) were identified as crucial genes for *S.grahami* growth. Our findings provide an important theoretical basis for guiding *S.grahami* breeding.



【**Yin YH** et al. 2022 ***Aquaculture Reports,*** IF= 3.385】

3. The artificial breeding, production and releasing in the wild of endangered fishes

In this year, we cultivated and produced more than 5 million fish fry of these fishes, including *Sinocyclocheilus grahami*, *Sinocyclocheilus tingi*, *Neolissochilus benasi*, *Schizothorax taliensis*, *Anabarilius liui chenghaiensis*, *Anabarilius grahami*, *Torqiaojiensis* and *Distoechodon macrophthalmus et al*. More than 0.8 million individuals were released in wild to rebuilt and restore the wild population of these fishes.

团队成员（Lab Member）

研究人员（Researchers）

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兽类生态与进化

蒋学龙，博士，研究员。立足于东喜马拉雅－横断山地区开展哺乳动物生态与进化研究，主要研究内容包括哺乳动物分类、系统演化与生物地理，灵长类动物行为生态，兽类资源考察、监测与保护，以揭示西南山地哺乳动物多样性形成及在特殊生态环境条件下的适应性进化与保护。近年来，主要以东喜马拉雅－横断山地区特有与常见小型哺乳动物、灵长类及地栖大中型兽类为研究对象，重点研究西南山地哺乳动物分布格局及其演化机制、西黑冠长臂猿行为生态及其适应性，并全面布局横断山区兽类资源监测网络与数据库建设，开展亚洲象生态学研究，为人象冲突防范与亚洲象保护提供科学对策。

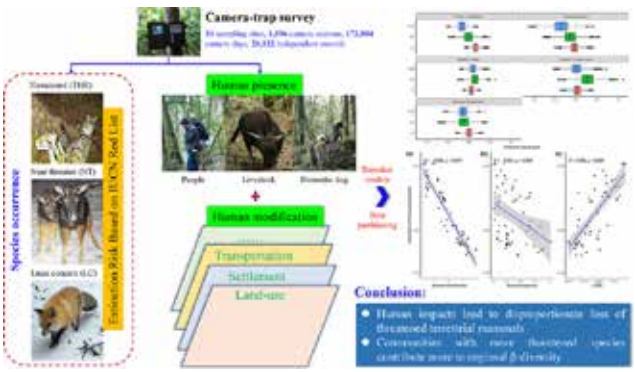
重要成果及产出：

1. **Li XY**#, **Hu WQ**, Bleisch WV, **Li Q**, **Wang HJ**, Ti B, Qin Z, Sun J, Zhang FY, **Jiang XL***. 2022. Disproportionate loss of threatened terrestrial mammals along anthropogenic disturbance gradients. ***Science of the Total Environment***, 850: 158038. IF10.240
2. Chen SD, Tang KY, Wang XM, Li FJ, Fu CK, Liu Y, Faiz A, **Jiang XL***, Liu SY*. 2022. Multi-locus phylogeny and species delimitations of the striped-back shrew group (Eulipotyphla, Soricidae): Implications for cryptic diversity, taxonomy and multiple speciation patterns. ***Molecular Phylogenetics and Evolution***, 177: 107619. IF5.019
3. Khanal L, Chalise MK, **Jiang XL***, Kyes RC. 2022. Mitochondrial genetic diversity and structure of the langur population in a complex landscape of the Nepal Himalaya. ***Diversity-Basel***, 14: 69. IF3.031
4. 宋文宇，**李学友**，**Onditi KO**，**蒋学龙**. 2022. 基于生态位理论研究群落构建的方法进展. ***兽类学报***，42(3): 312-324.
5. 魏辅文，杨奇森，吴毅，**蒋学龙**，刘少英. 2022.《中国兽类分类与分布》. 北京：科学出版社.

1. 人类活动加剧濒危兽类局域丧失

分析人类活动对不同受胁等级兽类物种多样性的影响，发现受胁物种集中分布在人类活动程度相对较低的区域，随着人类活动的增加，受胁物种比例急剧减少，在区域尺度验证了庇护所假说；相反，总的物种丰富度和常见物种丰富度及其比例均随人类活动的增加而增加，表明不同受胁等级兽类物种对人类活动的响应存在差异，总的物种丰富度并不能反映受胁物种的分布格局。研究还发现，群落中的受胁物种比例越高，该群落对β多样性的贡献越大，表明该类群落（样地）具有更高的保护价值。研究强调，仅以总的物种丰富度来评价、识别保护优先区难以保证濒危物种得到有效保护，在保护地空间优化及资源配置的过程中需要综合考虑物种丰富度、稀有度、受胁物种占比等多样性指标。

【Li XY et al. 2022 ***Science of the Total Environment,*** IF=10.240】



2. 参与编写《中国兽类分类与分布》

《中国兽类分类与分布》根据最新的形态学和分子遗传学证据，综合现代兽类分类学家意见，整理并收录了截至 2022 年 6 月在中国有确定分布记录的兽类 12 目 58 科 256 属 694 种。《中国兽类分类与分布》对每个物种的拉丁学名、中文名、英文名、曾用名、地方名、模式产地、同物异名及分类引证、亚种分化、国内外分布与重要的引证文献进行了详细的介绍，特别是对物种的原始定名文献及分类变更历史文献进行了详细考证，是对我国兽类物种分类和分布调查研究结果的系统性整理。

Mammal Ecology and Evolution

Prof. Xuelong Jiang, Professor, The laboratory is mainly interested in specimen-based investigations of biodiversity inventory, taxonomy and systematics, phylogenetics and phylogeography of small mammals with a special focus in the mountain region of southwest China, and also in mammal diversity distribution pattern and the driving forces, behavior ecology of western black crested gibbon, as well as conservation of rare species, such as Asian elephant and other large mammals.
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1. Multi-locus phylogeny and species delimitations of the striped-back shrew group (Eulipotyphla, Soricidae), Implications for cryptic diversity, taxonomy and multiple speciation patterns

Phylogenetic analyses of the concatenated mtDNA data revealed 14 sympatric and independently evolving lineages within the striped-back shrew group, including *Sorex bedfordiae*, *S. cylindricauda*, *S. excelsus*, *S. sinalis* and several cryptic species. All concatenated data (ten genes) showed a consistent genetic structure compared to the mtDNA lineages for the group, whereas the nuclear and the Y chromosome data showed a discordant genetic structure compared to the mtDNA lineages for the striped-back shrew group. Species delimitation analyses and deep genetic distance clearly support the species status of the 14 evolving lineages. The divergence time estimation suggested that the striped-back shrew group began to diversify from the middle Pleistocene (2.34 Ma), then flourished at approximately 2.14 Ma, followed by a series of rapid diversifications through the Pleistocene. Our results also revealed multiple mechanisms of speciation in the Mountains of Southwestern China and Adjacent Mountains with complex landscapes and climate. The uplifting of the Qinghai-Tibetan Plateau, Quaternary climate oscillations, riverine barriers, ecological elevation gradients, topographical diversity, and their own low dispersal capacity may have driven the speciation, genetic structure, and phylogeographic patterns of the striped-back shrew group.
【Chen SD et al. 2022 ***Molecular Phylogenetics and Evolution***, IF=5.019】

2. Mitochondrial Genetic Diversity and Structure of the Langur Population in a Complex Landscape of the Nepal Himalaya

This study assessed the population genetic structure of the Nepal Himalayan langurs (Semnopithecus spp.) across almost their entire distribution range in the complex landscape of the Nepal Himalaya using the mitochondrial cytochrome b (CYTB, 1140 bp), cytochrome c oxidase I (COI, 676 bp), and control region (1088 bp) sequences. Sequences were successfully retrieved from 52 samples belonging to 17 troops of wild Himalayan langurs in Nepal. The concatenated alignment of the three loci (2904 bp) defined 35 unique haplotypes with haplotype and nucleotide diversities of 0.961 ± 0.017 and 0.0204 ± 0.004, respectively. The results of a median joining haplotype network and of inter-haplotypic phylogenetic analyses revealed five major clades across the country: one from the eastern, two from the central, and two from the western region of Nepal. No haplotypes were shared among the regions. The Mantel test results indicated that the landscape heterogeneity of the Himalaya has shaped the population genetic structure of the Himalayan langurs due to the combined effects of isolation by resistance and isolation by distance phenomena. The strong population genetic structure and deep mtDNA divergence warrants a detailed taxonomic assessment of the Himalayan langurs across their entire range.
【Khanal L et al. 2022 ***Diversity-Basel***, IF=3.031】

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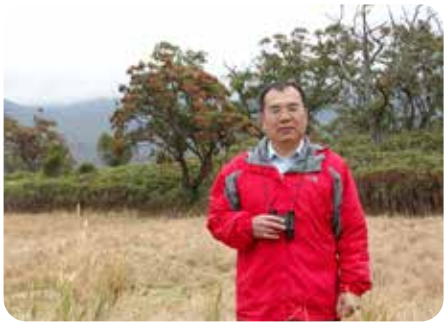
汪思远 Siyuan Wang	硕士生 2021 级
Sambaya Brian Anoto	硕士生 2021 级
朱中旭 Zhongxu Zhu	硕士生 2022 级
白 如 Ru Bai	硕士生 2022 级



鸟类学研究组

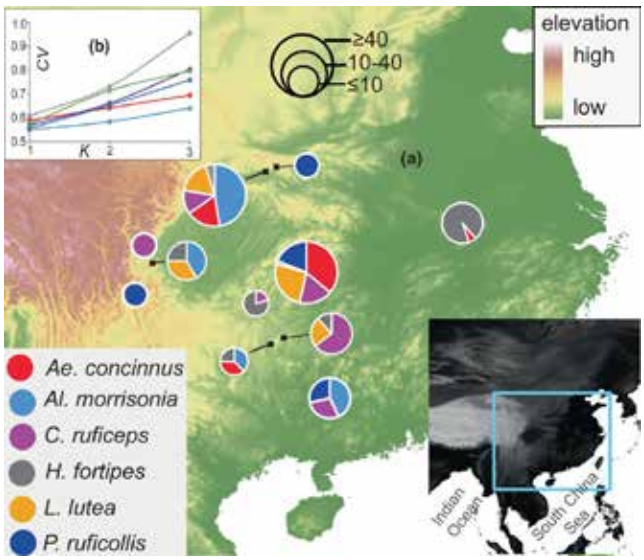
杨晓君，研究员，主要从事西南地区鸟类分类区系、系统演化、生物地理、群落生态学及珍惜鸟类的行为生态学和保护生物学研究。近年来更关注青藏高原旗舰物种 — 黑颈鹤的保护及鸟类系统演化研究。目前已出版执行主编和副主编专著 9 部，发表论文 100 余篇。

重要成果及产出：

1. Potential millennial-scale avian declines by humans in southern China. **Dong F**, Zhang Q, **Chen YL**, Lei MM, Li SH, **Wu F**, **Yang, XJ**. ***Global Change Biology***, 2022; 28: 5505-5.
2. 西藏墨脱厚嘴苇莺的分布新记录 [J]. **单鹏飞**，**岩道**，**高建云**，**吴飞**，**袁兴海**，**杨晓君**. 四川动物 . 2022, 5: 535.
3. 西藏墨脱地区 6 种鸟类种和亚种的新分布记录 [J]. **岩道**，**单鹏飞**，**吴飞**，**董锋**，**伍和启**，**高建云**，**杨晓君**. 动物学杂志 . 2022, 57(5): 766-774.

在中国南方，人类可能在千年尺度上导致鸟类数量减少

越来越多的观测记录表明，近几十年来人类造成的动物数量减少，而越来越多的考古证据表明，全新世期间人类活动对生物多样性产生了早期影响。一个基本的问题是，现代野生动物数量的下降是否始于早期人类的干扰。在这里，我们对东亚六种常见森林鸟类进行了种群基因组分析，以解决这个问题。对其中 5 个物种，基于每个物种 25-33 个基因组的人口历史推断显示，数千年来 (例如 2000-50 万年前)，种群数量急剧下降了 4-48 倍。然而，综合统计数据发现，这些种群规模轨迹与全新世温度变化之间的相关性不显著，生态位模型明确预测了全新世期间广泛的范围持续性，这意味着全新世气候变化对人口的影响有限。进一步的分析表明，重建种群数量下降与人类干扰强度之间存在高度负相关，并表明人类活动的潜在驱动因素。这些发现为最近认识到的鸟类物种减少提供了一个深入的时间和大规模的洞察，并支持了人类对生物多样性影响的早期起源假说。总的来说，我们的研究揭示了当前人类与环境长期相互作用背景下的生物多样性危机，并为定量评估人类干扰的生态后果提供了一个多证据。



抽样和总体结构的概要信息。(a) 中国南方抽样地形图。圆圈的颜色表示被研究的六种鸟类，包括 *Aegithalos coninnus* (*Ae. coninnus*)、morrisonia (*Al. morrisonia*)、ruficeps (*C. ruficeps*)、*Horornis fortipes* (*H. fortipes*)、*Leiothrix lutea* (*L. lutea*) 和 *Pomatorhinus ruficollis* (*P. ruficollis*)。圆圈的大小与样本大小成正比。地图上的颜色表示海拔高度，右上角的插图中显示了一个图例。右下方的插图显示了研究地点在东亚的位置，颜色越浅表示海拔越高。(b) 混合分析中交叉验证 (cv) 误差的散点图，K(假设的遗传簇数) 从 1 到 3。

Ornithology

Prof. Yang Xiaojun, Principle Investigator, Kunming Institute of Zoology, Chinese Academy of Sciences. My research interest lies at bird taxonomy and fauna, phylogeny, biogeography, community ecology, as well as behaviour ecology and conservation biology of endangered bird species. Till now, 8 books and more than 100 papers have been published.
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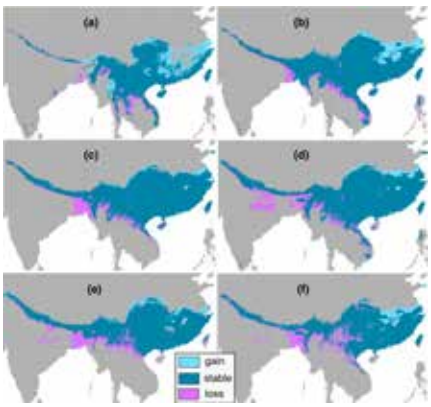
Potential millennial-scale avian declines by humans in southern China

Mounting observational records demonstrate human-caused faunal decline in recent decades, while accumulating archaeological evidence suggests an early biodiversity impact of human activities during the Holocene. A fundamental question arises concerning whether modern wildlife population declines began during early human disturbance. Here, we performed a population genomic analysis of six common forest birds in East Asia to address this question. For five of them, demographic history inference based on 25–33 genomes of each species revealed dramatic population declines by 4- to 48-fold over millennia (e.g. 2000–5000 thousand years ago). Nevertheless, summary statistics detected nonsignificant correlations between these population size trajectories and Holocene temperature variations, and ecological niche models explicitly predicted extensive range persistence during the Holocene, implying limited demographic consequence of Holocene climate change. Further analyses suggest high negative correlations between the reconstructed population declines and human disturbance intensities and indicate a potential driver of human activities. These findings provide a deep-time and large-cale insight into the recently recognized avifaunal decline and support an early origin hypothesis of human effects on biodiversity. Overall, our study sheds light on the current biodiversity crisis in the context of longterm human–environment interactions and offers a multi-evidential framework for quantitatively assessing the ecological consequences of human disturbance.



Species distributional changes in the potential suitable habitats from the mid-Holocene to the present day for the six studied birds. (a) Alcippe morrisonia, (b) Cyanoderma ruficeps, (c) Pomatorhinus ruficollis, (d) Aegithalos concinnus, (e) Leiothrix lutea and (f) Horornis fortipes. Species distribution models during the mid-Holocene were constructed under the CCSM4 model.

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生态学与环境保护中心

Douglas W. Yu, 博士，研究员。生态学与环境保护中心负责人，首批云南省高端人才项目引进人才。主要关注两个方面的研究内容：生物多样性快速评估方法和互利共生研究。目前已发表超过 100 篇论文于国际期刊 *Nature, Science, PNAS, PLoS Biology, Ecology Letters, Ecological Monographs, Ecology, American Naturalist, Evolution* 等上。

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重要成果及产出：

1. **Ji, Y.**[#], Baker, C.C.M.[#]*, Popescu, V.D., **Wang, J., Wu, C.**, Wang, Z., **Li, Y., Wang, L.**, Hua, C., Yang, Z., **Yang, C.**, Xu, C.C.Y., Diana, A., Wen, Q., Pierce, N.E.*, **Yu, D.W.***, 2022. Measuring protected-area effectiveness using vertebrate distributions from leech iDNA. ***Nature Communications***. 13: 1555. https://doi.org/10.1038/s41467-022-28778-8
2. **Li, Z.**[#], Linard, B., Vogler, A.P., **Yu, D.W.***, Wang, Z.[#], 2022. Phylogenetic diversity only weakly mitigates climate-change-driven biodiversity loss in insect communities. ***Molecular Ecology***. mec.16747. https://doi.org/10.1111/mec.16747
3. **Luo, M.**[#], **Ji, Y.,** Warton, D., **Yu, D.W.***, 2023. Extracting abundance information from DNA-based data. ***Molecular Ecology Resources***. 23: 174-189. https://doi.org/10.1111/1755-0998.13703

1. 利用蚂蝗 iDNA 来评估自然保护区的管理成效

生物多样性的灾难性丧失是目前全球面临的重大问题之一，而建立自然保护区是公认的保护生物多样性的最重要措施。如何判断这些保护区是否真正有效地保护了当地的生物多样性，成为了一个全球性的难题。为了解决这一难题，中国科学院昆明动物研究所 Douglas 课题组首次利用蚂蝗吸食的脊椎动物血液中的 DNA（iDNA，invertebrate-derived DNA）进行了一次大规模的尝试，对占地 677 平方公里的哀牢山国家级自然保护区进行了一个全局的脊椎动物多样性的调查。本研究证明了基于蚂蝗 iDNA 的高通量条形码技术可以实际应用于大规模、高空间分辨率的野生脊椎动物多样性评估调查。研究结果表明，哀牢山自然保护区（主要在其核心区域）为具有高保护价值的脊椎动物提供了保护空间。本研究为哀牢山自然保护区建立了基于 iDNA 的脊椎动物多样性基线，未来的 iDNA 调查可以基于这个基线检测各个物种分布的变化，作为评估自然保护区的效率指标。

图 1. 哀牢山地图、吸血蚂蝗和本研究检测到的部分保护动物

2. 从 DNA 数据中提取丰度信息

宏条形码、宏基因组学（metabarcoding, metagenomics）可以对食性分析和食物网络重建、物种相互作用的推断、种群动态和物种分布的建模、环境状态和变化的生物监测，以及假阳性和假阴性的推断做出有用的贡献。然而，采样和处理过程中多种来源的偏差和噪声结合在一起，为 DNA 数据集注入了错误。因此，本文展示了如何使用 “DNA 内标（DNA spike-in）” 来纠正实验流程产生的噪声并恢复物种内的多度信息。本文还提出了一种基于模型的估计方法，可用于没有实际 DNA 内标添加的数据集，以估计并纠正该实验及测序的干扰。

Ecology, Conservation & Environment Center(ECEC)

Dr. Douglas W. Yu. Yu's research covers two fields, (1) game-theoretical models of symbiosis, and (2) rapid biodiversity assessment using genomics. In the first area, we have developed new genomics methods for biodiversity rapid assessment. In the second, we have been elucidating the mechanisms stabilizing cooperation among species, using in fig-wasp and ant-plant mutualisms as experimental models. Yu has 100 publications, including in *Nature*, *Science*, *PNAS*, *PLoS Biology*, *Ecology Letters*, *Ecological Monographs*, *Ecology.*

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1. Measuring protected-area effectiveness using vertebrate distributions from leech iDNA

Protected areas are key to meeting biodiversity conservation goals, but direct measures of effectiveness have proven difficult to obtain. We address this challenge by using environ_x0002_mental DNA from leech-ingested bloodmeals to estimate spatially-resolved vertebrate occupancies across the 677 km2 Ailaoshan reserve in Yunnan, China. From 30,468 leeches collected by 163 park rangers across 172 patrol areas, we identify 86 vertebrate species, including amphibians, mammals, birds and squamates. Multi-species occupancy modelling shows that species richness increases with elevation and distance to reserve edge. Most large mammals (e.g. sambar, black bear, serow, tufted deer) follow this pattern; the excep_x0002_tions are the three domestic mammal species (cows, sheep, goats) and muntjak deer, which are more common at lower elevations. Vertebrate occupancies are a direct measure of conservation outcomes that can help guide protected-area management and improve the contributions that protected areas make towards global biodiversity goals. Here, we show the feasibility of using invertebrate-derived DNA to estimate spatially-resolved vertebrate occupancies across entire protected areas.

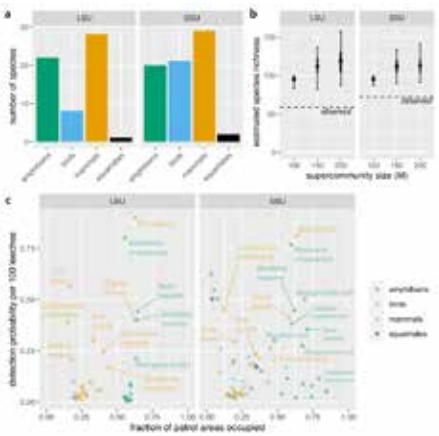

Figure 2. Species richness, occupancy and detection.

2. Extracting abundance information from DNA-based data

The accurate extraction of species-abundance information from DNA-based data (metabarcoding, metagenomics) could contribute usefully to diet analysis and food_x0002_web reconstruction, the inference of species interactions, the modelling of popula_x0002_tion dynamics and species distributions, the biomonitoring of environmental state and change, and the inference of false positives and negatives. However, multiple sources of bias and noise in sampling and processing combine to inject error into DNA-based data sets. we therefore demonstrate how to use a “DNA spike-in” to correct for pipeline noise and recover within-species abundance information. We also introduce a model based estimator that can be used on data sets without a physical spike-in to approximate and correct for pipeline noise.

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两栖爬行类多样性与进化

车　静，研究员，博士生导师。世界两栖爬行动物学大会执委；中国动物学会两栖爬行动物学分会副理事长；中华人民共和国濒危物种科学委员会委员；中国人与生物圈（MAB）国家委员会专家咨询委员会委员。2019 年度当选美国鱼类和两栖爬行动物联合学会（ASIH）终身外籍荣誉会员；入选国家高层次人才特殊支持计划科技创新领军人才（2019 年度）；获国家基金委杰出青年和优秀青年基金支持。

学科组长期立足中国及东南亚丰富的多样性资源，从宏观生物学问题出发，坚持多学科交叉，以整合的方法和进化的视角，瞄准两栖爬行动物多样性形成、演化、适应的前沿科学问题及濒危物种保护的重大需求开展工作。牵头出版专著 1 部《西藏两栖爬行动物 —— 多样性与进化》；作为通讯（第一）作者在 *Science*、*PNAS*、*Syst Biol*、*Nati Sci Rev* 等一系列国际学术期刊发表 136 篇 SCI 论文。

重要成果及产出：

1. **Fu TT**#, Sun YB#, **Gao W**#, Long CB, Yang CH, Yang XW, **Zhang Y**, Lan XQ, Huang S, **Jin JQ**, Murphy RW, **Zhang Y***, **Lai R***, Hillis DM*, **Zhang YP***, **Che J***. 2022. The highest-elevation frog provides insights into mechanisms and evolution of defenses against high UV radiation. *Proceedings of the National Academy of Sciences of the United States of Americ*.119(46): e2212406119.
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4. **Chai J**#, **Lu CQ**#, **Yi MR**#, Dai NH, Weng XD, Di MX, Peng Y, Tang Y, Shan QH, **Wang K**, Liu HZ, Zhao HP, **Jin JQ**, **Cao RJ**,Lu P, Luo LC, Murphy RW*, **Zhang YP***, **Che J***. 2022. Discovery of a wild, genetically pure Chinese giant salamander creates new conservation opportunities. *Zoology Research*. 43(3): 469-480.
5. **Gao W**#, **Yu CX**#, Zhou WW#, **Zhang BL**, Chambers EA, Dahn HA, **Jin JQ**, Murphy RW, **Zhang YP***, **Che J***. 2022. Species Persistence with hybridization in toad-headed lizards driven by divergent selection and low recombination. *Molecular Biology and Evolution*. 39(4): msac064.
6. **Wu YH**#, Chatmongkon Suwannapoom#, Poyarkov NA, **Gao W**, Karuno AP, Yuan ZY, **Che J***. 2022. First record of *Kurixalus odontotarsus* (Ye Et Fei, 1993) and *Raorchestes longchuanensis* (Yang Et Li, 1978) (Anura: Rhacophoridae) in Thailand. *Russian Journal of Herpetology*. 29(1): 1-18
7. ZY#, Wu DY#, Wen Y#, **Xu W**, **Gao W**, Dahn HA, Liu XL, **Jin JQ**, **Yu CX**, Xiao H*, **Che J***. 2022. Historical mitochondrial genome introgression confounds species delimitation: evidence from phylogenetic inference in the *Odorrana grahami* species complex. *Current Zoology*. Doi: 10.1093/cz/zoac010
8. **Wu YH**#, Chen JM#, Pawangkhanant P, Yothawut C, Karuno AP, Suwannapoom C*, **Che J***. 2022. Distribution extension of *Leptobrachella eos* (Ohler, Wollenberg, Grosjean, Hendrix, Vences, Ziegler & Dubois, 2011): first record from Thailand. *Herpetozoa*. 35: 25-32.

1. 生物多样性科学考察及监测研究顺利推进，发表系列新类群

围绕生物多样性保护、生态文明建设的国家战略需求，积极推进第二次青藏高原综合科学考察研究、高黎贡山生物多样性保护以及中科院 STS 区域重点等系列项目。2022 年度发表两栖、爬行动物新种共 2 个，国家新纪录种 4 个，省级新纪录种 2 个。

基于监测数据，报道在江西九岭山国家级自然保护区发现的大鲵野外种群。综合形态学和遗传分化证据，描述一新种 —— 江西大鲵 *Andrias jiangxiensis*。为期 18 个月的野外监测共记录包括成体、亚成体和新孵化幼鲵在内的 700 余尾个体，并连续两年观察到野外繁殖。这是我国首个遗传身份明确且野外稳定繁殖的大鲵纯种种群。也是中国首个可记录大鲵完整自然生活史的野外种群，为系统收集物种的基础生物学和栖息地生态学资料等提供了宝贵机会。

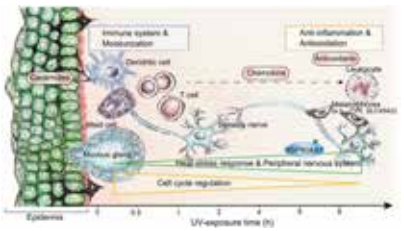
江西大鲵成体与共栖鱼类

该研究进展受到国内外媒体的广泛关注和报道。5 月 26 日，*Science* 杂志以 A new hope 为题，在 Research Highlight (Conservation) 撰文对该进展进行了介绍。英国 BBC 旗下 *Wildlife* 杂志将江西大鲵列入 “2022 年度已发现的 20 个新物种 ”（20 of the new species discovered so far this year）。

【Chai J et al. 2022 *Zool Res*, IF5-year= 4.811】

2. 解析高山倭蛙皮肤适应强紫外环境的分子机制

强紫外是高原主要的极端环境特点之一，不同于其它类群具有毛发、鳞片等覆盖，高原蛙类皮肤裸露，没有任何物理防护，其皮肤抵御高原强紫外辐射的机制一直不清楚。研究组以世界上海拔分布最高的蛙类 — 高山倭蛙（*Nanorana parkeri*）为研究对象，结合生理学、代谢组学、基因组学及转录组学以及生物化学等技术手段，对其皮肤适应高海拔强紫外环境的分子调控机制进行了研究，发现高山倭蛙皮肤面对紫外照射，具有更快速清除自由基的能力，免疫反应、炎症及抗氧化、热激反应、细胞周期调节等不同应答功能通路时空表达互作，协同完成紫外抵御，其中多个与紫外抵御相关基因在高山倭蛙中受到显著的正选择作用。该研究揭示了生物个体水平对于强紫外的抵御机制，也对人类皮肤方面的医学健康具有重要的参考和应用价值。

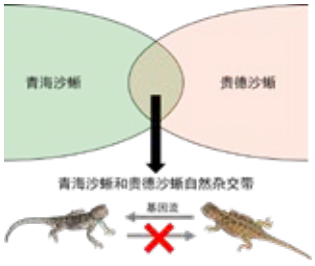


高山倭蛙皮肤抵御紫外辐射的分子调控网络

【Fu TT et al. 2022 *PNAS*, IF5-year= 13.451】

3. 揭示青藏高原沙蜥物种形成和维持的基因组学机制

物种形成是进化生物学中一个基础而又重要的问题，生殖隔离的建立和维持是物种形成过程中不同的阶段，目前大多数全基因组水平的研究关注在生殖隔离的建立方面，而对于生殖隔离维持的分子机制并不清楚。研究组对青海沙蜥（*P. vlangalii*）和贵德沙蜥（*P. putjatai*）在青藏高原存在的一个自然杂交带（接触区）体系开展群体基因组学研究，发现两物种的基因组高分化区中包含多个与生殖相关的基因，在接触区存在非随机的基因流，提示二者已经形成了一定的生殖隔离；而基因组高分化区的基因流则受到限制，且检测到明显的歧化选择信号，并显示出较低的重组水平，表明歧化选择和低重组在物种间生殖隔离的维持中发挥了重要作用。该研究为物种多样性形成和维持的基因组学机制研究开拓思路。



【Gao W et al. 2022 *Mol Biol Evol*, IF5-year= 20.074】

Herpetological Diversity and Evolution

Dr. Jing Che, Principal Investigator. Using amphibians and reptiles as model, we explore biodiversity and evolutionary questions within a phylogenetic framework. We are interested in how historical and ongoing processes have shaped the patterns of biodiversity of amphibians and reptiles that exist today, and how the species have adapted to and evolved.

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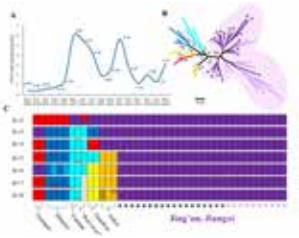
1. New progress in biodiversity research

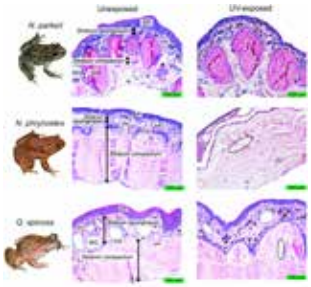
In 2022, a total of 2 new species of amphibians and reptiles, 6 new record species in China have been published. Following 18-month long field monitoring, we reported the discovery of a wild population of CGS in a closed nature reserve in Jiangxi Province, China. Genomic assessments reveal its genetic distinctiveness and do not detect genetic admixture with other species. Based on morphological and molecular evidences, we describe this CGS as a new species *Andrias jiangxiensis*. This is the only known species of CGS today with a genetically pure, reproducing, in situ population. This discovery emphasizes the important role that closed nature reserves play in protecting species, and the necessity of integrating long-term field monitoring and genetic assessments. It sets a new pathway for discovering and conserving endangered species, especially for those biotas that are similarly being extirpated by anthropogenic translocations and overexploitation.



Results of field-monitoring surveys and genetic distinctiveness of *A. jiangxiensis*

2. The highest-elevation frog provides insights into mechanisms and evolution of defenses against high UV radiation

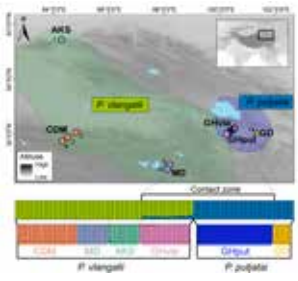
High-elevation species may face increased ultraviolet (UV) exposure as a consequence of climate change. By comparing the highest-elevation frog, *Nanorana parkeri*, with its low-elevation relatives, we showed higher UV tolerance in *N. parkeri* after a time course UV exposure. Combined a chromosome-level reference genome of *N. parkeri* with large-scale transcriptomic and microRNA (miRNA) profiling, we showed a temporal expression pattern of UV defense genes in *N. parkeri*. Moreover, multiple temporal-expressed genes also exhibit positive selection with function-enhancing substitutions in *N. parkeri*, such as *TYR*. This work provides a comprehensive genetic framework of UV defense, which will guide future study of skin cancer and evolution of defense.



Skin structures of the unexposed and the UV-exposed frogs.

3. Species persistence with hybridization in toad-headed lizards driven by divergent selection and low recombination

Speciation plays a central role in evolutionary studies, and particularly how reproductive isolation evolves. However, we know little about how species persist in face of gene flow. Here, we evaluate a contact zone of two closely related toad-headed lizards (*Phrynocephalus*) using population genomics. To some extent, recent asymmetric introgression from *P. putjatai* to *P. vlangalii* reduces their genomic differences. However, their highly divergent regions (HDRs) have heterogeneous distributions across the genomes. And many genes within HDRs are involved in reproduction and reproductive isolation. Compared to allopatric populations, contact areas exhibit recent divergent selection on the HDRs and a lower population recombination rate. Taken together, this implies that divergent selection and low genetic recombination help maintain reproductive isolation.



Geographic distribution and genetic structure of *P. vlangalii* and *P. putjatai.*

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分子进化与基因组多样性研究

张亚平，博士，研究员，中国科学院院士，发展中国家科学院院士，欧洲科学院院士。中国科学院副院长，遗传资源与进化国家重点实验室学术委员会主任，Hum Mol Genet 编委。近年来重点围绕家养动物复杂性状遗传的分子基础、遗传育种与新品种创制以及人社交障碍疾病的动物模型创建与应用开展研究工作。2022 年联合多家研究机构，组织开展合作研究了非洲野生猪科动物遗传资源挖掘，为家猪抗病育种提供关键理论依据和技术支撑。利用群体基因组学分析揭示中亚人群的混合历史。再议家鸡的早期驯化和扩散历史，填补了其缺失环节。在国际 SCI 刊物上发表了论文 16 篇，其中 IF>10 的 7 篇，包括 ***Mol Biol Evol*** (3)，***PANS***(3)，***Nat Sci Rev*** (1)。

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重要成果及产出：

1. **Xie HB[1], Yan C[1], Adeola AC[1],** Wang K[1], **Huang CP[1], Xu MM**, Qiu Q, Yin X, Fan CY, **Ma YF, Yin TT, Gao Y, Deng JK**, Okeyoyin AO, Oluwole OO, Omotosho O, Okoro VMO, Omitogun OG, Dawuda PM, Olaogun SC, Nneji LM, Ayoola AO, Sanke OJ, Luka PD, Okoth E, Lekolool I, Mijele D, Bishop RP, Han JL*, **Wang W*, Peng MS*, Zhang YP***. African suid genomes provide insights into the local adaptation to diverse African environments. *Molecular Biology and Evolution*, 2022, 39(12): msac256.
2. **Dai SS[1], Sulaiman X[1]**, Isakova J[1], Xu WF[1], Abdulloevich NT, Afanasevna ME, Ibrohimovich KB, Chen X, Yang WK, Wang MS, **Shen QK,** Yang XY, Yao YG, Aldashev AA, Saidov A, Chen W, Cheng LF*, **Peng MS*, Zhang YP***. The genetic echo of the Tarim mummies in modern Central Asians. *Molecular Biology and Evolution*, 2022: msac179.
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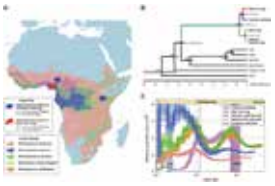
4. **Tao L**[1], Wang LG[1], **Adeola A.C.**, Zhang LC, **Li LW, Li QL, Cen DJ, Yan C, Ma ZS**, Wang LX*, **Xie HB*, Zhang YP***. Associations of autozygosity with economic important traits in a cross of Eurasian pigs. *Journal of Genetics and Genomics*, 2022.
5. **Wu YQ[1], Zhang YD[1], Liu H, Gao Y,** Liu YY, Chen L, **Liu L**, Iwrin DM, **Hou CH, Zhou ZY*, Zhang YP***. Genome-wide identification of functional enhancers and their potential roles in pig breeding. *Journal of Animal Science and Biotechnology*, 2022, 13(1): 75.
6. **Xu MM**[1], Gu LH[1], **Lv WY**[1], Duan SC, Li LW, Du Y, Lu LZ, Zeng T, Hou ZC, Ma ZS, Chen W, **Adeola AC**, Han JL, Xu TS*, Dong Y*, **Zhang YP*, Peng MS***. Chromosome-level genome assembly of the Muscovy duck provides insight into fatty liver susceptibility. *Genomics*, 2022, 114(6): 110518.

1. 非洲野生猪科动物遗传资源挖掘

非洲猪瘟（African Swine Fever，ASF）是由非洲猪瘟病毒（ASFV）感染引起的猪的一种急性、烈性、高度接触性传染病，非洲野生猪科动物是 ASFV 的天然宿主。运用三代长片段测序技术构建了普通疣猪和红河猪的高质量基因组，揭示了非洲猪科动物的基因组进化模式。发现非洲猪科共同祖先支上发生的结构变异和选择信号与 T 细胞免疫、病毒感染和淋巴组织发育相关。其中，体细胞重排后参与编码 T 细胞受体的 TRBV27 基因在非洲猪科动物中存在 284 bp 缺失，导致相关 T 细胞受体缺乏 CDR1 编码区，影响其 T 细胞受体对抗原呈递细胞的识别。本研究表明非洲猪科动物的基因组资源有助于筛选家猪受 ASFV 感染和致病的关键基因，为家猪抗病育种提供关键理论依据和技术支撑。

【Xie HB et al. 2022 ***Molecular Biology and Evolution,*** IF= 20.074】



2. 群体基因组学分析揭示中亚人群的混合历史

中亚位于欧亚大陆的交界处，一直是研究人类生物多样性与文化多样性的热点地区。在过去的二十年内，关于中亚民族人群的群体历史开展了大量研究。但是由于所采用遗传标记的限制以及缺乏周边古代人群的遗传学数据，难以剖析中亚人群真正的祖先。我们对中亚的塔吉克族和柯尔克孜族进行了高深度的测序，通过整合大量已发表的中亚及周边地区的古代人群和当代人群的基因组数据，我们发现，当代塔吉克族的祖先可以追溯到青铜时代的安德罗诺沃和中亚南部巴克特里亚 - 马尔吉纳亚文化人群。此外，高原塔吉克人群额外接收到来自小河人群 ANE 的基因流。而柯尔克孜族则是与历史时期的新疆人群保持了遗传上的连续性。并且柯尔克孜族和塔吉克族都受到近期东部游牧民族扩张的影响。我们的研究加深了我们对于中亚人群起源、迁徙以及混合历史的认识。

【Dai SS et al. 2022 ***Molecular Biology and Evolution,*** IF=20.074】

3. 再议家鸡的早期驯化和扩散历史

家鸡驯化一直是多学科关注的科学问题。近期 Peters 等人分析了大量考古学证据，提出家鸡最早驯化在泰国中部，时间距今约 3600 – 3200 年前，并随后快速扩散到世界各地。我们对相关证据和分析方法进行评估，发现在考古学资料整理、统计计算方法以及动物学野外调查方面存在问题，并补充了中国（特别是西南地区）的考古学资料，指出当前关于家鸡的早期驯化历史还存在明显的缺失环节。而与中国和东南亚地区的学者开展广泛深入的合作是填补缺失环节的关键途径。

【Peng MS et al. 2022 ***Proceedings of the National Academy of Sciences,*** IF= 13.451】

Molecular Evolution and Genome Diversity

Prof. YaPing Zhang, Academician of Chinese Academy of Sciences (CAS), The World Academy of Sciences, and Academia Europaea. He serves as Vice President of CAS and the editorial board of ***Hum Mol Genet.*** He focuses on the molecular basis of complex traits inheritance in domestic animals, genetic breeding and creation of new breeds, creation and application of animal models of human social disorders. In 2022, Prof. Zhang organized joint team to conduct series of evolutionary genomic research on domestic animals, including the excavation of African wild suid genetic resources, providing key theoretical basis and technical support for domestic pig disease resistance breeding. Further, his research team revealed the admixture history of Central Asian populations using population genomics analysis, and reconsideration of the early domestication and dispersal history of Chicken. Prof. Zhang's group has published 16 SCI-indexed papers, including ***Mol Biol Evol*** (3) , ***PANS***(3), ***Nat Sci Rev*** (1).

1. Adaptive evolution of the immune system in African wild suids

African swine fever is caused by the African swine fever virus (ASFV), and the African wild suids are the natural reservoirs of the ASFV. We have assembled the genomes of the common warthog and the red river hog, and analyzed the adaptive evolution of the African wild suids. We found that the common ancestor of the African wild suids have experienced adaptive evolution regarding the T-cell adaptive immunity. We identified a 284-bp deletion in *TRBV27* gene that results in a loss of CDR1 domain in relevant T cell receptors (TCRs), putatively impairing the recognition of antigen-presenting cells by the TCRs. This study is important to explore the key genes for the ASFV resistance and offer important variants for future pig breeding.

【Xie HB et al. 2022 ***Molecular Biology and Evolution***, IF= 20.074】

2. Population genomic analysis reveals admixture episodes in Central Asians

Central Asia, located at the crossroads of Eurasia, is a key area for studying human evolution. During the past two decades, massive genetic studies have been conducted to investigate the population history of Central Asian. Due to limited resolution of genetic markers and lacking of source panels of ancient populations, it is difficult to dissect the potential ancestries in the Central Asians. We conducted high-depth sequencing for 131 novel genomes from two Central Asian representative groups: Tajik and Kyrgyz. By integrating ancient DNA, we found that the major ancestry of present-day Tajik populations can be traced back to the admixture of the Bronze Age Bactria–Margiana Archaeological Complex and Andronovo related populations. Tajik from Pamirs further received additional gene flow from the Tarim mummies. The Kyrgyz showed the genetic continuity with the Historical Era populations in Xinjiang of China. Furthermore, the recent admixture signals detected in both Tajik and Kyrgyz are ascribed to the expansions of Eastern Steppe nomadic pastoralists during the Historical Era.

【Dai SS et al. 2022 ***Molecular Biology and Evolution***, IF=20.074】

3. Missing puzzle piece for the origins of domestic chickens

Chicken domestication is a milestone in human civilization. The most recent publication in PNAS entitled "The biocultural origins and dispersal of domestic chickens" by Peters presents direct evidence of the appearance of early domestic chickens in central Thailand, and then proposed the domestication and dispersal history for chicken was recent. Nevertheless, the archaeological sites in southwestern China, one candidate chicken domestication center inferred by various researches, were underrepresented. In addition, the discussion of linguistic and ecological link between chicken/red junglefowl and bamboo is misleading. Taken all above, we provide information of candidate sites with chicken remains and artifacts in southwestern China to highlight the possibility of earlier contacts humans and red junglefowls or chickens in this region than in Southeast Asia. And we also propose the wide international collaboration is necessary to unveil the early domestication and dispersal history for chicken.

【Peng MS et al. 2022 ***Proceedings of the National Academy of Sciences***, IF= 13.451】

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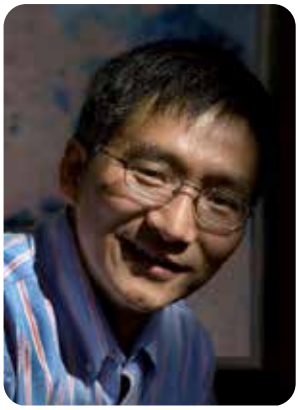
宋修成	Song XC	陈　星	Chen X
Lameck Ajuma Odongo			
Maina Susan Muthoni			



进化基因组学与基因起源

王　文，中国科学院昆明动物研究所，研究员、博士生导师，进化基因组学与基因起源学科组负责人。长期以来一直致力于进化基因组学的研究。目前已经在 *Science*、*Cell*、*Nature Biotechnology*、*Nature Communications*、*Nature ecology & evolution*、*Molecular plant* 等重要学术杂志上发表论文 240 余篇，2022 年在国际权威杂志上发表了论文 12 篇，其中 IF>10 的有 3 篇，包括 *Cell* (1)，*Science Bulletin* (1)，*Nature Communications* (1) 。 两项 973 项目首席科学家，国家基金委创新群体项目负责人，中科院战略性先导专项 (B) 两个首席科学家之一， 2012 年获得 “ 国家自然科学二等奖 ”(第一完成人)，2017 年获得两项 “ 云南省自然科学二等奖 ”(分别为第一完成人和第二完成人)，2019 年获得 “ 云南省自然科学奖一等奖 ”(第三完成人)，2021 年获得 “ 云南省技术发明一等奖 ”(第四完成人)。

实验室主页：http://internal.kiz.ac.cn/wangw2013/WenWang_Labweb/page0002.htm

重要成果及产出：

1. Tong X, Han MJ, Lu K, Tai S, Liang S, Liu Y, ... **Wang W***, Xiang ZH* & Dai F. 2022. High-resolution silkworm pan-genome provides genetic insights into artificial selection and ecological adaptation. ***Nat Commun***, 13(1): 1-15.
2. Wang ST, Teng DQ, **Li XY**, Yang PW, Da W, Zhang YM, Zhang YB, **Liu GC**, Zhang XS, **Wan WT**, **Dong ZW**, …**Wang W** & Zhang W. 2022. The evolution and diversification of oakleaf butterflies. ***Cell***, 185(17): 3138-3152.
3. Chen CY[1], Yin Y[1], Li HR[1], Zhou BT, Zhou J, Zhou XF, Li ZP, **Liu GC**, Pan XY, Zhang R, Lin ZS, Chen L*, Qiu Q*, Zhang YE*, **Wang W***. 2022. Ruminant-specific genes identified using high-quality genome data and their roles in rumen evolution. ***Sci Bull***, 67(8): 825-835.
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5. **He JW**[1], Zhang R[1], Yang J[1], **Chang Z**[1], Zhu LX[1], Lu SH#, Xie FA, Mao JL, **Dong ZW**, **Liu GC**, **Hu P**, Dong Y, **Wan WT**, **Zhao RP**, Xiong TZ, León-Cortés JL, **Mao CY**, Zhang W, Zhan S, **Li J**, Chen L*, **Wang W***, **Li XY***. 2022. High-quality reference genomes of tribe-level swallowtail butterflies provide insights into their coloration evolution. ***Zool Res***, 43(3): 367-379.
6. **Wan WT**, **Hu P**, **Chang Z**, Ren YD, **Dong ZW**, Yang J, Pan XY, **He JW**, Liu W, **Liu GC**, **Zhao RP**, **Mao CY**, **Li J**, **Wang W***, **Li XY***. 2022. Genome-wide survey of open chromatin regions in two swallowtail butterflies *Papilio machaon* and *P. bianor*. ***Arch Insect Biochem Physiol***, e21952.
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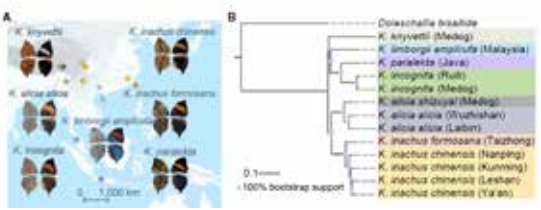
9. **Li J**, Zhou Z, **Mao CY**, Pan Z, Yao YH, **He JW**, Lin Y, **Dong ZW**, **Liu GC**, **Zhao RP**, **Wang W**, **Li XY***. 2022. Complete mitogenome and phylogenetic significance of *Metoecus javanus* (Pic, 1913) (Coleoptera: Ripiphoridae) from Southwest China, with notes on morphological traits of adult and immature stages. ***Zootaxa***, 5205(3): 231-248.

1. 昆虫复杂性状适应性进化的遗传基础

昆虫是地球上多样性最为丰富的动物群体，其复杂性状的适应性进化一直是生物学的一个重要研究内容。研究利用枯叶蛱蝶属 6 个物种以及蛱蝶科其他 20 个属共计 105 份蝴蝶样本，对枯叶蛱蝶属遗传多样性和物种多样性进行了全面分析，结果表明喜马拉雅山脉东部地区为该属蝴蝶的分化中心。同时我们进一步对 78 个枯叶蛱蝶中华亚种个体进行基因组重测序，并结合全基因组关联分析、基因表达、染色质相互作用分析和 CRISPR/Cas9 介导的基因组编辑，发现了一个已知的翅型调节因子 *cortex* 基因，它在控制叶翅形多态性中发挥着重要作用，可能是通过调节一个潜在的下游基因 *snake* 参与色素沉着和颜色转换。本研究表明保守的翅发育工具盒基因在蝴蝶翅表型适应性演化中的重要作用，进一步阐释了在保守的发育约束下产生表型多样性的可演化性。

另一项研究利用三代长读长技术解析了 11 种凤蝶的高质量参考基因组并构建了族级系统发育树。研究结果提示位于模式基因（决定蝴蝶翅膀上不同形态和色素类型鳞片的时空定位）和效应基因（决定鳞片内色素合成）上游调控区的凤蝶科特异的非编码保守元件和转录因子结合位点的进化，以及效应基因的快速进化，可能促进了凤蝶色素的起源与进化。这些结果不仅为了解颜色多样性的基因组基础尤其是凤蝶色素的起源提供了新见解，并为探索蝴蝶的进化、生态学和保护提供了重要的数据资源。

【Wang *et al*., 2022, ***Cell***; He *et al*., 2022, ***Zoological Research***】



2. 云南昆虫多样性研究

地球上到底有多少物种一直是世界最前沿的科学问题之一，而对西南山地生物多样性的本底调查与编目是中国和云南生物多样性保护的重要战略任务之一。目前云南昆虫物种多样性数据仍十分缺乏，亟待开展系统全面的云南昆虫多样性调查研究。研究以云南蝴蝶为例，通过对云南境内不同生境类型进行连续多年的野外调查和标本采集、对昆明动物所标本库馆藏蝴蝶标本的检视、以及对相关文献调研工作，完成了一个较为全面可靠的云南蝴蝶名录，共统计得到 6 科 356 属 1300 种，其中包括 2 个中国蝴蝶新纪录属 18 个中国新纪录种以及 36 个云南新纪录种。研究结果显示云南蝴蝶的属种数分别约占中国蝴蝶属种总数的 79.8% 和 58.6%，证明了云南拥有极高的蝴蝶多样性。该研究进一步完善云南蝴蝶的物种信息，为云南蝴蝶研究及多样性保护工作提供了重要的参考。

【Yu *et al*., 2022, ***Zoological Research***】

3. 家蚕高质量泛基因组解析及图谱绘制

家蚕是重要的经济昆虫和模式生物，也是支撑工业与科学研究的生物和遗传资源。为了能更加全面地反映家蚕的所有基因组信息，研究对 1078 份蚕种质资源进行了深度二代测序，并对 545 份代表性资源进行了三代测序，共鉴定出 7308 个新基因，4260 个核心基因和 3432266 个非冗余结构变异 (SVs)。本研究还绘制了世界首个家蚕泛基因组图谱，对深化家蚕功能基因组学研究及改良育种具有重要意义。

【Tong *et al*., 2022, ***Nature Communacations***】

Evolutionary Genomics and Origin of New Genes

Prof. Wen Wang, Professor, Head of Evolutionary Genomics and Origin of New Genes Research Group, KIZ, CAS. Prof. Wang has been focusing on evolutionary genomics. So far, he published more than 240 papers in such scientific journals as Science, Cell, Nature Biotechnology, Nature Communications etc., He is Chief Scientist of both 973 project (Scientific and technology Ministry) and Strategic Priority Research Program B (CAS), and also the leader of Innovative research group (NSFC). He received one second prize in China's National Natural Science Award in 2012, two second prize in Yunnan Natural Science Award in 2017, one first prize in Yunnan Natural Science Award in 2019, one first prize in Yunnan Technical Invention Award in 2021.
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1. Genomic basis of adaptive evolution of complex phenotypic traits in insects

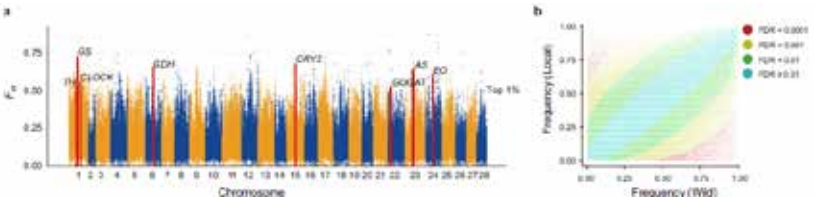
Insects are the most diverse group of animals on earth, and the adaptive evolution of their phenotypic traits is an important topic in biology. We traced the origin of the genus *Kallima* by sequencing the genomes of 105 butterflies from 21 nymphalid genera. The result indicate that the eastern Himalayas are a center of *Kallima* diversification. To dissect the genomic basis of leaf wing polymorphism, we focused on *K. inachu*s and performed genome-wide association studies (GWASs) by sequencing the genomes of 78 *K. inachus* butterflies with polymorphic phenotypes. A combination of evidence obtained from de novo genome assembly, gene expression, chromatin interaction analyses, and CRISPR-Cas9 genome editing led to the identification of a known wing pattern regulator, the *cortex* gene, that plays a major role in controlling leaf wing polymorphism, likely by regulating a potential downstream gene, *snake*, involved in butterfly pigmentation and color switching we show that leaf mimicry is maintained by balancing selection, possibly as a type of negative frequency-dependent selection, providing a rare and remarkable example with clear survival value supporting the role of long-term balancing selection in adaptive evolution.
The second study on high-quality reference genomes of swallowtail butterflies provides novel insights into the genomic basis of color diversity, especially papiliochrome origin in swallowtail butterflies. We obtained high-quality reference genomes of 11 swallowtail butterfly species covering all tribes of Papilioninae and Parnassiinae using long-read sequencing technology. Combine with previously published butterfly genomes, we obtained robust phylogenetic relationships among tribes, overcoming the challenges of incomplete lineage sorting (ILS) and gene flow. Comprehensive genomic analyses indicated that the evolution of Papilionidae-specific conserved non-exonic elements (PSCNEs) and transcription factor binding sites (TFBSs) of patterning and transporter/cofactor genes, together with the rapid evolution of transporters/cofactors, likely promoted the origin and evolution of papiliochromes. This study provide important data resources for exploring the evolution, ecology, and conservation of butterflies.
【Wang *et al*., 2022, ***Cell***; He *et al*., 2022, ***Zoological Research*** 】

2. Biodiversity of Yunnan's insects

Discovering how many insect species inhabit the Earth remains a fundamental quest of biology. Background survey and species catalogue of the mountains of Southwest China is still the most important challenge to China and Yunnan's biological protection. However, the insect species biodiversity is still overlooked in the present. A comprehensive and systematic investigation of insect diversity in Yunnan is necessary and urgent. We conducted a continuous survey of butterfly species and collected a large number of specimens from different habitats in Yunnan. We checked all collected butterfly specimens in the Kunming Institute of Zoology (KIZ) and in the private collection of Zhou Chang (CZC). We also retrieved and reviewed relevant literature and the Zoological Record database. In total, 356 genera and 1 300 species of butterflies were included in our Yunnan checklist, including 89 species endemic to Yunnan, two genera and 18 species newly recorded from China, and 36 species first recorded from Yunnan.
【 Yu *et al*., 2022, ***Zoological Research*** 】

3. High-resolution silkworm pan-genome analysis and mapping

Silkworm is an important economic insect and model organism as well as one of biological and genetic resource that supports key industrial and scientific research. In order to reflect the entire genomic information of silkworm, we deeply re-sequence 1,078 silkworms and assemble longread genomes for 545 representatives. We construct a high-resolution pangenome dataset representing almost the entire genomic content in the silkworm. We find that the silkworm population harbors a high density of genomic variants and identify 7308 new genes, 4260 (22%) core genes, and 3,432,266 non-redundant structure variations (SVs). We also provide the world's first super pan-genome map. This population-scale genomic resources will promote functional genomics studies and breeding improvement for silkworm.
【Tong *et al*., 2022, ***Nature Communacations*** 】



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比较基因组学

宿　兵，博士，研究员，中国科学院“百人计划”项目引进人才，国家自然科学基金杰出青年科学基金获得者，“新世纪百千万人才工程”国家级人选，国务院政府特殊津贴获得者，云南省有突出贡献优秀专业技术人才，中科院知识创新工程学科带头人，云南省万人计划“云岭学者”、“兴滇人才”与“科技领军人才”。2022 年度，本实验室围绕人类起源与适应性进化的遗传学机制研究等方向，在国际权威杂志上发表了 3 篇论文，包括基于古 DNA 研究揭示 1.4 万年前云南马鹿洞“蒙自人”的遗传演化特征（***Current Biology***）；利用分子进化学和功能基因组学手段发现藏族人群适应高原强紫外线的遗传机制（***PNAS***）；以及基于大规模表型分析发现高原新生儿出生体重的季节变化和性别差异（***Phenomics***）。

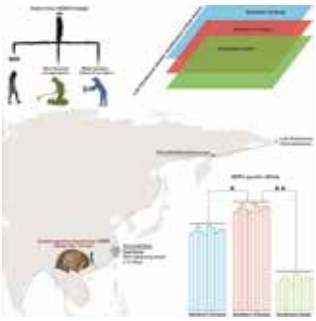
重要成果及产出：

1. Yang Z*, Cui C, Pu Y, Kong Q, Guo Y, Ouzhuluobu, Gengdeng, Liu X, Zhao Q, Qiu Z, Zheng W, He Y, Lin Y, Deng L, Zhang C, Xu S, Baimayangji, Cirenyangji, Bai C, Baimakangzhuo, Bianba, Pan Y, Xin J, Wang Y, Liu S, Wang L, Guo H, Feng Z, Wang S, Shi H, Jiang B, Wu T, Qi X*, **Su B***. Genetic adaptation of skin pigmentation in highland Tibetans. ***PNAS*** (2022) 119: e2200421119.
2. Zhang X, Ji X, Li C, Huang J, Wu Y, Ma S, He Y*, **Su B*.** Ancient genome of hominin cranium reveals diverse population lineages in southern East Asia during Late Paleolithic. ***Current Biology*** (2022) 32: 3095-3109.
3. He Y, Li J, Yue T, Zheng W, Guo Y, Zhang H, Chen L, Li C, Li H, Cui C, Ouzhuluobu*, Qi X*, **Su B***. Seasonality and sex-biased fluctuation of birth weight in highlanders. ***Phenomics*** (2022) 2: 64-71.

1、古 DNA 研究揭示 1.4 万年前云南马鹿洞“蒙自人”的遗传演化模式

云南从史前到现在都有极其复杂的生物多样性和人类文化多样性，包括禄丰古猿、元谋猿人，以及 1.4 万年前的“蒙自人”等多个古人类化石。为了揭示“蒙自人”的神秘面纱，中国科学院昆明动物研究所与多家单位合作对“蒙自人”开展了古 DNA 遗传学分析。古 DNA 证据表明，“蒙自人”是亚洲早期现代人的一位女性，而非古老型人类。“蒙自人”的线粒体遗传世系属于一种未知的 M9* 支系，反映了晚更新世东亚南部人群丰富的遗传多样性。作为晚更新世的“中国南方人”，“蒙自人”与最早的美洲原住民存在深度的古老祖源遗传联系。本研究表明，晚更新世不仅存在中国南北方人群的遗传分化，该时期中国南方人群与东南亚人群的遗传分歧程度更加明显。东亚大陆人群一些体质人类表型可能在约 7,500 年前就已经形成，这不仅反映了自然选择在最近一万年以来的全新世仍然在影响东亚地区人群的遗传结构和相应的体质表型，同时为中华文明探源工程提供了线索。

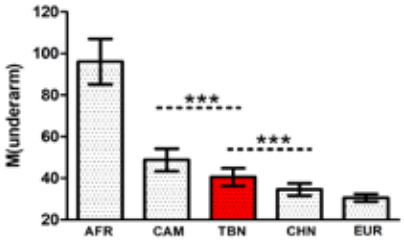
【Zhang XM et al. 2022 ***Current Biology***】



2、基因组学分析发现藏族人群适应高原强紫外线的遗传机制

东南亚分布许世居高原的藏族人群是研究人类如何适应极端环境的理想人群。然而，对高原紫外辐射这一重要的环境胁迫的适应性机床机制鲜有研究，关于强紫外刺激下的深肤色是否可以遗传及其适应的遗传机制仍然是未解之谜。通过对藏族群体全基因组数据的分析，研究人员发现了参与机体黑色素合成的基因 GNPAT 在藏族人群中存在很强的达尔文正选择信号。位于该基因上游的一个增强子调控元件发生了点突变（rs75356281），其衍生等位基因频率在藏族人群中达 58%，而在世界其他人群中的比例仅为 0-18%。综合遗传学和细胞生物学的实验证据，揭示了 GNPAT 基因在藏族人群中发生了适应性突变的富集，导致藏族人群黑色素合成能力的增强和肤色变深。

【Yang ZH et al. 2022 ***PNAS***】



Comparative Genomics

Prof. Bing Su, Principle Investigator. Director of academic committee of Kunming Institute of Zoology, Chinese Academy of Sciences, the leader of Comparative Genomics Lab of CAS. Prof. Bing Su focuses on primate comparative genomics and genetic mechanism of origin of human intelligence, and human population genetics. In 2022, Prof. Su's group conducted series of genomic researches on human evolution and adaptation, including sequenced the genome of a Late Pleistocene hominin (MZR) (***Current Biology***); revealed genetic adaptation of skin pigmentation in highland Tibetans (***PNAS***); and found the seasonality and sex-biased fluctuation of birth weight in Tibetan populations (***Phenomics***).
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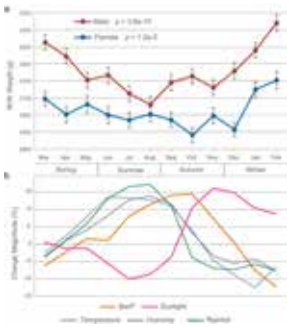
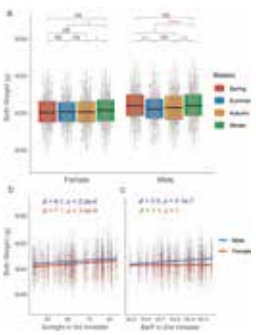
1. A Late Pleistocene human genome from Southwest China

Southern East Asia is the dispersal center regarding the prehistoric settlement and migrations of modern humans in Asia-Pacific regions. However, the settlement pattern and population structure of paleolithic humans in this region remain elusive, and ancient DNA can provide direct information. Here, we sequenced the genome of a Late Pleistocene hominin (MZR), dated ~14.0 thousand years ago from Red Deer Cave located in Southwest China, which was previously reported possessing mosaic features of modern and archaic hominins. MZR is the first Late Pleistocene genome from southern East Asia. Our results indicate that MZR is a modern human who represents an early diversified lineage in East Asia. The mtDNA of MZR belongs to an extinct basal lineage of the M9 haplogroup, reflecting a rich matrilineal diversity in southern East Asia during the Late Pleistocene. Combined with the published data, we detected clear genetic stratification in ancient southern populations of East/Southeast Asia and some degree of south-vs-north divergency during the Late Pleistocene, and MZR was identified as a southern East Asian who exhibits genetic continuity to present day populations. Markedly, MZR is linked deeply to the East Asian ancestry that contributed to First Americans.
(Zhang XM et al. 2022 ***Current Biology***)

2. Seasonality and Sex-biased Fluctuation of Birth Weight in Tibetans

Birth weight (BW) is a key determinant of infant mortality. Previous studies have reported seasonal fluctuation of BW. However, the responsible environmental factors remain disputable. High-altitude environment provides a great opportunity to test the current hypotheses due to its distinctive climate conditions. We collect BW data of ~9000 Tibetan singleton borns at Lhasa during 2014 to 2018. We observe a significant seasonal pattern of BW in Tibetans, with a peak in winter and a trough in summer. Notably, we see a marked sex-biased pattern of BW seasonality (more striking in males than in females). Sunlight exposure in the 3rd trimester and barometric pressure exposure in the 2nd trimester is significantly correlated with BW, and the latter can be explained by seasonal change of oxygen partial pressure. In particular, due to the male-biased BW seasonality, we find a more serious birth weight reduction and higher prevalence of low-BW in males, and a skewed sex ratio in highlanders. Infant BW of highland Tibetans have a clear pattern of seasonality. The winter BW is larger than the summer BW, due to the longer sunlight exposure during the late-trimester. Male infants are more sensitive to hypoxia than female infants during the 2nd trimester, leading to more BW reduction and higher mortality.
(He YX et al. 2022 ***Phenomics***)





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进化与功能基因组学

施　鹏，研究员，中科院昆明动物研究所党委书记、副所长，“遗传资源与进化国家重点实验室”主任，进化与功能基因组学研究室负责人。长期从事进化基因组学和功能基因组学研究。本研究室的研究兴趣集中在以下两个方向：（1）利用新一代测序技术，运用自然选择理论在基因组范围内探讨基因型和表型的关系，结合生物信息学和功能实验的方法来研究动物适应环境的分子机制；（2）通过对非模式生物的基因组研究，从新的视角理解人类长寿、心血管疾病和肿瘤的发病机理及新的疾病相关基因资源的挖掘。

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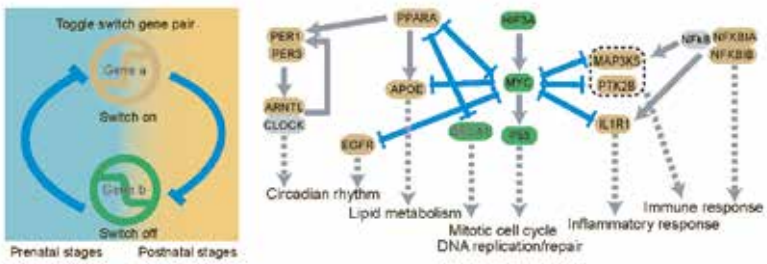
重要成果及产出：

1. **Hao JJ,** Hao WL, **Liu Z*, Shi P*.** The Toggle Switch Model for Gene Expression Change during the Prenatal-to-Postnatal Transition in Mammals. *Mol Biol Evol*. 2022, 39(3): msac036.
2. **Zheng ZZ[1], Hua R[1],** Xu GQ, **Yang H*, Shi P***. Gene losses may contribute to subterranean adaptations in naked mole-rat and blind mole-rat. *BMC Biology*. 2022, 20(1): 44.
3. **Zhang T, Lei ML, Zhou H,** Chen ZZ*, **Shi P*.** Phylogenetic relationships of the zokor genus *Eospalax* (Mammalia, Rodentia, Spalacidae) inferred from whole-genome analyses, with description of a new species endemic to Hengduan Mountains. *Zool Res*. 2022, 43(3): 331-342.
4. **Liu Z[1], Chen P[1], Xu DM[1], Qi FY[1], Guo YT, Liu Q, Bai J, Zhou X, Shi P*.** Molecular convergence and transgenic evidence suggest a single origin of laryngeal echolocation in bats. *iScience*. 2022, 25(4): 104114.
5. **Chen P[1], Hao JJ[1], Li MW, Bai J, Guo YT, Liu Z*, Shi P*.** Integrative functional transcriptomic analyses implicate shared molecular circuits in sensorineural hearing loss. *Front Cell Neurosci*. 2022, 16: 857344.
6. Tu Q[1], Liu XY[1], **Yao XQ[1]**, Li RX[1], Liu GJ[1], Jiang HL, LiKQ, Chen QF, Huang XY, Chang Q, Xu GQ*, Zhu H*, **Shi P***, Zhao B*. RETSAT associates with DDX39B to promote fork restarting and resistance to gemcitabine based chemotherapy in pancreatic ductal adenocarcinoma. *J Exp Clin Cancer Res*. 2022, 41(1): 274.
7. Hu YB[1], Wang XP[1], Xu YC[1], **Yang H[1]**, Tong ZY[1], Tian R[1], Xu SH[1], Yu L*, Guo Y L*, **Shi P*,** Huang SQ*, Yang G*, Shi SH*, Wei FW*. Molecular mechanisms of adaptive evolution in wild animals and plants. *Sci China Life Sci*, 2022.
8. Li JM[1], An ZF[1], Wei LN[1], Xu B[1], Wang ZJ, Gao CH, Wei L, Qi DL, **Shi P***, Zhang TZ*, Dengbang Wei*. A New Homotetramer Hemoglobin in the Pulmonary Surfactant of Plateau Zokors (*Myospalax Baileyi*). *Front Genet.* 2022, 13: 824049.
9. An ZF[1], Wei LN[1], Xu B[1], Wang ZJ, Gao CH, Li JM, Wei L, Qi DL, **Shi P***, Zhang TZ*, Wei DB*. A homotetrameric hemoglobin expressed in alveolar epithelial cells increases blood oxygenation in high-altitude plateau pika (*Ochotona curzoniae*). *Cell Rep*. 2022, 41(1): 111446.

1. 哺乳动物胎 - 幼转变中基因表达变化的开关模型

出生前到出生后的转变是生命周期中的一个关键过程，生物体在此过程中从对宫内信号的反应转变为适应宫外应激。我们通过构建计算共表达网络，分析了五个哺乳动物物种在发育时间点上的七个器官的转录组，并报告了围产期基因表达的发育转变。这些基因往往形成相互抑制的开关基因对来适应环境变化。该研究揭示了胎盘哺乳类胎 - 幼转换过程中保守的分子切换模式，为深入理解哺乳动物对出生前后巨大环境变化的适应变化奠定了基础。（Hao JJ et al., ***Mol Biol Evol***）

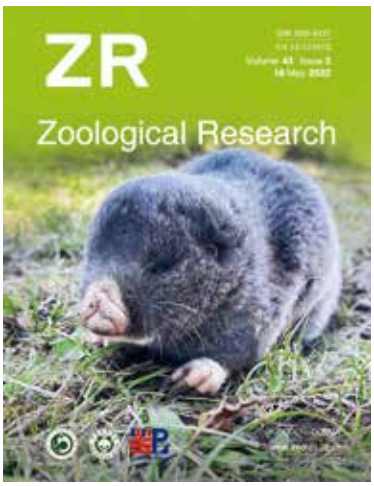


2. 假基因对裸鼹鼠和盲鼹鼠地下生活适应的贡献

假基因的作用一直是生物学研究中颇有争议的话题。运用比较基因组学分析手段，我们对裸鼹鼠和盲鼹鼠的假基因进行了系统研究，发现这两个物种中趋同发生了基因丢失事件，并且这些假基因多富集于与地下洞穴生活适应相关的通路中。以 *TRIM17* 基因为例，细胞功能实验提示该基因的丢失对低氧下神经细胞受到的损伤有保护作用。我们的研究提示，不同于传统观点，基因丢失事件可能对地下生活物种的适应具有积极贡献，在哺乳动物进化过程中可能发挥着重要作用。(Zheng ZZ et al., ***BMC Biology***)

3. 凸颅鮃鼠属的系统发育及分类学

为厘清凸颅鮃鼠属的分类学及系统学，课题组对该属物种进行了系统全面的采样及全基因组深度测序，构建了可靠且稳健的系统发育关系。基因组学、形态学及生物地理学证据表明凸颅鮃鼠属至少包含 7 个有效物种，且存在 2 个主要适应性进化方向。值得注意的是，本研究时隔一个世纪发现凸颅鮃鼠属新物种 - 木里鮃鼠。新物种在系统发育上处于较为基部的位置，且其在形态上保留更多的祖先性状，表明凸颅鮃鼠属可能起源于横断山脉地区。（Zhang T et al., ***Zool Res***）



Evolutionary and Functional Genomics

Prof. Peng Shi, Principal Investigator, has long been engaged to the researches on evolutionary and functional genomics. The work in Shi's laboratory covers two fields:

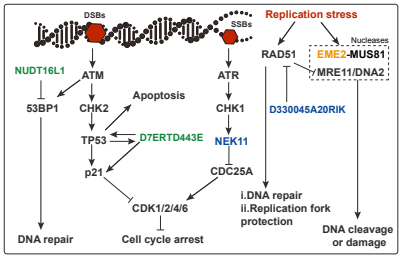
(1) molecular mechanism of adaptation to various environments in animals. We study the genotype-phenotype relationship at the genomic level under the guidance of natural selection theory, while combining multiple advanced techniques including NGS, bioinformatics and functional assays, etc.

(2) novel disease-related gene identification and the etiopathogenesis study. Through genomic analyses using non model organisms, we try to aid the comprehensive understanding of the etiopathogenesis in human longevity, cardiovascular diseases and tumors from a different angle.

1. The Toggle Switch Model for Gene Expression Change during the Prenatal-to-Postnatal Transition in Mammals

The prenatal-to-postnatal transition is a pivotal process in the life cycle whereby an organism shifts from responding to intrauterine cues to undergoing extrauterine stresses. We analyze the transcriptomes of seven organs across developmental time points from five mammalian species by constructing computational coexpression networks and report a developmental shift of gene expression at the perinatal stage. The genes around the perinatal stage tend to form the mutually inhibitory toggle switch gene pairs in response to the environmental changes. This study reveals conserved molecular switching patterns during prenatal-to-postnatal transition in placental mammals.Which provides a basis for further understanding of adaptive changes before and after birth.

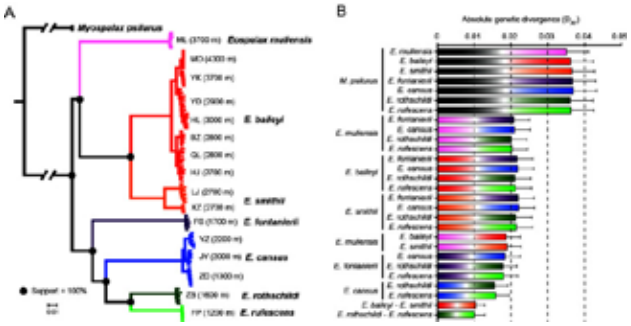
2. Gene losses may contribute to subterranean adaptations in naked mole-rat and blind mole-rat



It has been controversial that gene losses play an adaptive role in mammalian evolution. In this study, we performed systematic analyses on pseudogenes in naked mole-rat and blind mole-rat, taking advantage of the -omics development. We identified convergent gene loss events in these species, which enriched in functional groups of subterranean life style related pathways. Functional assay suggested a beneficial role of *TRIM17* loss in neuronal survival under hypoxia. Our study provides new insights into the molecular underpinnings of subterranean adaptations and highlights the importance of gene losses in mammalian evolution.

3. Phylogeny and taxonomy of genus *Eospalax*

To clarify the taxonomy and phylogeny of the genus *Eospalax*, we performed systematic and comprehensive sampling and whole-genome high-depth sequencing and constructed reliable and robust phylogeny of *Eospalax*. Genomic, morphological, and biogeographical evidence supports that *Eospalax* contains at least seven valid species and evolved to two main adaptive directions. Notably, after a century of quiescence, we discovered a new species, Muli zokor in *Eospalax*. This new species is located in the relatively basal phylogenetic position and possesses more supposedly plesiomorphic characters, suggesting a possible origin of *Eospalax* in the Hengduan Mountains.



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真核细胞进化基因组学

文建凡，博士，研究员，遗传资源与进化国家重点实验室副主任。研究方向为“真核细胞进化基因组学”。以处在真核生物进化的关键地位的单细胞生物（如贾第虫、衣藻、眼虫、领鞭毛虫等）为主要研究对象，向下追溯到原核生物，向上扩展到多细胞生物，开展真核细胞的结构和功能，特别是基因、基因家族、功能途径基因群和基因组的多样性形成与进化研究，以及从适应性进化角度开展有害生物（如寄生虫）防治靶标的发掘利用，有益生物（如藻类）的高效、特异代谢途径的进化形成机制及其应用的基础研究。

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重要成果及产出：

1. **Ye Q-Q**, **Lyu Z-X**, Guo X-L, **Xue M**, **Li Y-J**, **Deng Q**, **Bai H-X**, **Wen J-F***. A Multi perspective Systematic Analysis Uncovers the Riddle of *Giardia*'s Evolutionary Position. 2022. ***Systematic Biology***. (under review)
2. **Lyu Z-X, Shen J, Cheng J-N, Wen J-F***. The determinant role of the specific feces eating behaviour of hamsters in the speciation of *Giardia cricetidarum*. (submitted)
3. **Li Y-J, Deng Q, Bai H-X, Wen J-F***. Transport mechanisms of energy and reducing equivalent in *Chlamydomonas reinhardtii* chloroplast. (submitted)

1. 宿主的特异性食粪行为对仓鼠贾第虫的成种起了决定性作用

本研究组首次发现宿主食粪行为对其特有的肠道寄生虫贾第虫成种具有决定性贡献。某些动物为了适应环境不利条件和吸收粪便内多种必需营养而摄取粪便的行为统称为食粪行为。我们通过比较发现仓鼠的食粪行为与其它动物存在很大的不同，并发现一种专性寄生仓鼠的仓鼠贾第虫（*G. cricetidarum*），该种贾第虫在感染和流行方面存在一些独特的特点，如群体内“全有或全无”的感染状况、阳性带虫量极高、自愈现象和包囊壁薄（图 1）等。通过包括基因组、转录组和代谢组的多组学联合分析，揭示食粪行为对仓鼠贾第虫这些独特特点的形成起了决定性作用。一方面，由于食粪而使得该寄生虫的传播距离短、重复感染几率高，对包囊的保护作用、免疫逃避形成了选择压力的放松。具体表现在包囊壁蛋白成分的减少、包囊壁的变薄；起免疫逃避功能的 VSP 种类数量的大幅减少。另一方面，由于食粪而使得肠道内的营养成分的改变，如短链脂肪酸的大量存在，氨基酸成分的改变，使得该寄生虫能够进行由短链脂肪酸合成长链脂肪酸，不同于别的贾第虫而保留了相关的合成代谢途径，以及通过水平基因转移获得的某些氨基酸代谢途径（图 2）。该研究首次揭示了宿主的一种特殊行为竟然能对其特异寄生虫的物种形成起了决定性作用。

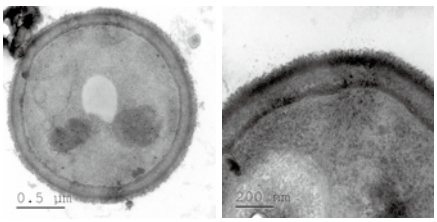

图 1. 仓鼠贾第虫包囊扫描电子显微镜照片

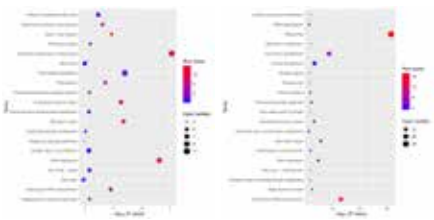

图 2. KEGG 富集的不同条件下仓鼠贾第虫的差异表达基因

2. 莱茵衣藻叶绿体能量和还原力的运输机制

单细胞绿藻莱茵衣藻细胞仅具有一个叶绿体，约占整个细胞体积的 40%。除了众所周知的卡尔文循环以外，衣藻中很多重要的生物合成反应（如淀粉、脂肪的合成）均发生在叶绿体中。因此，确保叶绿体中能量（ATP）和还原力（NAD(P)H）的供应和平衡对于衣藻的生长不可或缺。但能量和还原力进出叶绿体的具体运输机制一直不甚清楚。我们基于莱茵衣藻高质量的基因组数据，通过生物信息学分析，结合基因编辑和蛋白质的亚细胞定位等实验研究，发现衣藻叶绿体中的能量和还原力的运输（包括输入和输出）均有两种机制：其一是通过磷酸丙糖转运蛋白（TPT）将 G3P 和 3-PGA 运输进出叶绿体，从而完成 ATP 和 NAD(P)H 在细胞质和叶绿体之间的运输（图 1）；另外一种机制，则是由专门的运输途径分别负责 ATP 和 NAD(P)H 的运输（图 2）：ATP 的运输通过质体核苷酸转运蛋白（plastidic nucleotide transporter, NTT），而 NAD(P)H 的运输则依赖分别定位于叶绿体和细胞质的苹果酸酸脱氢酶介导的苹果酸穿梭的方式完成。从而，首次清晰地揭示出了莱茵衣藻叶绿体能量和还原力的具体运输机制。

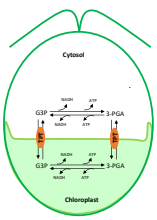

图 1. TPT 介导的能量和还原力在莱茵衣藻叶绿体和细胞质之间的运输

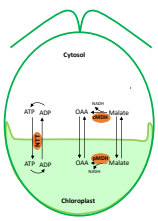

图 2. NTT 和 MDH 介导的能量和还原力在莱茵衣藻叶绿体和细胞质之间的运输

Evolutionary Genomics of Eukaryotic Cells

Prof. Jian-Fan Wen, Principal Investigator, Vice Director ofthe State Key Laboratory of Genetic Resources and Evolution.His group is mainly interested in the origin and evolution of theeukaryotic cell. Taking the protists, which occupy key positions inthe eukaryotic cell evolution, as models, and combining with thedata of prokaryotes and multicellular organisms, they study thebiodiversity and origin and evolution of the structures and functions, especially of genes, gene families, gene groups offunctional pathways and genomes, of the eukaryotic cells. Based on these basic studies, they also explore the new waysfor the control and treatment of some harmful organisms (e.g. parasitic protozoa and schistosomes) and the applications of the effective and specifc metabolic pathways.

1. The determinant role of the specific feces eating behaviour of hamsters in the speciation of *Giardia cricetidarum*

For the first time, our group found that host feces eating behaviour makes a decisive contribution to the speciation of the intestinal parasite *Giardia*. The behaviour of certain animals that ingest feces in order to adapt to unfavourable environmental conditions and to absorb many essential nutrients from the feces is collectively known as coprophagy. We found that the coprophagy of hamsters differs from other animals, and have identified some unique characteristics of *G. cricetidarum*, which is exclusively parasitic on hamsters. This parasite species has unique features in infection and prevalence, such as 'all or none' infection within hamster populations, extremely high trophozoites load in positive individuals, self-healing and loose cyst walls. Our multi-omics analyses with the combination of genome, transcriptome and metabolome revealed that coprophagy plays a determinant role to the form of the specific features of *G. cricetidarum*. On one hand, coprophagy creates a shortcut transmission and repeat infection, consequently makes the selection pressure relaxed in immune evasion and cyst protection, which are exhibited by the reduction of cyst wall proteins, looser and thinner cyst wall structure and the significant reduction in the number of VSP responsible for immune evasion role. On the other hand, coprophagy changes the nutrient in intestines, such as the high concentration of short-chain fatty acids and different amino acid composition, *G. cricetidarum* thus retained the de novo synthesis pathways of long-chain fatty acid from short-chain fatty acids, and some other lipid relevant metabolic pathways. And *G. cricetidarum* also acquired some amino acid metabolic pathways to adapt coprophagy through horizontal gene transfer. This study reveals that a specific behaviour of the host plays a determinant role in the speciation of its specific parasite for the first time.

2. Transport mechanisms of energy and reducing equivalent in *Chlamydomonas* reinhardtii chloroplast

The green single-cell alga *Chlamydomonas reinhardtii* cells possess a single chloroplast that occupies ~40% of the cell volume. In addition to the well-known Calvin cycle, many important biosynthetic reactions in *C. reinhardtii* (e.g., starch and fat synthesis) occurs in the chloroplast. Therefore, ensuring the supply and balance of energy (ATP) and reducing equivalent (NAD(P)H) in chloroplast is indispensable for the growth of *C. reinhardtii*. However, the specific transport mechanism of energy and reducing equivalent in and out of chloroplasts has not been well understood yet. Based on the high-quality genomic data of *C. reinhardtii*, we found that there are two mechanisms for energy and reducing equivalent transport (including input and output) in *C. reinhardtii* chloroplast through bioinformatics analysis combined with experimental studies such as gene editing and subcellular localization of proteins. One is triose phosphate transporter (TPT) – mediated transport of G3P and 3-PGA in and out of chloroplast, thereby completing the transport of ATP and NAD(P)H between chloroplast and cytoplasm (Figure 1); the other mechanism is that specialized transport pathways are responsible for ATP and NAD(P)H transport respectively (Figure 2): ATP transport is via plastidic nucleotide transporter (NTT), while NAD(P)H transport relies on malate shuttle mediated by malate dehydrogenase that localized to chloroplast and cytoplasm, respectively. Thus, for the first time, the specific transport mechanisms of chloroplast energy and reducing equivalent of *C. reinhardtii* was clearly revealed.

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重要成果及产出：

1. Ma ZS & Zhang YP (2022) Ecology of Human Medical Enterprises: From disease ecology of zoonoses, cancer ecology through to medical ecology of human microbiomes. *Frontiers in Ecology and Evolution. 10: 879130.*
2. Ma ZS & Yang LX (2022) CDC (Cindy and David's Conversations) Game: Advising President to Survive Pandemic. *iScience* (Accepted)
3. Li WD & Ma ZS (2022) The upper respiratory tract microbiome network impacted by SARS-CoV-2. *Microbial Ecology, 84: 1-10.*
4. Ma ZS, Li WD & Shi P (2022) Microbiome-host-phylogeny relationships in animal gastrointestinal tract microbiomes. *FEMS Microbiology Ecology,* 98(2): fiac021.
5. Xiao WM & Ma ZS (2022) Influences of Helicobacter pylori infection on diversity, heterogeneity, and composition of human gastric microbiomes across stages of gastric cancer development. *Helicobacter,* 27(4): e12899.
6. Ma ZS (2022) Coupling power laws offers a powerful modeling approach to certain prediction/estimation problems with quantified uncertainty. *Applied Mathematics and Statistics,* 8: 801830.
7. Ma ZS & Mei JD (2022) Stochastic neutral drifts seem prevalent in driving human virome assembly: Neutral, near-neutral and non-neutral theoretic analyses. *Computational and Structural Biotechnology Journal,* 20: 2029-2041.
8. Chen HJ & Ma ZS (2022) Further Quantifying the Niche-Neutral Continuum of Human Digestive Tract Microbiomes with Near Neutral Model and Stochasticity Analysis. *Evolutionary Bioinformatics,* 18:11769343221128540.
9. Chen HJ & Ma ZS (2022) Niche-neutral continuum seems to explain the global niche differentiation and local drift of the human digestive tract microbiome. *Frontiers in Microbiology.* 13: 912240.
10. Liu SL *et al.* ADAM10 and γ-secretase-dependent cleavage of the transmembrane protein PTPRT attenuates neurodegeneration in the mouse model of Alzheimer's disease. *The FASEB Journal*, 37(2): e22734.

代表性成果 (Research Highlights)

CDC (Cindy and David's Conversations) Game: Advising President to Survive Pandemic

Ongoing debates on anti-COVID19 policies have been focused on coexistence vs. zero-out strategies, which can be simplified as “always open (AO)” vs. “always closed (AC).” We postulate that, the middle ground between the two extremes, dubbed LOHC (low-risk open and high-risk closed), is likely more favorable, precluding obviously irrational HOLC (high-open-low-closed). From a meta-strategy perspective, these four policies cover the full spectrum of anti-pandemic policies. We argue that, among numerous factors influencing strategic policy-making, the competence of advisory body such as CDC chief-scientist (say, Cindy) and politics in decision-making body such as president (David), and their cooperation/communication can be critical. Here we investigate anti-pandemic policy-making by harnessing the power of evolutionary game theory in modeling competition/cooperation/communication (three critical processes underlying biological and social evolutions). Specifically, we apply the Sir Philip Sydney (SPS) game, a 4x4 signaler-responder evolutionary game with 16 strategic interactions, which was devised to investigate the reliability of communication that can modulate competition and cooperation, to capture rich idiosyncrasies surrounding today's anti-pandemic policies. By emulating the reality of anti-pandemic policies today, the study aims to identify possible cognitive gaps and traps. The extended SPS, dubbed CDC (Cindy and David's Conversations) game, offers a powerful cognitive model for investigating the coexistence/zero-out dichotomy and possible alternatives. The rigorous analytic solutions and extensive simulations suggest a take-home message—keep it persistently simple and rational: while apparently preferred middle-ground LOHC seems to be small-probability (~0.053) event counter-intuitively, the AO and AC policies appear to be large-probability (~0.41-0.53) events.

【Ma ZS & Yang LX (*iScience*)】

Computational Biology and Medical Ecology Lab

Bio-sketch of the lab Principal Investigator (PI): Zhanshan (Sam) Ma received his double PhDs in Computer Science, and Entomology in 2008, and 1997, respectively, both from the University of Idaho (UI), USA. In November 2010, he was retained as a Professor and PI by Kunming Institute of Zoology (KIZ), the Chinese Academy of Sciences (CAS) through "The 100 Talents PI Program" of the CAS. Prior to joining in KIZ, he was a Research Scientist (in Computational Biology & Computer Science) at UI. He was senior software engineer from 1998 to 2006 in the computer industry in Silicon Valley, USA. Dr. Ma has been keeping dual track publishing in both Computer Science and Biology with more than 120 peer-refereed papers in premier platforms such as *IEEE Transactions on Reliability*, *Science Translational Medicine*, *The ISME Journal, Ecological Monographs,* and *Advanced Science*. He was a member of London-based "*Faculty 1000 of Biology and Medicine*".

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MD Motiur Rahman（博士生；概率统计；深度学习）

邹　权（博士、客座教授；计算机科学；人工智能）

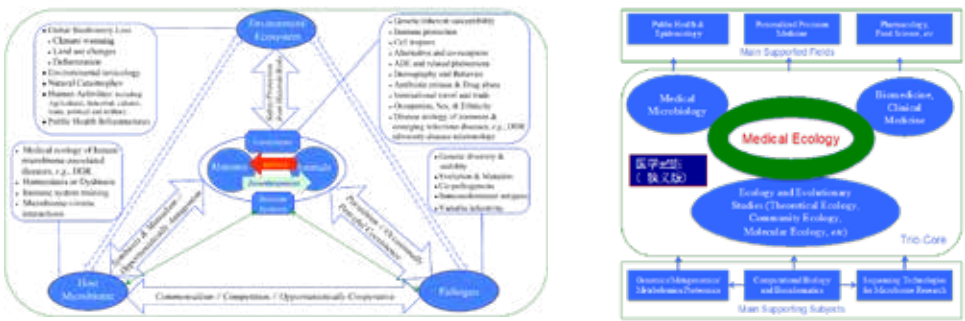
姓　名（学位；早期背景；目前研究方向）

陈红菊（博士生；数学；复杂网络与神经疾病）

乔玉亭（博士生：生物信息学；机器学习）

Review & Perspective: 生物信息革命、计算生物学支持的医学生态学与人类健康和福祉密切相关

In nature, the interaction between pathogens and their hosts is only one of a handful of interaction relationships between species, including parasitism, predation, competition, symbiosis, commensalism, and among others. From a non-anthropocentric view, parasitism has relatively fewer essential differences from the other relationships; but from an anthropocentric view, parasitism and predation against humans and their well-beings and belongings are frequently related to heinous diseases. Specifically, treating (managing) diseases of humans, crops and forests, pets, livestock, and wildlife constitute the so-termed medical enterprises (sciences and technologies) humans endeavor in biomedicine and clinical medicine, veterinary, plant protection, and wildlife conservation. In recent years, the significance of ecological science to medicines has received rising attentions, and the emergence and pandemic of COVID-19 appear accelerating the trend. The facts that diseases are simply one of the fundamental ecological relationships in nature, and the study of the relationships between species and their environment is a core mission of ecology highlight the critical importance of ecological science. Nevertheless, current studies on the ecology of medical enterprises are highly fragmented. Here, we (i) conceptually overview the fields of disease ecology of wildlife, cancer ecology and evolution, medical ecology of human microbiome- associated diseases and infectious diseases, and integrated pest management of crops and forests, across major medical enterprises. (ii) Explore the necessity and feasibility for a unified medical ecology that spans biomedicine, clinical medicine, veterinary, crop (forest and wildlife) protection, and biodiversity conservation. (iii) Suggest that a unified medical ecology of human diseases is both necessary and feasible, but laissez-faire terminologies in other human medical enterprises may be preferred. (iv) Suggest that the evo-eco paradigm for cancer research can play a similar role of evo-devo in evolutionary developmental biology. (v) Summarized 40 key ecological principles/theories in current disease-, cancer-, and medical-ecology literatures. (vi) Identified key cross-disciplinary discovery fields for medical/disease ecology in coming decade including bioinformatics and computational ecology, single cell ecology, theoretical ecology, complexity science, and the integrated studies of ecology and evolution. Finally, deep understanding of medical ecology is of obvious importance for the safety of human beings and perhaps for all living things on the planet.



Ma ZS & Zhang YP (2022) Ecology of Human Medical Enterprises: From Disease Ecology of Zoonoses, Cancer Ecology Through to Medical Ecology of Human Microbiomes. *Frontiers in Ecology and Evolution.* 10:879130.

人类进化与疾病基因组学

孔庆鹏，中科院昆明动物所，研究员、博导。迄今在 *Genome Res*、*Mol Biol Evol*、*Sci Adv*、*Natil Sci Rev*、*Aging Cell*、*Aging Dis* 等国际重要 SCI 期刊上发表论文 100 余篇，论文被各类 SCI 刊物累计引用 5000 余次，H 指数 35。主持有国家重点研发计划专项（任首席科学家）、国家基金委重点国际合作、重大研究计划等项目；2013 年入选科技部科技创新中青年领军人才计划；2016 年入选“国家高层次人才特殊支持计划”领军人才；2020 年先后入选昆明市“春城科技领军人才”、云南省万人计划“云岭学者”。研究组目前的主要研究方向：人群起源演化及健康长寿分子机制。

重要成果及产出：

1. **Xiao FH**[#], **Yu Q**[#], Deng ZL[#], Yang K, Ye YS, **Ge MX**, Yan DJ, **Wang HT**, Chen XQ, **Yang LQ**, Yang BY, Lin R, Zhang W, Yang XL, Dong L, He YH, Zhou JM, Cai WW*, Li J*, **Kong QP*.** *ETS1* acts as a regulator of human healthy aging via decreasing ribosomal activity. ***Science Advances***, 2022, 8(17): eabf2017. (IF=14.957)
2. **Li GH**, Han FF, **Xiao FH**, Gu KSY, Shen Q, Xu WH, Li WX, Wang YL, Liang B, Huang JF*, Xiao WZ*, **Kong QP***. System-level metabolic modeling facilitates unveiling metabolic signature in exceptional longevity. ***Aging Cell***. 2022, 21(4): e13595. (IF=11.005)
3. **Huang YQ**[#], **Ge MX**[#], **Li YH**[#], Li JL, **Yu Q**, **Xiao FH**, **Ao HS, Yang LQ**, Li J*, He YH*, **Kong QP***. Longevity-associated transcription factor *ATF7* promotes healthspan by suppressing cellular senescence and systematic inflammation. ***Aging and Disease***, 2022 (in press). (IF=9.968)
4. **Ge MX**[#], **Yu Q**[#], **Li GH**, **Yang LQ**, He YH, Li J, **Kong QP***. Multiple time-series expression trajectories imply dynamic functional changes during cellular senescence. ***Computational and Structural Biotechnology Journal***, 2022, 20: 4131-4137. (IF=6.155)
5. **Ge MX**[#], **Jiang JJ**[#], **Yang LQ**, Yang XL, He YH, **Li GH**, **Kong QP***. Specific gain and loss of co-expression modules in long-lived individuals indicate a role of circRNAs in human longevity. ***Genes***, 2022, 13(5): 749. (IF=4.141)

1. 揭示 ETS1 调控的核糖体功能降低是人类健康老化的新型机制

对长寿人群 271 例样本（185 例长寿老人，86 例老年对照）的外周血白细胞进行转录组测序，信息学分析发现，长寿老人核糖体通路基因显著低表达；进一步分析发现，长寿老人核糖体编码基因低表达的转录调控因子很可能是 ETS Proto-Oncogene 1（*ETS1*）。进而，研究人员利用人真皮成纤维细胞（HDF）和 IMR-90 等复制衰老细胞模型进行功能验证，发现敲降 ETS1 可降低核糖体编码基因表达，并延缓细胞衰老。该研究表明，降低核糖体参与的蛋白质翻译功能对延缓衰老 / 健康老化具有重要作用，转录调控因子 ETS1 参与该过程调控（**Xiao et al. 2022, *Science Advances***）。

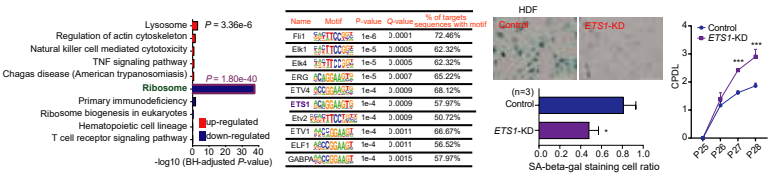


图 1. 长寿人群转录组揭示 ETS1 调控的核糖体功能降低是人类健康老化的新型机制

【Xiao et al.2022, *Science Advances*】

2. 利用新型代谢网络分析方法发现脂氧化代谢功能增强是百岁老人健康老化的重要代谢特征

自主开发全新的、更高准确性的代谢网络模拟方法 GPMM，系统重建并分析比较了我国百岁老人及年轻对照的代谢网络（包括 3977 个代谢反应），发现脂肪酸氧化（FAO）增强是百岁老人中最显著的代谢特征。样本血清代谢组数据，也表明百岁老人血清中脂类物质总体较年轻对照显著降低。该项研究首次揭示脂肪酸氧化增强是百岁老人最为显著的代谢特征，提示其可能是长寿老人实现健康老化的重要代谢机制，这为老年疾病的早期防治提供了新的视角和策略（**Li et al. 2022, *Aging Cell***）。

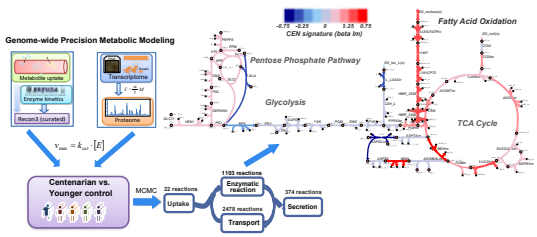


图 2.GPMM 代谢模拟流程及主要发现

【Li et al.2022, *Aging Cell*】

3. 揭示 ATF7 调控的细胞衰老和全身慢性炎症的抑制促进人类的健康衰老

利用长寿人群转录组数据，发现长寿老人的多种炎症因子表达水平下调，而这种低炎症水平可能受转录调控因子 *ATF7*（activating transcription factor 7）的调控。利用细胞衰老模型进行功能验证发现：过表达或敲降 ATF7 可分别延缓或促进细胞衰老；*ATF7* 还可通过抑制 NF-κB 通路、增强靶基因 H3K9me2 水平，从而抑制衰老相关分泌表型（SASP）的分泌，而 SASP 正是衰老相关炎症的重要来源。此外，过表达 *ATF7* 可以抑制线虫的衰老表型，延长线虫的健康寿命。这一研究提示：*ATF7* 可通过延缓细胞衰老和降低老年个体的炎症水平，从而促进健康长寿（**Huang et al. 2022, *Aging and Disease***）。

Human Evolution and Disease Genomics

Dr. Qing-Peng Kong, Principal Investigator, Kunming Institute of Zoology, Chinese Academy of Sciences.

The main research interests of my laboratory are: (1) tracing the origin and evolutionary history of modern humans and (2) disclosing the molecular mechanism of healthy aging by studying longevity individuals. Our research group has already published over 100 papers on the international peer-reviewed journals such as *Am J Hum Genet*, *PNAS*, *Genome Res*, *Mol Biol Evol*, *Natil Sci Rev*, *Theranostics* with total citations over 5,000 times.

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1. Reduced ribosome function regulated by ETS1 is a novel mechanism for human healthy aging and longevity

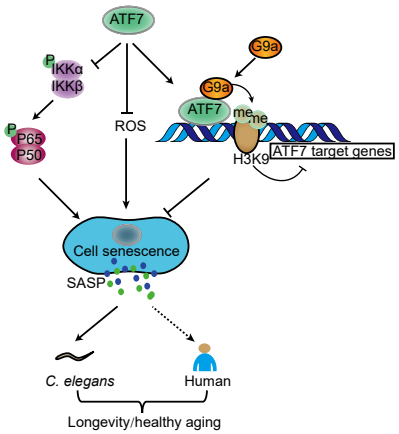
To illustrate the longevity mechanisms, we obtained and analyzed the peripheral blood leukocyte transcriptome data (RNA-seq) in 185 long-lived individuals (LLIs) and 86 spouses of LLI-children (F1SPs) in Lingshui (LS) Prefecture and Lingao (LG) Prefecture, Hainan Province. We found a new but very significant signal in the LLIs: ribosomal pathway genes were markedly downregulated in both LS and LG longevity cohorts. The researchers further showed that the observed downregulation of ribosome protein-coding genes (RPGs) is most likely regulated by a transcriptional regulator *ETS1*. Further functional assays using different replicated senescent cells showed that knockdown of *ETS1* reduced RPG expression and alleviated cellular senescence. Therefore, the study shows that the decreased ribosome function plays an important role in human healthy aging and longevity, and the transcriptional regulator *ETS1* is involved in the regulation of this process **(Xiao et al. 2022, *Science Advances*).**

2. Enhanced fatty acid oxidation as a key metabolic signature in centenarians

To better understand the metabolic mechanisms of healthy aging, we developed a method of genome-wide precision metabolic modeling (GPMM), also systematically reconstructed and analyzed the metabolic network (including 3977 metabolic reactions) of centenarians and young controls, and found that enhanced fatty acid oxidation (FAO) was the most significant metabolic feature in centenarians. By measuring the serum metabolome data of the same longevity and control samples, the results showed that the lipids in centenarians were significantly lower than that of young controls, further supporting the conclusion that centenarians had enhanced fatty acid oxidation. Given that FAO declines with normal aging and is impaired in many age-related diseases, this study suggests that the elevated FAO is a novel mechanism of healthy aging of humans **(Li et al. 2022, *Aging Cell*).**

3. ATF7 promotes healthspan by suppressing cellular senescence and systematic inflammation

Based on RNA-sequencing data of a cohort of longevous families, a transcriptional repressor *ATF7* was identified as a potential longevity-promoting factor as it was upregulated in the long-lived individuals (LLIs) but downregulated in senescent cells. Functional experiments demonstrated that *ATF7* can suppress cellular senescence and the secretion of senescence-associated secretory phenotype (SASP) factors, delay aging and finally extend the lifespan in model animal (*C. elegans*) **(Huang et al. 2022, *Aging and Disease*).**



Schematic role of *ATF7* in senescence process.【**Huang et al. 2022, *Aging and Disease*** 】

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生物多样性基因组学研究

张国捷，中国科学院昆明动物研究所客座研究员，哥本哈根大学兼职教授，浙江大学生物演化研究中心讲席教授。长期担任 *Nature, Science, Genome Research, Current Biology* 等顶尖国际期刊和各国基金会评审委员。目前已在 *Science, Nature, Cell, Science Advances, Nature Communication, PNAS, Current Biology* 等国际高影响力杂志发表论文 200 余篇。2022 年，课题组建立了世界上首个全面覆盖一个蚂蚁社会中所有分工角色的单细胞图谱，揭示了蚂蚁不同等级大脑结构与功能的重塑；解析了蚂蚁个体发育分化的基因表达图式，发现等级分化与细胞分化类似，支持了蚂蚁等级分化的渠化模型；重建了保存在白垩纪琥珀中蚂蚁最完整的内部软组织结构。在 ***Cell*** (1), ***Nature Ecology & Evolution*** (2), ***Nature Communications*** (1), ***Genome Research*** (1), ***Science Advances*** (1), ***BMC Ecology & Evolution*** (1) 等国际刊物发表 SCI 文章 20 篇。

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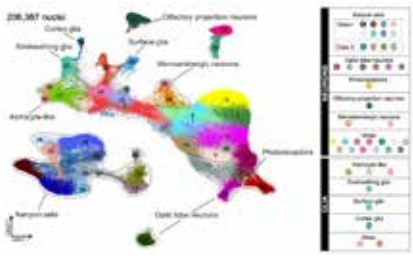
重要成果及产出：

1. Feng S[#], Bai M[#], Rivas-González I, Li C, Liu S, Tong Y, Yang H, Chen G, Xie D, Sears KE, Franco LM, Gaitan-Espitia JD, Nespolo RF, Johnson WE, Yang H, Brandies PA, Hogg CJ, Belov K, Renfree MB, Helgen KM, Boomsma JJ, Schierup MH, **Zhang G**[*]. Incomplete lineage sorting and phenotypic evolution in marsupials. *Cell*, 2022, 185(10): 1646-1660. e18.
2. Li Q[#], Wang M[#], Zhang P[#], Liu Y[#], Guo Q, Zhu Y, Wen T, **Dai X, Zhang X**, Nagel M, Dethlefsen BH, Xie N, **Zhao J**, Jiang W, Han L, Wu L, **Zhong W**, Wang Z, Wei X, Dai W, Liu L, Xu X, Lu H, Yang H, Wang J, Boomsma JJ, Liu C[*], **Zhang G**[*], **Liu W**[*]. A single-cell transcriptomic atlas tracking the neural basis of division of labour in an ant superorganism. *Nat Ecol & Evol*, 2022, 6(8):1191-1204
3. Cole TL[#*], Zhou C[#], Fang M[#], …**Zhang G**[*]. Genomic insights into the secondary aquatic transition of penguins. *Nat Commun*, 2022, 13(1): 3912.
4. Ji Y[#], Feng S, Wu L, Fang Q, Brüniche-Olsen A, DeWoody JA, Cheng Y, Zhang D, Hao Y, Song G, Qu Y, Suh A, **Zhang G**[*], Hackett SJ[*], Lei F[*]. Orthologous microsatellites, transposable elements, and DNA deletions correlate with generation time and body mass in neoavian birds. *Sci Adv*, 2022, 8(35): eabo0099.
5. Ferrández-Peral L[#], Zhan X[#], Alvarez-Estape M, Chiva C, Esteller-Cucala P, García-Pérez R, Julià E, Lizano E, Fornas Ò, Sabidó E, Li Q, Marquès-Bonet T[*], Juan D[*], **Zhang G**[*]. Transcriptome innovations in primates revealed by single-molecule long-read sequencing. *Genome Res*, 2022, 32(8): 1448-62.
6. Qiu B[#], **Dai X**[#], Li P, Larsen RS, Li R, Price AL, **Ding G**, Texada MJ, **Zhang X**, **Zuo D**, **Gao Q**, Jiang W, Wen T, Pontieri L, Guo C, Rewitz K, Li Q, **Liu W**, Boomsma JJ[*], **Zhang G**[*]. Canalized gene expression during development mediates caste differentiation in ants. *Nat Ecol & Evol*, 2022, 6(11): 1753-1765.
7. Zhuang Y[#], Xu W[#], **Zhang G**, Mai H, Li X, He H, **Ran H**[*], Liu Y[*]. Unparalleled details of soft tissues in a Cretaceous ant. *BMC Ecol & Evol*, 2022, 22(1):146.

1. 蚂蚁超有机体全等级大脑单细胞图谱

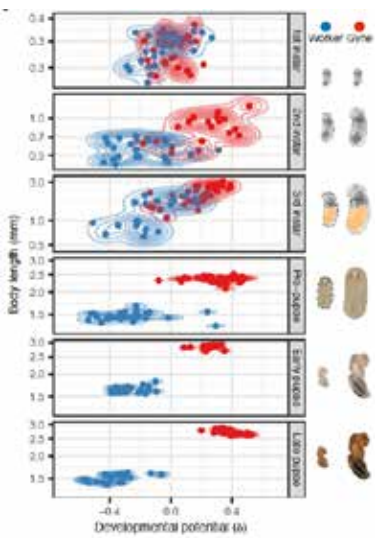


研究团队以法老蚁（*Monomorium pharaonis*）为研究对象，利用单细胞转录组测序技术，获得了涵盖法老蚁工蚁、处女繁殖蚁、蚁后、雄蚁 4 种全等级大脑总共 206367 个高质量的单细胞核转录组数据。这是世界上首个全面覆盖一个蚂蚁社会中所有分工角色的单细胞图谱。通过比较法老蚁四种成体大脑的细胞组成，发现蚂蚁不同等级个体的大脑有不同方向和程度的特化。

这提示了不同等级的蚂蚁其神经环路发生了重大重塑。不同等级个体的大脑有不同方向和程度的特化，彼此之间又功能互补，执行不同的社会行为和功能，从而使得整个蚁群能够同时拥有生殖、育幼、觅食、防御等全面的功能。（Li *et al*., 2022, *Nat Ecol & Evol*）

2. 蚂蚁等级分化个体发育渠化模型

研究团队揭示了蚂蚁群体和多细胞生物在发育和演化上的相似之处，为蚂蚁超有机体概念提供了证据支持。该研究以法老蚁和切叶蚁为研究对象，对不同发育阶段的蚂蚁个体进行微量 RNA 测序，分析蚂蚁个体发育分化的基因表达图式。随着时间推移，蚁后与工蚁的基因表达差异逐渐增大，而同一等级个体间的基因表达则愈加相像。该发现意味着蚁后和工蚁的等级分化与细胞分化类似，其形态发育会限制在特定的分化渠道中（渠化，canalization）并朝着特定的目标前进，而保幼激素在其中起到了重要作用。此外，研究还发现了一个最显著的渠化基因 Freja，这个基因只在蚁后卵巢特异表达。这提示渠化基因在蚂蚁等级分化中与等级特征的发育和维持相关，并可能影响着蚂蚁的等级演化。（Qiu *et al*., 2022, *Nat Ecol & Evol*）

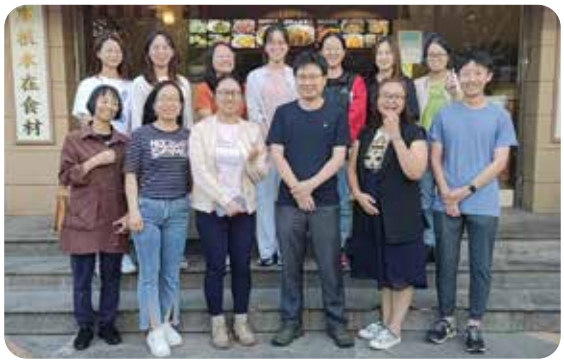


3. 解析白垩纪蚂蚁化石内部软组织解剖结构

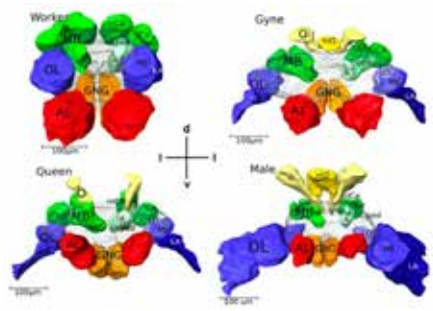
研究团队与云南省古生物重点实验室合作，报道了蚂蚁白垩纪琥珀中的软组织结构。研究人员通过 Micro-CT 的方法，解析了现已灭绝的蚂蚁（*Zigrasimecia*）其内部软组织结构。这些软组织涵盖完整的器官系统，包括大脑、主要的外分泌系统、消化道的一部分和一些肌肉群。对蚂蚁内部组织结构的重构有助于我们理解其社会行为和演化。此外，研究人员还发现该化石中雌性处女蚁在形态上具有独特的唇状结构，这表明早期蚂蚁在白垩纪时期可能具有特殊生态习性。（Zhuang *et al*. 2022, *BMC Ecol & Evol*）

Biodiversity Genomics Lab

Dr. Guojie Zhang, Head of Biodiversity Genomics Group, Kunming Institute of Zoology, CAS, adjunct professor in University of Copenhagen and chair professor of the Evolutionary & Organismal Biology Research Center, Zhejiang University. Dr. Zhang has published more than 200 articles, including *Science, Nature, Cell, Science Advances, Nature Communications, PNAS* and *Current Biology*. In 2022,we produced a single-cell transcriptomic atlas of the full panel of castes in *Monomorium pharaonis*, identifying the brain specializations across different castes, indicating permanent caste and extreme sex-differentiation induced major changes in the neural circuitry of ants; we analyzed the individual developmental transcriptomic trajectories of two ant species, showing that caste differentiation is analogous to cell differentiation and demonstrating that caste differentiation is increasingly canalized from early development onwards; we reconstructed the anatomy of *Zigrasimecia* ant preserved in Cretaceous amber with an almost complete internal organ systems. 20 high profile SCI papers were published, including ***Cell*** (1), ***Nature Ecology & Evolution*** (2), ***Nature Communications*** (1), ***Genome Research*** (1), ***Science Advances*** (1).



1. Decoding the brain of ants: single cell transcriptomic atlas of ant superorganism

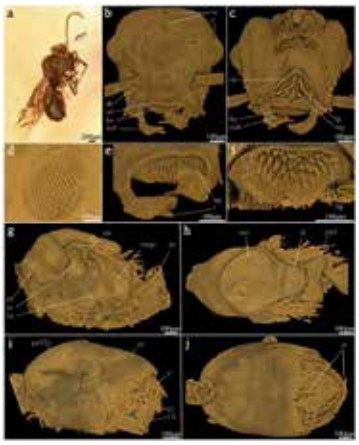


We produced the brain single cell transcriptomic atlas covering the full panel of castes – queens, gynes (virgin queens), workers and males of *Monomorium pharaonis* by obtaining 206,367 brain single-nucleus transcriptomes. We found that the brains of different castes are differentially specialized in directions and degrees. The observation suggests permanent caste differentiation and extreme sex-differentiation induced major changes in the neural circuitry of ants. The brains of different castes in the colony are specialized for different functions and complementary at superorganismal level for totipotent functions such as reproduction, nursing, foraging and defense (Li *et al*., 2022, *Nat Ecol & Evol*).

2. Deciphering the development of ants: caste canalization

We reconstructed the individual developmental trajectories of two ant species, *Monomorium pharaonis* and *Acromyrmex echinatior* by obtaining >1,400 individual transcriptomes, detecting that caste differentiation is increasingly canalized from early development onwards and that the juvenile hormone signaling pathway plays a key role in this process. This study also identified a highly canalized gyne-biased ovary gene *Freja*, suppression of which disturbed pupal development by induceing non-adaptive intermediate phenotypes between gynes and workers. Our results were consistent with natural selection actively maintaining canalized caste phenotypes while securing robustness in the life cycle ontogeny of ant colonies (Qiu *et al*., 2022, *Nat Ecol & Evol*).

3. Reconstructing the anatomy of internal soft tissue: Cretaceous Zigrasimecia ant



We collaborated in a research which rereported a female specimen (gyne) of the extinct ant group—*Zigrasimecia*—included in a Cretaceous amber piece from Kachin, Myanmar, with an almost complete system formed by various internal organs. These included the brain, the main exocrine system, part of the digestive tract, and several muscle clusters. This research expanded our knowledge of internal anatomy in stem group ants. As the gyne bears a morphologically unique labrum, our specimen's internal and external features supported the notion that the early ant may have special ecological habits during the Cretaceous period (Zhuang *et al*., 2022, *BMC Ecol & Evol*).

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Dashuang Zuo, Ph.D. candidate 2021
杞燕梅
Yanmei Qi, Ph.D. candidate 2022
钟文江
Wenjiang Zhong, Master candidate 2021
王 娇
JiaoWang, Master candidate 2022

进化生态与多维组学动态

吕雪梅，博士，研究员，博士生导师，中国科学院引进海外高层次人才、“西部之光”引进人才、云南省引进高层次人才，同时担任云南省西南及跨境生物多样性数据信息重点实验室主任、中国科学院昆明动物研究所生物多样性大数据中心主任、中国科学院昆明动物研究所进化发育中心主任。近年来课题组研究主要以群体遗传和进化生态学理论为核心，利用多组学测序等技术手段，结合大数据和高性能计算，解析生物多样性的形成与稳定过程、适应性进化的遗传机制以及肿瘤疾病的发生发展与演化。目前已在 *National Science Review*、*Science Advances*、*Nature Communications*、*Molecular Biology and Evolution*、*PNAS*、*Genome Research*、 *Science Bulletin* 等期刊上累计发表 SCI 论文 63 篇，成果得到中国科学报 ScienceDaily、央视晚间新闻等国内外媒体的报道。

重要成果及产出：

1. Guanghao Li[#], Zuyu Yang[#], Dafei Wu, Sixue Liu, Xuening Li, Tao Li, Yawei Li, Liji Liang, Weilong Zou, Chung-I Wu, Hurng-Yi Wang*, **Xuemei Lu*.** Evolution under spatially heterogeneous selection in solid tumors. *Molecular Biology and Evolution*, 2022, 39(1): msab335.
2. Yongsen Ruan, Haijun Wen, Mei Hou, Weiwei Zhai, Shuhua Xu, **Xuemei Lu*.** On the epicenter of COVID-19 and the origin of the pandemic strain. *National Science Review*, 2022, nwac286.
3. Yanan Cao, Lingling Chen, Hua Chen, Yupeng Cun, Xiaofeng Dai, Hongli Du, Feng Gao, Fengbiao Guo, Yalong Guo, Pei Hao, Shunmin He, Shunping He, XiongLei He, Zheng Hu, Boon-Peng Hoh, Xin Jin, Qian Jiang, Qinghua Jiang, Asifullah Khan, Hong-Zhi Kong, Jinchen Li, Shuai Cheng Li, Ying Li, Qiang Lin, Jianquan Liu, Qi Liu, Jian Lu, **Xuemei Lu**, Shujin Luo, Qinghua Nie, Zilong Qiu, Tieliu Shi, Xiaofeng Song, Jianzhong Su, Shengce Tao, Chaolong Wang, ChuanChao Wang, GuoDong Wang, Jiguang Wang, Qi WU, Shaoyuan Wu, Shuhua Xu, Yu Xue, Wenjun Yang, Zhaohui Yang, Kai Ye, YuanNong Ye, Li Yu, Fangqing Zhao, Yiqiang Zhao, Weiwei Zhai, Dandan Zhang, Liye Zhang, Houfeng Zheng, Qi Zhou, Tianqi Zhu, Yaping Zhang*. Was Wuhan the early epicenter of the COVID-19 pandemic? – A critique. *National Science Review*, 2022, nwac287.

1. 结构化种群的进化驱动力和动态进程及其预测

实体肿瘤空间上的遗传和表型异质性已被充分报道。然而，这种异质性如何影响肿瘤发生的群体动态变化还没有得到充分解析，其难点是由于实体肿瘤受到较强的空间约束，进化过程不遵循传统的群体遗传学模型。为了解决这个问题，本研究提出了一个中性空间 (NS, neutral spatial) 模型，为了验证 NS 模型，我们对两个肝细胞肿瘤（T1 和 T2）进行了三维多点微采样和全基因组测序（图 1）。结果显示，肿瘤外围样本检测到的突变是内部样本的 2 倍，肿瘤外部细胞具有更高的分裂速度，从而积累更多的突变，通过刻画肿瘤内克隆的大小和分布，在两个肿瘤中都检测到了自然选择。由于肿瘤细胞迁移能力有限，优势克隆快速生长从而占据肿瘤的大部分空间，早期出现的小克隆由于优势克隆的扩张而灭绝。检测肿瘤进化过程中的自然选择颇具挑战性，在肿瘤发生发展的不同阶段进行采样得到的结论可能有所不同，不同阶段起主导作用的驱动力也有所不同（图 2）。通过引入中性空间模型，揭示了中性进化和自然选择的交替作用，驱动了肿瘤内遗传结构、克隆多样性的形成以及肿瘤的克隆扩张和取代。

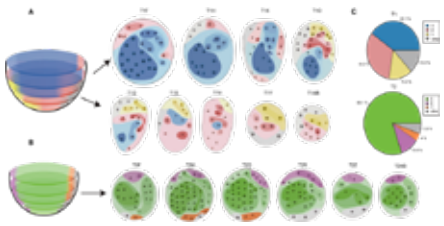

图 1. 3D 微采样

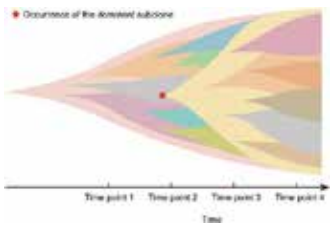

图 2. 肿瘤随时间的进化过程

【Li et al., 2022, *Molecular Biology and Evolution*, IF20.074】

2. 从科学角度分析新冠病毒的溯源问题

2022 年，Pekar、Worobey 等研究团队在 Science 连发两篇关于新冠病毒起源的文章，作者根据新冠疫情爆发早期的数据，通过一定的演化和溯源分析，都得出了 COVID-19 起源于武汉的一致结论。针对此问题，我们指出 Pekar et al.(2022) 中存在的分析错误。他们混淆了 tMRCA 的概念，错误地将最近共同祖先时间等同于病毒由动物传播至人的时间。病毒有可能在人群中少量传播已久再近期爆发，此时以爆发后的毒株数据计算所得的最近共同祖先时间往往要比真正的跨种传播时间要近得多。此外，在合作团队发表的 Ruan et al.(2022) 中，对病毒突变体进行科学分析，明确了病毒起源地（PL0）和传播起始地的定义（PL1）；前者代表冠状病毒由动物入侵至人类，而后者表示冠状病毒在人群中的传播；病毒由 PL0 到 PL1 后，可能引起地区性的传播或消失的历史，大规模疫情爆发的地区不一定是唯一的起始地。

【Ruan et al., 2022, *National Science Review*, IF23.920】

4–D Genomic Dynamics in Ecology and Evolution

Dr. Xuemei Lu, Professor, Principal Investigator. Our group focuses on the genetic and regulatory basis of adaptation, population dynamics in natural species and cell evolution by integrating ecological and evolutionary theory, population genetics, system biology approaches and multi-omics techniques. For example, we are asking how the life-history tradeoffs shape the evolutionary processes and the formation of genetic diversity in different species, and what the consequences are in terms of adaptation or resistance in metapopulations. We are also interested in the interaction and co-evolution of genomic variations, three-dimensional (3D) genome organization and their effects on adaptation.

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1. Evolution under spatially heterogeneous selection in solid tumors

We propose a neutral spatial (NS) model whereby the mutation accumulation increases toward the periphery; the genealogical relationship is spatially determined and the selection efficacy is blunted (due to kin competition). In this model, neutral mutations are accrued and spatially distributed in manners different from those of advantageous mutations. Importantly, the distinctions could be blurred in the conventional model. To test the NS model, we performed a three-dimensional multiple microsampling of two hepatocellular carcinomas. Whole-genome sequencing (WGS) revealed a 2-fold increase in mutations going from the center to the periphery. The operation of natural selection can then be tested by examining the spatially determined clonal relationships and the clonal sizes. Due to limited migration, only the expansion of highly advantageous clones can sweep through a large part of the tumor to reveal the selective advantages. Hence, even multiregional sampling can only reveal a fraction of fitness differences in solid tumors. Our results suggest that the NS patterns are crucial for testing the influence of natural selection during tumorigenesis, especially for small solid tumors.

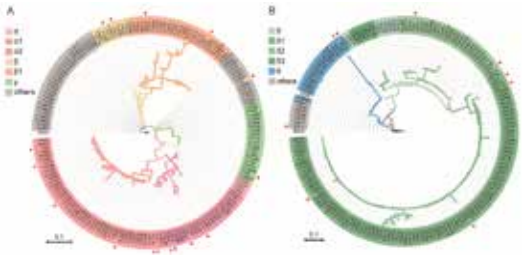

Fig 3. Extended sample phylogenetic relationships

2. On the epicenter of COVID-19 and the origin of the pandemic strain

We point out the error in Pekar et al.(2022) that they estimated tMRCAs of SARS-CoV-2 found in humans, which means the time to the most recent common ancestor of the viral variants. However, the authors interpret tMRCA to mean the timing of the viral jump from animal hosts to humans. Specifically, Ruan et al. (2022) published in National Science Review (NSR) an analysis that concludes two early centers in the spread of COVID-19. Since the strain (referred to as DG1111) that spread globally to cause the pandemic has never been found in Wuhan prior to its arrival from outside Asia in March 2020, Wuhan is a local center, rather than the “global epicenter”. Citing observations from Europe , we suggest that the jump from animal hosts to humans must be earlier than the fall of 2019 to permit the evolution from the ancestral DG0000 strain to the global DG1111 (0 and 1 designating the ancestral and derived variant, respectively).

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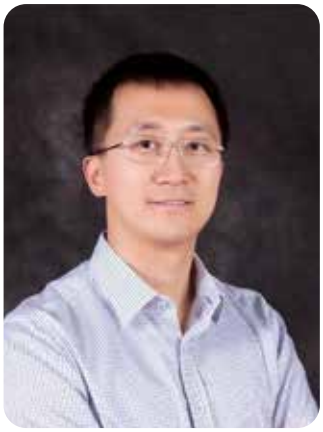
刘 灿 Can Liu



行为遗传和进化

王国栋，博士，研究员，博士生导师。入选中组部万人计划青年拔尖人才，中国科学院青年促进会优秀会员，云南省中青年学术和技术带头人。获 2019 年度中国科学院青年科学家奖，作为发起人之一创建家犬基因组研究国际联盟。现任中国动物学会动物行为学分会第二届理事会理事（2019 年 11 月 -2023 年 11 月）和中国科学院昆明动物研究所人类疾病的家犬模型省创新团队带头人（2019- 至今）。主要研究方向为群体遗传、适应性进化、复杂表型和行为的遗传机制等研究。以第一作者和通讯作者（含并列）在 *Nat Genet*、*Nat Commun*、*Cell Res*、*PNAS*、*Mol Biol Evol* 和 *Nucl Acids Res* 等 SCI 杂志发表论文三十余篇。获 Sanofi-Cell Research 优秀论文和第三届中国科协优秀科技论文，研究结果被 *Nature*、*The New York Times*、*The Guardian*、*National Geographic*、*Scientific American* 等国际杂志报道。

重要成果及产出：

1. **Zhou QJ**[1], Liu XY[1], Zhang LL[1], Wang R, Yin TT, Li XL, Li GM, He YQ, Ding ZL, Ma PC, Wang SZ, Mao BY*, Zhang SH*, **Wang GD***. A single-nucleus transcriptomic atlas of the dog hippocampus reveals the potential relationship between specific cell types and domestication. *National Science Review*, 2022, 9(11): nwac147. (IF:23.178)
2. **王国栋**，张树润，李欣懿。一种犬脐带来源的间充质干细胞培养基和培养方法。授权专利号：ZL 2020 1 0976166.2

1. 家犬海马单细胞图谱的绘制

为探究海马不同细胞类型与神经性疾病间的对应关系，研究团队从比格犬的海马中共捕获了 105,057 个单细胞核，使用 SPLiT-seq 构建了标准化的单核 rna 测序 (snRNA-seq) 流程。利用 Leiden 群落检测算法最终鉴定出 26 个细胞簇（cluster）及其差异表达基因集合（图 1A 和 1B），并根据小鼠和人体内的已知标记定义出 8 种细胞类型（cell type），以及使用免疫荧光及免疫组化技术验证验证了其中 5 种细胞的标记基因（图 1C-H）。

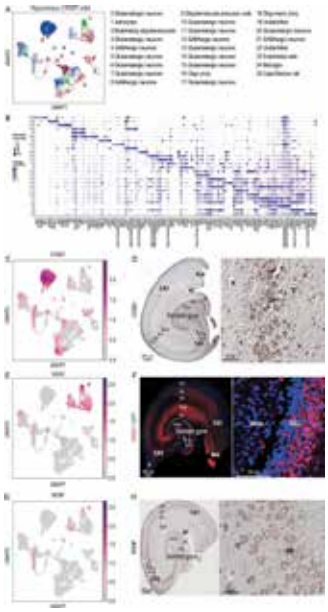


图 1. 家犬海马细胞图谱

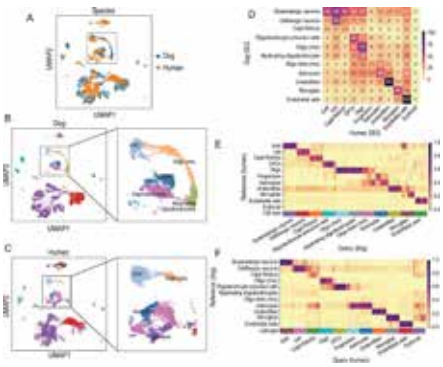


图 2. 家犬与人联合分析

2. 家犬和人类海马的联合分析

为了验证细胞注释的准确性和海马细胞类型的保守性，下载了人类海马的单细胞转录组数据进行联合分析。整合结果显示家犬和人类细胞类型较为保守（图 2A-C）且共享差异表达基因（图 2D）。跨物种细胞分型和整合工具 CAME 被用于交叉验证，研究团队分别用人类的数据作为参考预测家犬海马的细胞类型（图 2E）和用家犬的数据作为参考预测人类海马的细胞类型（图 2F），证明了海马细胞类型在家犬和人类之间是保守的。

Genetics and Evolution of Behavior

Prof. Guodong Wang, researcher, Ph.D. Supervisor. The 2019 Young Scientist Award of the Chinese Academy of Sciences and as one of the initiators to create the Dog10K Consortium. Recently years we focused on genomic evolution, adaptive evolution, the genetic basis of complex traits and behavior. Research progress published on *Nat Genet*, *Nat Commun*, *Cell Res*, *PNAS*, *Mol Biol Evol*, *Nucl Acids Res* and other science citation index (SCI) journals.

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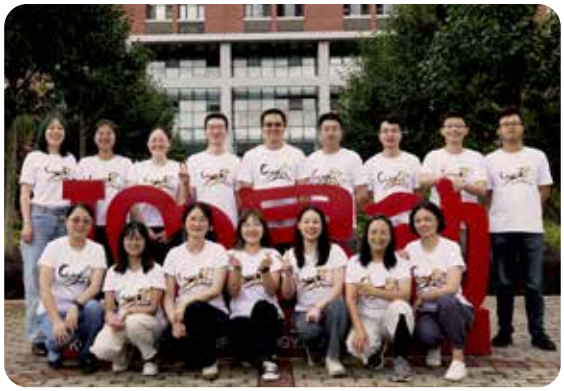

3. Putative trajectory analysis reveals the conserved oligodendrocyte development trajectory

With the defined cell-type markers, Clusters 2 and 9 were inferred to be myelinating oligodendrocytes and OPCs, respectively (Fig. 3A). Consistently with this classification, CNP, a myelin-related marker gene of Cluster 2, was highly expressed in the hilus, ML, SLM, F and A areas (Fig. 3B). AGAP1 was a DEG in Cluster 9 and could be used as a new marker of OPCs (Fig. 3B). Cluster 16 was linked to Clusters 2 and 9 (Fig. 1A), with few specifically expressed genes to assign its identity. Therefore, we inferred that Clusters 2, 9 and 16 might form a development trajectory from OPCs to myelinating oligodendrocytes, which was also found in the mouse hippocampus.

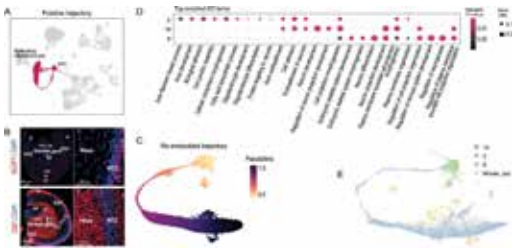

Figure 3. Putative trajectory analysis and cross-species transcriptome comparison between dog and mouse oligodendrocyte.

4. Significant convergence between DEGs and putative PSGs in domestication

Glutamate neurons play an important role in domestication and may play a role in learning, memory and stress response. *GRIK3* is highly expressed in glutamate neurons, plays an important role in reducing stress responses in domestic animals, making them more likely to be kept in captivity. *GAD2* is a marker gene of GABA neurons, which is associated with fear response, reducing fear is an important step in animal domestication. *MBP* is a myelin protein coding gene which is highly expressed in oligodendrocytes, and changes in myelination may be associated with behavioral differences between domestic dogs and wolves (Figure 4). All of these suggest that domestication has influenced the behavior of domestic dogs by changing the hippocampus.

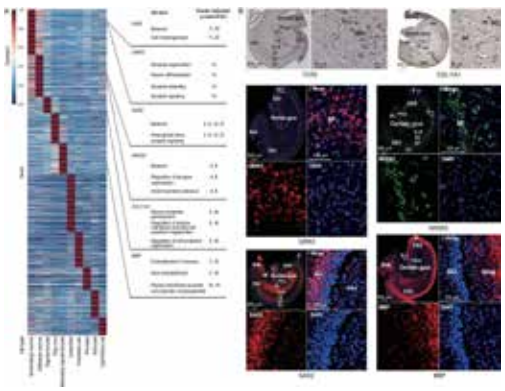

Figure 4. The mean expression of DEGs in different cell types.

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神经发育与进化

毛炳宇，博士，研究员，中德马普青年科学家小组组长，遗传资源与进化国家重点实验室副主任。先后获得国家自然科学基金委杰出青年基金、重点项目等资助。实验室主要以小鼠、非洲爪蛙和文昌鱼为动物模型研究神经系统的早期发育机制及其演化。

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重要成果及产出：

1. **Ma P#, Li Wan L#, Li Y#,** He C#, Song N, Zhao S**, Wang H**, Ding Y***, Mao B***, **Sheng N***. RNF220 is an E3 ubiquitin ligase for AMPA receptors to regulate synaptic transmission. ***Sci Adv***, 2022, 8(39): eabq4736.
2. **Zhou Q#**, Liu X#**, Zhang L#,** Wang R**, Yin T,** Li X**, Li G**, He Y, **Ding Z**, **Ma P, Wang S**, **Mao B***, Zhang S*, **Wang G***. A single-nucleus transcriptomic atlas of the dog hippocampus reveals the potential relationship between specific cell types and domestication. ***National Science Review***, 2022, 9(11): nwac147.
3. **Ma P#**, Liu X#, Xu Z#, Liu H#, Ding X#, Huang Z#, Shi C, Liang L, Xu L**, Li X, Li G, He Y, Ding Z**, Chai C, Wang H, Qiu J, Zhu J, Wang X, Ding P, Zhou S, Yuan Y, Wu W, Wan C, Yan Y, Zhou Y, Zhou Q, **Wang G**, Zhang Q,* Xu X,* Li G*, Zhang S*, **Mao B***, Chen D*. Joint profiling of gene expression and chromatin accessibility during amphioxus development at single-cell resolution. ***Cell Reports***, 2022, 39(12): 110979.
4. **Li Y#, Yang C#**, **Wang H**, Zhao L, Kong Q, Cang Y, Zhao S, **Lv L,** Li Y, **Mao B***, and **Ma P***. Sequential stabilization of RNF220 by RLIM and ZC4H2 during cerebellum development and Shh-group medulloblastoma progression. ***Journal of Molecular Cell Biology***, 2022, 14(1): mjab082.

1. 构建文昌鱼胚胎单细胞水平的细胞分化谱系

得益于近年来单细胞测序技术和计算生物学的发展，以“DNA 条形码”为代表的谱系示踪技术取得了长足发展；文昌鱼是介于无脊椎动物和脊椎动物之间的过渡型动物，是最原始的脊索动物（Chordate），一直是研究脊椎动物起源和演化的理想对象，在探索脊索动物细胞命运决定保守机制和进化发育上有着极其重要的地位。我们联合 Split-seq 单细胞转录组测序（snRNA-seq）和 10× Genomics 单细胞表观组测序（scATAC-seq）技术，以单细胞分辨率绘制了文昌鱼早期胚胎发育全细胞命运图谱和成体文昌鱼各组织的单细胞基因表达图谱和染色质开放特性图谱；分析了文昌鱼胚胎各谱系分化过程中的基因转录动态；以及通过跨物种的整合分析，构建了文昌鱼胚胎各谱系分化过程中保守的基因调控网络，计算筛选 并通过原位杂交实验验证到组织 特异表达的新标记基因。这是第一张文昌鱼胚胎发育过程中的单细胞分辨 率全细胞命运图谱，这项研究产生的 数据对于研究脊椎动物各组织器官的演化具有重要意义（*Cell Reports*，2022）。

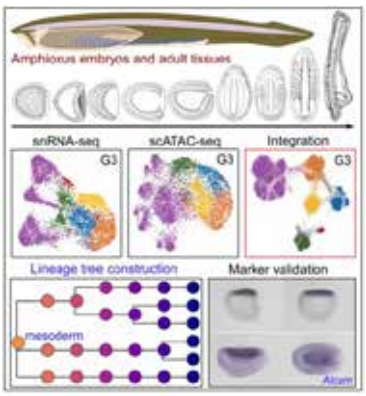

图 1. 文昌鱼单细胞水平转录组和表观组整合分析

2. 揭示 RLIM/RNF220/ZC4H2 轴调控 Shh 信号和小脑发育

我们前期的研究工作揭示了泛素连接酶 RNF220 通过调控 Shh 信号通路参与神经管图式形成和小脑发育；同时课题组的研究还发现小核蛋白 ZC4H2 作为 RNF220 的蛋白稳定因子参与了 Shh 信号调控和神经图式形成。进一步研究发现，ZC4H2 在小鼠胚胎的小脑颗粒祖细胞中特异高表达；并且在 Ptch1+/- 小鼠自发髓母细胞瘤和人 Shh 亚型髓母细胞瘤中，RNF220/ZC4H2 蛋白异常累积和高表达。为了探究 RNF220/ZC4H2 在小脑颗粒祖细胞特异表达以及在髓母细胞瘤中异常累积的机制，我们通过酵母双杂交方法筛选发现泛素连接酶 RLIM 与 ZC4H2 特异结合，通过非降解的泛素化修饰促进 RNF220/ZC4H2 蛋白复合体的稳定性。另外，研究人员还在 RLIM 的启动子上鉴定出有功能的 Gli 结合位点，提示 RLIM 是 Shh/Gli 信号通路的直接靶基因。免疫荧光实验证明 RLIM 在位于 EGL 的小脑颗粒祖细胞中特异高表达；同时，在 Ptch1+/- 小鼠自发髓母细胞瘤以及人的 Shh 亚型髓母细胞瘤临床样本中，RLIM 与 RNF220 /ZC4H2 的蛋白水平表现出正相关。该研究进一步揭示了 RNF220/ZC4H2 蛋白在小脑颗粒祖细胞特异高表达及其在 Shh 亚型髓母细胞瘤中异常累积的分子机制（*JMCB*, 2022）。

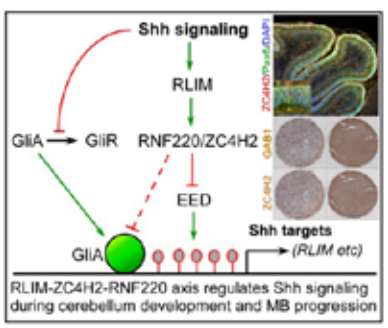

图 2. Shh 靶基因 RLIM 通过稳定 RNF220/ZC4H2 蛋白复合体参与 Shh 信号通路调控的分子机制

Mechanisms of Neural Patterning and Evolution

Dr. Bingyu Mao, Principal Investigator, Ph. D. (1998, Shandong University, China). The molecular mechanisms of neural patterning and how these mechanisms evolved during vertebrate origin are the focuses of our lab. We use mouse, the amphibian *Xenopus* and the cephalochordate amphioxus as our model animals.
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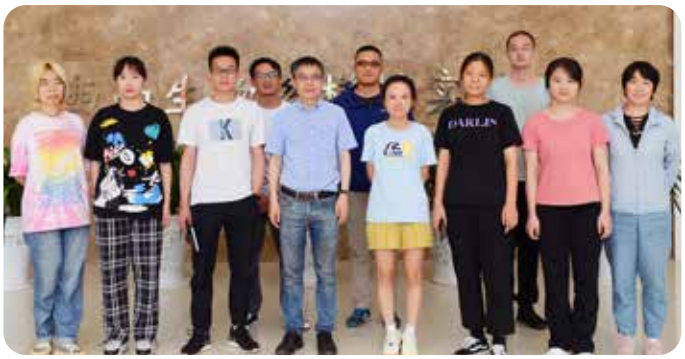

1. Joint profiling of gene expression and chromatin accessibility during amphioxus development at single-cell resolution

Vertebrate evolution was accompanied by two rounds of whole-genome duplication followed by functional divergence in terms of regulatory circuits and gene expression patterns. As a basal and slow-evolving chordate species, amphioxus is an ideal paradigm for exploring the origin and evolution of vertebrates. Single-cell sequencing has been widely used to construct the developmental cell atlas of several representative species of vertebrates (human, mouse, zebrafish, and frog) and tunicates (sea squirts). Here, we perform single-nucleus RNA sequencing (snRNA-seq) and single-cell assay for transposase accessible chromatin sequencing (scATAC-seq) for different stages of amphioxus (covering embryogenesis and adult tissues). With the datasets generated, we constructed a developmental tree for amphioxus cell fate commitment and lineage specification and characterize the underlying key regulators and genetic regulatory networks. The data are publicly available on the online platform Amphioxus Atlas (***Cell Reports***, 2022).

2. Sequential stabilization of RNF220 by RLIM and ZC4H2 during cerebellum development and Shh-group medulloblastoma progression

Sonic hedgehog (Shh) signaling is essential for the proliferation of cerebellar granule neuron progenitors (CGNPs), and its misregulation is linked to various disorders, including cerebellar cancer medulloblastoma (MB). During vertebrate neural development, RNF220, a ubiquitin E3 ligase, is involved in spinal cord patterning by modulating the subcellular location of glioma-associated oncogene homologs (Glis) through ubiquitination. RNF220 is also required for full activation of Shh signaling during cerebellum development in an epigenetic manner through targeting embryonic ectoderm development. ZC4H2 was reported to be involved in spinal cord patterning by acting as an RNF220 stabilizer. Here, we provided evidence to show that ZC4H2 is also required for full activation of Shh signaling in CGNP and MB progression by stabilizing RNF220. In addition, we found that the ubiquitin E3 ligase RING finger LIM domain-binding protein (RLIM) is responsible for ZC4H2 stabilization via direct ubiquitination, through which RNF220 is also thus stabilized. RLIM is a direct target of Shh signaling and is also required for full activation of Shh signaling in CGNP and MB cell proliferation. We further provided clinical evidence to show that the RLIM–ZC4H2–RNF220 cascade is involved in Shh-group MB progression. Disease-causative human RLIM and ZC4H2 mutations affect their interaction and regulation. Therefore, our study sheds light on the regulation of Shh signaling during cerebellar development and MB progression and provides insights into neural disorders caused by RLIM or ZC4H2 mutations (***JMCB***, 2022).

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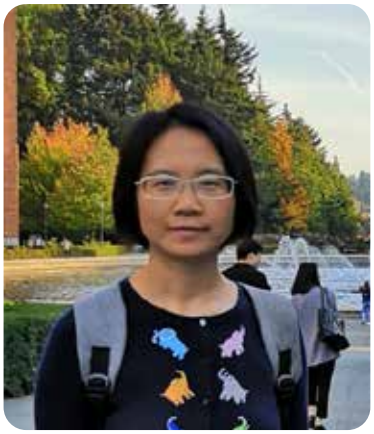


哺乳动物胚胎发育

郑　萍，博士，研究员，课题组长。2009年入选中国科学院“百人计划”，组建实验室。主要研究方向：1）干细胞维持基因组稳定性的调控机制；2）灵长类精原干细胞的基础生物学及其在基因修饰技术中的应用研究；3）灵长类早期胚胎发育。

重要成果及产出：

1. **Zhang WD**[1], **Tang M**[1], **Wang L**, Zhou H, Gao J, Chen ZL, Zhao B*, **Zheng P***. Lnc956-TRIM28-HSP90B1 complex on replication forks promotes CMG helicase retention to ensure stem cell genomic stability and embryogenesis. ***Science Advances***, 2023, 9(4): eadf6277.
2. **Ma HX**[1,*], **Ning YQ**[1], **Wang L**[1], **Zhang WD**, **Zheng P***. Lnc956 regulates mouse embryonic stem cell differentiation in response to DNA damage in a p53-independent pathway. ***Science Advances***, 2023, 9(3): eade9742.

1. 发现干细胞维持基因组稳定的新机制

1.1 干细胞调控复制叉稳定的新机制

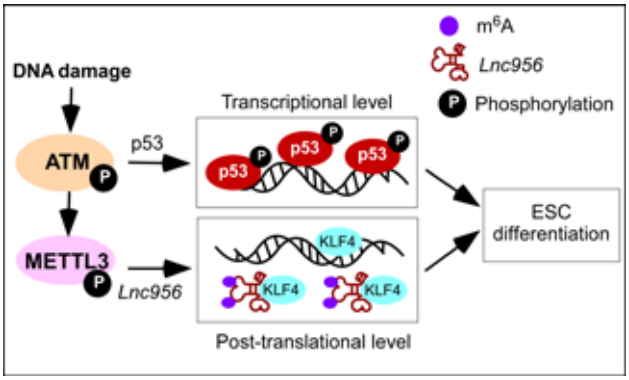
基因组变异和致瘤性是制约干细胞临床应用的主要障碍。研究干细胞维持基因组稳定的机制，是理解并有效解决基因组变异的基础。基于前期工作，我们推测干细胞复制叉上可能存在 lncRNA，调控 DNA 复制压力反应。为此，我们建立了新的方法，系统分析了胚胎干细胞 DNA 复制叉上的 lncRNAs。发现干细胞复制叉上存在一些特异性 lncRNAs，且在复制压力下高度富集，提示它们在复制压力反应中起重要作用。我们以其中一个丰度最高且功能未知的 lncRNA –Lnc956 为例进行了研究。发现干细胞能通过复制叉上的 Lnc956-Trim28-Hsp90b1 蛋白质复合体，有效阻止复制压力下 DNA 复制小体的解离，避免复制叉坍塌产生基因组变异。Lnc956 也有重要的生理功能，敲除后导致胚胎着床后死亡。该工作揭示了干细胞调控复制叉稳定的新机制。

【Zhang W et al. 2023, *Science Advances*】

1.2 干细胞基因组质量监控的新机制

有效清除基因组损伤的细胞个体，是干细胞维持群体基因组稳定的重要方式。p53 是目前已知唯一的干细胞基因组质量监控分子。我们鉴定了一个新的干细胞基因组质量监控分子 Lnc956。在基因组受损后，DNA 损伤反应通路的核心激酶 ATM 激活，ATM 活化 Mettl3 (调控 RNA m6A 修饰），使 Lnc956 发生 m6A 修饰。发生 m6A 修饰的 Lnc956 大量结合干性维持关键蛋白 KLF4，阻止其结合到 DNA 上行使干性调控功能，使基因组损伤的干细胞快速发生分化，得以清除。Lnc956-KLF4 通路不依赖 p53，和 p53 通路平行，共同对干细胞基因组质量进行监控。

【Ma H et al. 2023, *Science Advances*】



p53 和 *Lnc956* 协调调控 ESCs 质量控制的工作模型

Mammalian Embryonic Development

Dr. Ping Zheng, Principal Investigator, joined in Kunming Institute of Zoology, Chinese Academy of Sciences in 2009. The laboratory studies 1) how stem cells safeguard their genomic stability, 2) the biology of primate spermatogonia stem cells, and 3) the early embryogenesis of non-human primates. We use mouse, monkey and tree shrew as animal models.
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1. Lnc956-TRIM28-HSP90B1 complex on replication forks promotes CMG helicase retention to ensure stem cell genomic stability and embryogenesis

Replication stress is a major source of endogenous DNA damage. Despite that numerous proteins have been identified on replication forks to modulate fork or replication machinery activities, it remains unexplored whether non-coding RNAs can localize on stalled forks and play critical regulatory roles. Here we identify an uncharacterized lncRNA NONMMUT028956 (Lnc956 for short) predominantly expressed in mouse embryonic stem cells. Lnc956 is accumulated on replication forks to prevent fork collapse and preserve genomic stability, and is essential for mouse embryogenesis. Mechanistically, it drives assembly of the Lnc956-TRIM28-HSP90B1 complex on stalled forks in an inter-dependent manner downstream of ATR signaling. Lnc956-TRIM28-HSP90B1 complex physically associates with MCM2-7 hexamer via TRIM28 and directly regulates the CMG helicase retention on chromatin. The regulation of Lnc956-TRIM28-HSP90B1 on CMG retention is mediated by HSP90B1's chaperoning function. These findings reveal a novel player which actively regulates replisome retention to prevent fork collapse (***Science Advances***, 2023, 9: eadf6277) .

2. Lnc956 regulates mouse embryonic stem cell differentiation in response to DNA damage in a p53-independent pathway

Maintaining genomic stability is crucial for embryonic stem cells (ESCs). ESCs with unrepaired DNA damage are eliminated through differentiation and apoptosis. To date, only tumor suppressor p53 is known to be implicated in this quality control process. Herein, we identified a novel and p53-independent quality control factor lncRNA NONMMUT028956 (Lnc956 for short) in mouse ESCs. Lnc956 is prevalently expressed in ESCs and regulates the differentiation of ESCs after DNA damage. Mechanistically, ATM activation drives m6A methylation of Lnc956, which promotes its interaction with KLF4. Lnc956-KLF4 association sequestrates the KLF4 protein and prevents KLF4's transcriptional regulation on pluripotency. This post-translational mechanism favors the rapid shut down of the regulatory circuitry of pluripotency. Thus, ATM signaling in ESCs can activate two pathways mediated by p53 and Lnc956, respectively, which act together to ensure robust differentiation and apoptosis in response to unrepaired DNA damage (***Science Advances***, 2023, 9: eade9742).

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施　文	Shi, Wen	2021
谢　恒	Xie, Heng	2022

表观遗传与发育调控

焦保卫，博士，研究员，博士生导师。2013 年国家海外高层次引进人才，2014 年云南省高端人才，2019 年云南省产业技术领军人才。兼任中国细胞生物学学会理事，云南省细胞生物学学会第六届理事会理事长。长期从事乳腺发育、乳腺癌、乳腺（癌）干细胞的研究。 研究团队发现 SGCE 在乳腺癌干细胞耐药中的新机制，以及 Rab13 在肿瘤微环境细胞与乳腺癌干细胞（BCSC）的互作过程中的调控作用。目前已经在 *Cell*、*PNAS*、*Nature Communications*、*Advanced Science*、*Cancer Research* 等国际期刊杂志发表论文 30 余篇。

重要成果及产出：

1. Xiyin Li[1], **Lina Zhao[1]**, Ceshi Chen[*], Jianyun Nie[*], **Baowei Jiao[*]**. Can EGFR be a therapeutic target in breast cancer? ***Biochim Biophys Acta Rev Cancer***, 2022, 1877(5): 188789.
2. **Lu Guo[1]**, Hao Ke[1], Honglei Zhang, **Li Zou, Qin Yang, Xuemei Lu, Limin Zhao, Baowei Jiao[*]**. TDP43 promotes stemness of breast cancer stem cells through CD44 variant splicing isoforms. ***Cell Death Dis***, 2022, 13(5): 428.
3. **Wang H**, Xu H, Chen W, Cheng M, **Zou L**, **Yang Q**, Chan CB, Zhu H, Chen C, Nie JY, **Jiao B***. Rab13 sustains breast cancer stem cells by supporting tumor-stroma crosstalk. ***Cancer Research***, 2022, 82(11): 2124-2140.

获奖情况：

云南省自然科学三等奖

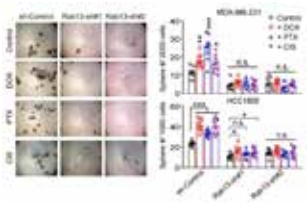
申请专利：

焦保卫，王慧，邹丽，杨钦．一种 Rab13 基因抑制剂及应用．专利申请号：202210304114.X; 申请日期：2022.03.26

1. 发现乳腺癌干细胞与微环境互作的调控因子

肿瘤微环境可以有效的支撑肿瘤干细胞。在特定的微环境下，非肿瘤干细胞可以被重塑为肿瘤干细胞，这导致靶向肿瘤干细胞临床治疗失败。深入了解肿瘤干细胞微环境的形成机制可以帮助改进靶向肿瘤干细胞临床治疗方案。我们发现小分子 GTP 酶 -Rab13 在乳腺癌干细胞中高表达。敲降 Rab13 可以通过减弱肿瘤和微环境之间的交流抑制乳腺癌干细胞干性、肿瘤发生以及化疗耐药性。Rab13 可以控制受体 CXCR1/2 的细胞膜转运，进而使得肿瘤细胞与肿瘤相关巨噬细胞 / 成纤维细胞互作，最终建立一个可以支撑肿瘤干细胞的微环境。甲基巴多索隆可以靶向 Rab13 调控的肿瘤微环境，在体内体外水平抑制乳腺癌干细胞干性。以上发现是肿瘤干细胞调控的新机制，对于靶向乳腺癌肿瘤微环境的治疗策略开发具有重要意义。

【Hui Wang et al. 2022 *Cancer Research*, IF=13.312】



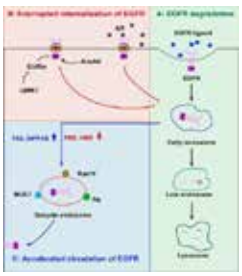
2. TDP43 通过 CD44 变异剪接异构体促进乳腺癌干细胞的干性

选择性剪接 (AS) 是在转录后水平上治疗癌症的一个有前途的临床靶点。我们之前在三阴性乳腺癌 (TNBC) 中发现了一个独特的 AS 基因，它是由剪接调节因子 TAR DNA 结合蛋白 -43 (TDP43) 调控的，因此表明 TDP43 在异质性 TNBC 中起着至关重要的作用。CD44 是乳腺癌干细胞 (BCSCs) 的一种广泛认可的标记物，在乳腺癌的发展过程中被广泛剪接到 CD44 变体 AS 亚型 (CD44v) 中。然而，目前 CD44v 的调控机制还不完全清楚。我们发现剪接因子 SRSF3 与 TDP43 通过 CD44 剪接调控而促进乳腺癌干细胞干性，该发现为乳腺癌中 CD44 的剪接提供新的理解。

【Lu Guo et al. 2022 *Cell Death Dis*, IF=9.685 】

3. 系统综述了乳腺癌中 EGFR 的调控机制

表皮生长因子受体 (EGFR) 在多种肿瘤细胞中高表达，并与肿瘤细胞增殖、转移和肿瘤干细胞干性维持密切相关，人们已经开发出多种靶向 EGFR 的抑制剂，并在肺癌和结直肠癌等取得不错疗效。多种肿瘤细胞中高表达，并与肿瘤细胞增殖、转移和肿瘤干细胞干性维持密切相关，人们已经开发出多种靶向 EGFR 的抑制剂，并在肺癌和结直肠癌等取得不错疗效。本文综述了 EGFR 蛋白在乳腺癌细胞中表达的调控机制，包括 EGFR 突变、扩增、内吞功能障碍、循环加速和降解障碍。【Xiyin Li et al. 2022 *Biochim Biophys Acta Rev Cancer*, IF=11.414】



Epigenetic and Developmental Regulation

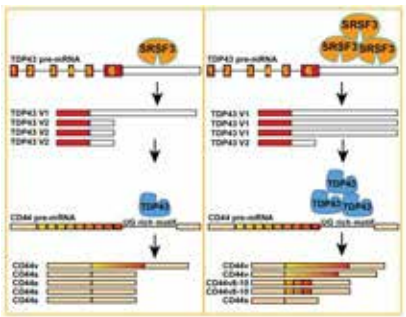
Dr. Baowei Jiao, Principal Investigator, doctoral supervisor. The research team is mainly interested in mammary gland development, breast cancer, normal and breast cancer stem cell. Research team found a novel mechanism of SGCE in breast cancer stem cell chemoresistance and the role of Rab13 in Sustaining Breast Cancer Stem Cells, over 30 papers have been published in international journals, such as *Cell, PNAS, Nature Communications, Advanced Science, Cancer Research*.
Email：jiaobaowei@mail.kiz.ac.cn

1. Rab13 Sustains Breast Cancer Stem Cells by Supporting Tumor–Stroma Cross-talk

Cancer stem cells (CSC) are supported by the tumor microenvironment, and non-CSCs can regain CSC phenotypes in certain niches, leading to limited clinical benefits of CSC-targeted therapy. A better understanding of the mechanisms governing the orchestration of the CSC niche could help improve the therapeutic targeting of CSCs. Here, we report that Rab13, a small GTPase, is highly expressed in breast CSCs (BCSC). Rab13 depletion suppressed breast cancer cell stemness, tumorigenesis, and chemoresistance by reducing tumor-stroma cross-talk. Accordingly, Rab13 controlled the membrane translocation of C-X-C chemokine receptor type 1/2 (CXCR1/2), allowing tumor cells to interact with tumor-associated macrophages and cancer-associated fibroblasts to establish a supportive BCSC niche. Targeting the Rab13-mediated BCSC niche with bardoxolone-methyl (C-28 methyl ester of 2-cyano-3, 12-dioxoolen-1, 9-dien-28-oic acid; CDDO-Me) prevented BCSC stemness in vitro and in vivo. These findings highlight the novel regulatory mechanism of Rab13 in BCSC, with important implications for the development of therapeutic strategies for disrupting the BCSC niche. 【Hui Wang et al. 2022 *Cancer Research*, IF=13.312 】

2. TDP43 promotes stemness of breast cancer stem cells through CD44 variant splicing isoforms

Alternative splicing (AS) is a promising clinical target for cancer treatment at the post-transcriptional level. We previously identified a unique AS profile in triple-negative breast cancer (TNBC), which is regulated by the splicing regulator TAR DNA-binding protein-43 (TDP43), thus indicating the crucial role of TDP43 in heterogeneous TNBC. Cluster of differentiation 44 (CD44), a widely recognized marker for breast cancer stem cells (BCSCs), is extensively spliced into CD44 variant AS isoforms (CD44v) during the development of breast cancer. At present, however, the regulatory mechanism of CD44v is not fully understood. In the current study, we found that loss of TDP43 inhibits BCSC stemness by reducing the abundance of CD44v. In addition, serine-arginine-rich splicing factor 3 (SRSF3), another splicing factor and partner of TDP43, acts as an upstream regulator of TDP43 to maintain CD44v isoforms and thereafter BCSC stemness. Mechanistically, SRSF3 stabilizes the mRNA of TDP43 by inhibiting nonsense-mediated decay (NMD). These findings illustrate the important role of complicated regulatory networks formedby splicing factors in TNBC progression, thus providing potential therapeutic targets from an AS perspective. 【Lu Guo et al. 2022 *Cell Death Dis*, IF=9.685 】



3. Can EGFR be a therapeutic target in breast cancer?

Epidermal growth factor receptor (EGFR) is highly expressed in certain cancer types and is involved in regulating the biological characteristics of cancer progression, including proliferation, metastasis, and drug resistance. Various medicines targeting EGFR have been developed and approved for several cancer types, such as lung and colon cancer. In this review, we summarize the regulatory mechanisms underlying EGFR protein expression in breast cancer cells, including EGFR mutations, amplification, endocytic dysfunction, recycling acceleration, and degradation disorders. We also discuss potential therapeutic strategies that act directly or indirectly on EGFR, including reducing EGFR protein expression, treating the target protein to mediate precise clearance, and inhibiting non-EGFR signaling pathways. This review should provide new therapeutic perspectives for breast cancer patients with high EGFR expression. 【Xiyin Li et al. 2022 *Biochim Biophys Acta Rev Cancer*, IF=11.414 】

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灵长类进化遗传与发育

吴东东，博士，研究员，PI，昆明动物研究所青年科学家小组组长。2011年1月于中科院昆明动物研究所获得博士学位，并破格晋升为副研究员，2013年获得硕士生导师资格，2016年获得博士生导师资格。2012年获得中国科学院百篇优秀博士论文，2013年获得云南省自然科学奖特等奖（个人排名第三），2014年获得中科院卢嘉锡青年人才奖，2015年获得国家自然科学奖二等奖（个人排名第三），2017年度获中科院青促会优秀会员，2018年获国家自然科学基金优青项目，2020年度获云南省自然科学奖一等奖（个人排名第二）。以第一作者或共同通讯作者在 ***Nat Genet, Nat Ecol Evol, Cell Res, Genome Biol, Mol Biol Evol***，***PNAS*** 等杂志发表论文40余篇。

重要成果及产出：

1. **Bao-Lin Zhang**#, Wu Chen#, Zefu Wang#, Wei Pang, Meng-Ting Luo, Sheng Wang, Yong Shao, Wen-Qiang He, Yuan Deng, Long Zhou, Jiawei Chen, Min-Min Yang, Yajiang Wu, Lu Wang, Hugo Fernández-Bellon, Sandra Molloy, Hélène Meunier, Fanélie Wanert, Lukas Kuderna, Tomas MarquesBonet, Christian Roos, Xiao-Guang Qi, Ming Li, Zhijin Liu, Mikkel Heide Schierup, David N. Cooper, Jianquan Liu, Yong-Tang Zheng*, Guojie Zhang*, **Dong-Dong Wu***. Comparative genomics reveals the hybrid origin of a macaque group. ***Science Advances***, 2022.
2. **Ming-Li Li**#, Sheng Wang#, Penghui Xu#, Hang-Yu Tian#, Mixue Bai, Ya-Ping Zhang, Yong Shao, Zi-Jun Xiong, Xiao-Guang Qi, David N. Cooper, Guojie Zhang, He Helen Zhu, Dong-Dong Wu*. Functional genomics analysis reveals the evolutionary adaptation and demographic history of pygmy lorises. ***PNAS***, 2022, 119(40): e2123030119.
3. **Yun-Mei Wang**#, Ling-Qun Ye#, Ming-Shan Wang#, Jin-Jin Zhang, Saber Khederzadeh, David M Irwin, XiaoDie Ren, Ya-Ping Zhang*, Dong-Dong Wu*. Unveiling the functional and evolutionary landscape of RNA editing in chicken using genomics and transcriptomics. ***Zoological Research***. 2022, 43(6): 1011-1022.
4. **Yong Shao***#, Xiao-Bo Wang#, Mei-Ling Zhang#, Yan Liu#, Sheng Wang, Bao-Lin Zhang,Min-Min Yang, Ming-Hai Yang,Ting Jia, Tian-Chun Pu, Yan Lu, He Liu, Zhe Xu, Bo Li, Ning Liu, Violet Magoma Onsongo, **Dong-Dong Wu**, Cheng-Lin Zhang*, Jue Ruan*, Yan Li*, Long-read genome sequencing provides molecular insights into scavenging and societal complexity in spotted hyena Crocuta crocuta, ***Mol Biology &Evolution***, doi:10.1093/molbev/msac011.

1. 揭示蜂猴适应性进化

蜂猴是一类濒危的灵长类动物，在进化过程中表现出较多不寻常的生理和行为特征，如低代谢率、行动缓慢和夜行性等。蜂猴为杂食动物，主要以野果为食，也能以有毒昆虫和树胶为食物。为探究蜂猴适应性进化的遗传机制，我们组装了倭蜂猴染色体水平的基因组序列，对50只倭蜂猴和6只孟加拉蜂猴进行全基因组重测序。研究发现，与解毒有关的 *GSTA* 基因家族在蜂猴肝脏中展现出特异性高的表达；*PITRM1* 基因在蜂猴和考拉之间表现出趋同进化；蜂猴的PITRM1酶活性降低，科学家认为，这可能是导致倭蜂猴低代谢率的原因。此外，科研人员还在倭蜂猴中鉴定到，与肌肉发育有关的正选择基因 *MYOF*，可能与其行动缓慢相关。相比较其他物种，倭蜂猴中正选择基因 *PER2* 与昼夜节律核心蛋白CRY的结合能力更弱，这可能与该物种不寻常的昼夜节律有关。研究显示，生活在同一地区的倭蜂猴和孟加拉蜂猴在过去100万年里，表现出逆相关关系，这意味着两个物种分化后存在物种间的竞争关系。这一研究成果发表在《美国国家科学院院刊》（*PNAS*）上，是当期的封面文章。

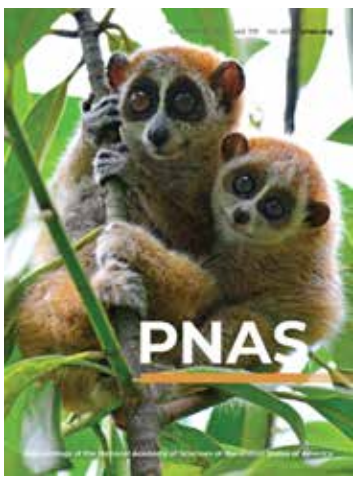

图1. 蜂猴适应性进化

2. 揭示猕猴属一古老杂交成种事件

同倍体杂交物种形成是物种形成的一个重要形式，但在整个哺乳动物类群中比较罕见。在本研究中，研究人员通过对12个猕猴物种的基因组进行分析，发现一古老的同倍体杂交物种形成事件，即食蟹猴种组是由狮尾猴种组和斯里兰卡种组在大约3.45-3.56百万年前杂交形成，杂交重组使得食蟹猴种组产生了新的生殖特征，如生殖器形态、性皮特征等，它们刚好介于两个亲本之间，并且在遗传上，与生殖相关的基因存在明显的重组痕迹并受正选择作用。同时，研究发现X染色体和基因组的低重组区在抵抗与亲本的基因交流方面发挥了重要功能，进而有利于维持杂交后代物种的完整性。另外，研究表明狮尾猴与北平顶猴有最近的亲缘关系，而非传统分类上认为的南、北平顶猴的关系最近，功能实验表明狮尾猴也可感染HIV病毒，表明狮尾猴是继南、北平顶猴之后另一可感染HIV病毒的旧大陆猴。本研究通过基因组分析不仅揭示了猕猴属全新的进化关系，报道了灵长类一古老的杂交事件，也揭示了杂交物种的形成和维持机制，相关成果发表在《Science Advances》上。

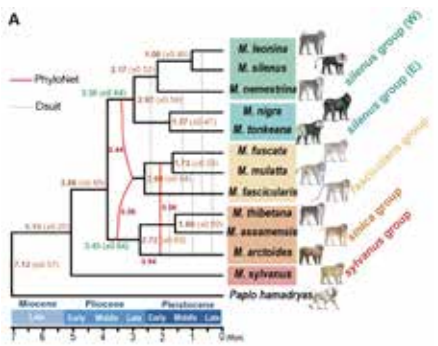

图2. 猕猴属各物种进化关系和基因交流示意图

Primate Evolutionary Genetics and Development

Dr. Dong-Dong Wu, Principal Investigator.

Dong-Dong Wu obtained his B.S at the Fudan University in 2006, and received his Ph.D from Kunming institute of Zoology, Chinese Academy of Sciences in 2011. He performed studies of artificial selection on domestic animals, particularly high altitude adaptation of domestic animals in Tibet. He has published more than 40 research papers in *Nat Genet, Cell Res, Genome Biol, Mol Biol Evol* etc, as first author or co-corresponding author.

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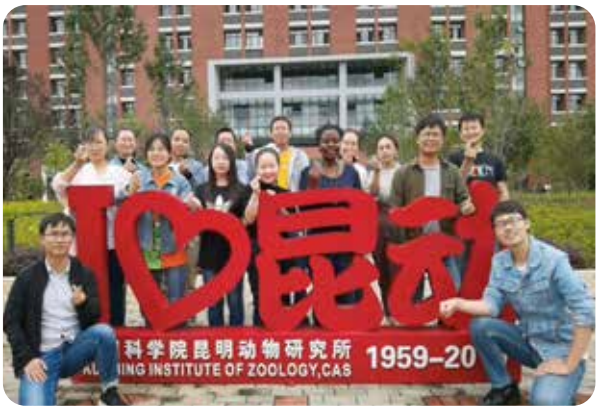

1. Functional genomics analysis reveals the evolutionary adaptation and demographic history of pygmy lorises

Lorises are a group of globally threatened strepsirrhine primates that exhibit many unusual physiological and behavioral features, including a low metabolic rate, slow movement, and hibernation. Here, we assembled a chromosome-level genome sequence of the pygmy loris (*Xanthonycticebus pygmaeus*) and resequenced whole genomes from 50 pygmy lorises and 6 Bengal slow lorises (*Nycticebus bengalensis*). We found that many gene families involved in detoxification have been specifically expanded in the pygmy loris, including the GSTA gene family, with many newly derived copies functioning specifically in the liver. We detected many genes displaying evolutionary convergence between pygmy loris and koala, including PITRM1. Significant decreases in PITRM1 enzymatic activity in these two species may have contributed to their characteristic low rate of metabolism. We also detected many evolutionarily convergent genes and positively selected genes in the pygmy loris that are involved in muscle development. Functional assays demonstrated the decreased ability of one positively selected gene, MYOF, to up-regulate the fast-type muscle fiber, consistent with the lower proportion of fast-twitch muscle fibers in the pygmy loris. The protein product of another positively selected gene in the pygmy loris, PER2, exhibited weaker binding to the key circadian core protein CRY, a finding that may be related to this species' unusual circadian rhythm. Finally, population genomics analysis revealed that these two extant loris species, which coexist in the same habitat, have exhibited an inverse relationship in terms of their demography over the past 1 million years, implying strong interspecies competition after speciation.

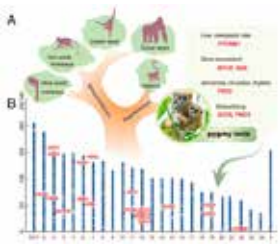

Fig 3. Study schematic

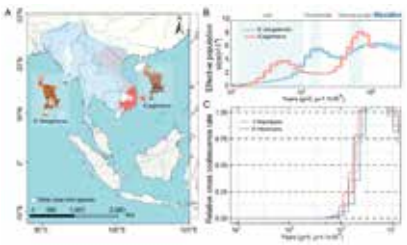

Fig 4. Evolutionary history of lorises

2. Comparative genomics reveals the hybrid origin of a macaque group

Although species can arise through hybridization, compelling evidence for hybrid speciation has been reported only rarely in animals. Here we present phylogenomic analyses on genomes from 12 macaque species and show that the fascicularis group originated from an ancient hybridization between the sinica and silenus groups ~3.45-3.56 million years ago. The X-chromosomes and low-recombination regions exhibited equal contributions from each parental lineage suggesting they were less affected by subsequent backcrossing and hence could have played an important role in maintaining hybrid integrity. We identified many reproduction-associated genes that could have contributed to the development of the mixed sexual phenotypes characteristic of the fascicularis group. The phylogeny within the silenus group was also resolved and functional experimentation confirmed that all extant Western silenus species are susceptible to HIV-1 infection. Our study provides novel insights into macaque evolution and reveals a hybrid speciation event that has occurred only very rarely in primates.

Fig 5. The genetic basis underlying the mixture of phenotypes in the fascicularis group macaques

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大脑进化发育与生理功能

盛能印，博士，研究员，博士生导师。中国科学院“率先行动”青年人才、云南省“云岭高层次人才”获得者。长期从事神经科学相关研究工作，包括中枢神经系统发育形成和神经突触信息传递作用分子机制。目前已在国际学术期刊发表研究论文 20 余篇，其中以第一作者或通讯作者（含共同）在 *Nature Communications*、*Science Advances*、*PNAS* 等期刊发表论文 10 余篇。目前实验室以小鼠、蜜袋鼯和貂为动物模型，主要研究：（1）大脑胼胝体结构的进化发育和功能调控；（2）大脑皮层沟回结构的进化发育与功能调控；（2）神经突触进化发育遗传机制与神经精神疾病的内在联系及分子机制。

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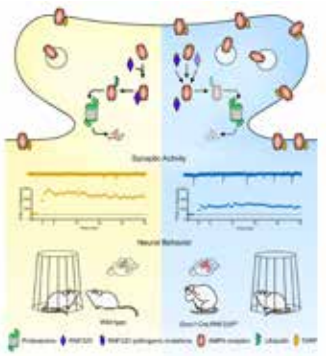
重要成果及产出：

1. Ma P[#], **Wan LP**[#], Li Y[#], He CH[#], Song NN, **Zhao S**, Wang H, Ding YQ[*], Mao B[*], **Sheng N**[*]. RNF220 is an E3 ubiquitin ligase for AMPA receptors to regulate synaptic transmission. ***Science Advances***, 2022, 8(39): eabq4736.
2. Li S[#], Ma C[#], Li Y[#], Chen R[#], Liu Y[#], **Wan LP**[#], Xiong Q, Wang C, Huo Y, Dang X, Yang Y, Lv L, Chen X, **Sheng N**[*], Li W[*], Luo XJ[*]. The schizophrenia-associated missense variant rs13107325 regulates dendritic spine density. ***Translational Psychiatry***, 2022, 12(1): 361.
3. Sun SY, Li XW, Cao R, Zhao Y, **Sheng N**[*], Tang AH[*]. Correlative Assembly of Subsynaptic Nanoscale Organizations During Development. ***Frontiers in Synaptic Neuroscience*** , 2022, 14: 748184.
4. Li QQ[#], Chen J[#], Hu P[#], Jia M, Sun JH, Feng HY, Qiao FC, Zang YY, Shi YY, Chen G, **Sheng N**, Xu Y, Yang JJ[*], Xu Z[*], Shi YS[*]. KKK879-881 motif is an ER-retention signal in GluN2A-NMDA receptor. ***Molecular Psychiatry***, 2022, 27(8): 3115.
5. Peng SX[#], Pei J[#], Rinaldi B[#], Chen J[#], Ge YH, Jia M, Wang J, Delahaye-Duriez A, Sun JH, Zang YY, Shi YY, Zhang N, Gao X, Milani D, Xu X, **Sheng N**, Gerard B, Zhang C, Bayat A, Liu N[*], Yang JJ[*], Shi YS[*]. Dysfunction of AMPA receptor GluA3 is associated with aggressive behavior in human. ***Molecular Psychiatry***, 2022, 27(10): 4092-4102.
6. Li QQ[#], Chen J[#], Hu P[#], Jia M, Sun JH, Feng HY, Qiao FC, Zang YY, Shi YY, Chen G, **Sheng N**, Xu Y, Yang JJ[*], Xu Z[*], Shi YS[*]. Enhancing GluN2A-type NMDA receptors impairs long-term synaptic plasticity and learning and memory. ***Molecular Psychiatry***, 2022, 27(8): 3468-3478.

1. 突触分子蛋白稳定性调控与大脑生理功能

泛素化 - 溶酶体降解系统介导的突触分子蛋白稳定性在突触功能调控中发挥重要作用，其 E3 泛素连接酶突变导致的该调控紊乱被认为是神经精神疾病的重要发病因素。携带 RNF220 突变的病人会表现出智力障碍等症状，利用前脑敲除小鼠动物模型，我们发现 RNF220 是兴奋性突触关键分子 AMPA 受体的特异性 E3 泛素连接酶，通过调控 AMPA 受体的蛋白稳定性和突触转运，参与调控突触传递活性和可塑性 LTP 的产生。RNF220 前脑缺失会造成小鼠多种神经行为活动异常，包括认知能力、空间学习和社交记忆。更为重要的是， RNF220 分子的神经疾病相关突变则导致其调控 AMPAR 泛素化和降解能力下降，从而影响其调控兴奋性突触活性的能力（Ma et al.，*Science Advances*，2022）。该研究阐明了 AMPA 受体蛋白稳定性调控在突触活性和大脑生理功能调控中的作用机制，有助于进一步深入研究突触分子蛋白稳定性调控在大脑生理和病理过程中的作用机理。



2. 大脑胼胝体结构的进化发育

在动物演化过程中，胼胝体是胎盘哺乳动物所特有的创新性性状，是大脑半球对侧 2-3 层神经元相互连接构成的神经纤维束，是实现语言和高级认知等生理功能所必须的，而在人类胼胝体缺失或发育异常则与多种神经精神疾病发生密切相关。为研究其进化起源的遗传机制，我们以 4 种非胎盘类动物为外群，整合比较分析 116 种胎盘类动物基因组，发现 32 万条胎盘类所特有的保守保守非编码元件（Placental Specific Conserved Noncoding Elements，PSCNE），同时整合已发表的小鼠胼胝体投射神经元 CPN 发育形成时期（E15.5 天）scRNA-seq 和 scATAC-seq 组学数据，利用生物信息学分析构建其分子调控网络，筛选出在 CPN 命运决定期开放的、有潜在活性的 PSCNE 约 2.1 万条。在此基础上，我们结合小鼠胚胎宫内电转和 MPRA 等技术手段，研究这些 PSCNE 在 CPN 发育过程中的转录调控活性，进一步利用 CRISPR 表观调控技术，增强或抑制其活性，研究对胼胝体发育的影响，以及调控的下游基因和作用机制。

3. 神经突触环路进化和功能调控机制

哺乳动物大脑的形态结构和突触环路的演化，是实现物种表型和功能多样性的重要物质基础。目前研究发现，诸多灵长类 / 人类特有基因在皮层沟回等形态结构进化调控中发挥重要作用，但对于其在神经突触进化调控中的作用机制知之甚少。嗜乳脂蛋白 Butyrophilin 家族属于免疫球蛋白超家族，我们通过跨物种整合基因组比较分析，阐明了其家族成员的演化历史，发现 BTN2A1、BTN3A1、BTN3A2 为灵长类所特有，而 BTN3A3 在胎盘哺乳类中经历起源、丢失和灵长类再起源的复杂过程，而它们的 mRNA 在人类大脑中都具有一定的表达。当将它们异位表达于大鼠海马 CA1 锥体神经元中，则分别影响兴奋性或抑制性突触传递活性。我们构建了 BTN3A2 前脑特异表达的小鼠动物模型，神经行为学检测发现，该小鼠表现出认知能力下降、社交和空间记忆能力受损和焦虑水平上升等症状；BTN3A2 分子在兴奋性突触后有表达定位，且通过抑制突触前神经递质释放，降低兴奋性突触传递活性，且使得突触可塑性 LTP 产生能力丧失。我们将深入研究其中的分子机制，以从分子 - 突触 - 环路 - 整体动物多个层次，系统解析该灵长类特有基因在神经突触进化和功能调控中的作用。

Brain Evolutionary Development and Physiological Function

Prof. Nengyin Sheng, Principal Investigator, joined in Kunming Institute of Zoology, Chinese Academy of Sciences in 2017. The research of Sheng's lab focuses on central nervous system (CNS) and will study the following topics using mice, mink and ***Petaurus notatus*** as model systems: (1) The mechanism and function of corpus callosum evolutionary development; (2) The mechanism and function of evolution and development of cortical gyrification; (3) The genetic bases underlying evolution and development of synapse, and its internal relationship with neuropsychiatric disorders.

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1. Protein stability regulation of synaptic molecules and brain physiological functions

The protein stability regulation of synaptic molecules mediated by the ubiquitination-lysosomal degradation system plays an important role for synaptic physiological functions, and its dysregulation caused by the mutation of its E3 ubiquitin ligase is considered to be an important pathogenic factor of neuropsychiatric diseases. Patients carrying RNF220 mutations show symptoms such as intellectual disability. Using the forebrain knockout mouse animal model, we found that RNF220 is a specific E3 ubiquitin ligase for AMPA receptors, a key molecule for excitatory synaptic transmission. Through regulating the protein stability and synaptic trafficking of AMPA receptors, RNF220 is involved in synaptic basal transmission and synaptic plastic of LTP. Depletion of RNF220 in mice forebrain leads to several neurobehavioral abnormalities, including cognitive ability, spatial learning, and social memory. More importantly, neurological disease-associated mutations of RNF220 decrease its ability to regulate AMPAR ubiquitination and degradation, thereby affecting its ability to regulate excitatory synaptic activity (Ma et al., Science Advances, 2022). This study clarified the mechanism of AMPA receptor protein stability maintenance in synaptic activity regulation and brain physiological functions. And it would be helpful to further study the internal relationship between the protein stability regulation of synaptic molecules and brain physiological functions, as well as the related pathological processes.

2. The evolutionary development of corpus callosum

In the process of animal evolution, the corpus callosum is a unique innovative trait of placental mammals. It is a nerve fiber bundle connecting the contralateral cerebral hemisphere, especially the 2-3 layers excitatory projection neurons. It is known to be necessary for executing brain physiological functions such as language and advanced cognition, and its absence or abnormal development in humans is closely related to the occurrence of various neuropsychiatric diseases. In order to study the genetic mechanism underlying the evolutionary origin of corpus callosum, using 4 non-placental animals as outgroups, we integrated the genomes of 116 placental animals for comparatively analyses. We have identified 320,000 placental-specific conserved non-coding elements (Placental Specific Conserved Noncoding Elements, PSCNE). Then combining the published scRNA-seq and scATAC-seq omics data of the developmental formation stage of mouse corpus callosum projection neuron (CPN) on E15.5 days, we used bioinformatics analyses to construct its molecular regulatory network and have found that there are around 21,000 opening and potential active PSCNEs during the fate-determining stage of CPN. On these bases, we will combine mouse embryo in utero electroporation and MPRA to study the transcriptional regulation activity of these PSCNEs during the development of CPN, and further use CRISPR epigenetic regulation technology to enhance or inhibit their activity, thereby study the PSCNEs function and mechanism during corpus callosum development.

3. The evolution of neural synaptic circuit and brain funciton

The evolution of brain morphological structure and neural synaptic circuit are important material bases for mammalian phenotypic and functional diversity. Currently, it has found that many primate/human-specific genes play important roles in the evolution of cortex morphological structures including cortical folding, however, little is known about their regulatory function for synaptic circuit evolution. The Butyrophilin family belongs to the immunoglobulin superfamily, and we have clarified the evolution history of its family members through comparison analyses of mammalian genomes, and have found that BTN2A1, BTN3A1, and BTN3A2 are unique for primates, while BTN3A3 is specific for placental mammals but undergoes a complex evolutionary process. Moreover, their mRNAs are expressed in the human brain. When ectopically expressed in rat hippocampal CA1 pyramidal neurons, they affect excitatory or inhibitory synaptic transmission activity, respectively. We have constructed a mouse animal model to specifically express BTN3A2 in forebrain. Neurobehavioral tests have found that the mice showed symptoms such as cognitive decline, social and spatial memory impairment, and increased anxiety levels. BTN3A2 is expressed and localized at the postsynapse, and by inhibiting the release of presynaptic neurotransmitters, it reduces the activity of excitatory synaptic transmission and impairs the capability of synaptic plastic LTP. We will study the molecular mechanism in depth to systematically analyze the role of this primate-specific gene in the evolution and functional regulation of synapses from the levels of molecular-synaptic-circuit-whole animal.

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进化发育生物学

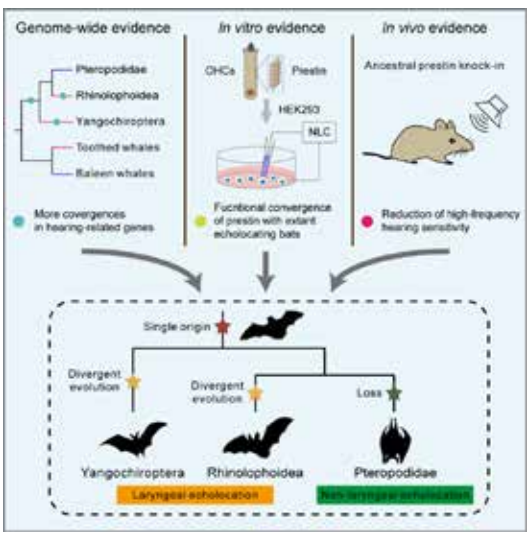
刘　振，博士，研究员，博士生导师，国家优秀青年基金获得者，省万人计划青年拔尖人才。主要以非模式动物为研究对象，结合比较基因组学、进化遗传学和功能基因组学的理论和方法，从进化发育生物学的角度揭示动物适应性复杂性状的分子遗传机制。目前以第一或通讯作者在 *Science, Science Advances, PNAS, Current Biology, Molecular Biology and Evolution* 等国际著名期刊发表研究论文二十余篇。

重要成果及产出：

1. **Liu Z[1], Chen P[1], Xu DM[1], Qi FY[1], Guo YT, Liu Q, Bai J, Zhou X, Shi P*** (2022) Molecular convergence and transgenic evidence suggest a single origin of laryngeal echolocation in bats. ***iScience***, 25(4): 104114.
2. **Chen P[1], Hao JJ[1], Li MW, Bai J, Guo YT, Liu Z*, Shi P*** (2022) Integrative functional transcriptomic analyses implicate shared molecular circuits. ***Frontiers in Cellular Neuroscience***. 16: 857344.
3. **Hao JJ, Hao WL, Liu Z*, Shi P*** (2022) The toggle switch model for gene expression change during the prenatal-to-postnatal transition in mammals. ***Molecular Biology and Evolution***, 39(3): msac036.

分子和转基因证据支持了回声定位在蝙蝠中一次起源的假说

一直以来，对动物适应性复杂性状起源问题的研究很大程度上依赖于化石证据，但由于化石形成和发现的偶然性，化石形态数据的有限性等因素的限制，在大部分情况下很难对动物适应性复杂性状起源的时间和演化路径做出明确的判断，其中一个典型案例是回声定位何时以及如何在蝙蝠中起源和演化的。有些化石证据支持回声定位起源于蝙蝠共同祖先（“一次起源”假说），而有些化石证据则支持回声定位独立起源于不同的回声定位蝙蝠支系（“多次起源”假说）。通过对蝙蝠祖先支（LCAB）、不具备回声定位能力的旧大陆果蝠祖先支（LCAP）等不同的祖先支系与具有回声定位能力的齿鲸进行分子趋同进化分析，发现与 LCAP 不同，听觉相关基因在 LCAB 与齿鲸之间具有显著的趋同演化信号。同时，通过重构 LCAB 和 LCAP 的回声定位相关基因 prestin，发现与 LCAP 相比，LCAB 的 prestin 功能与现生回声定位蝙蝠更相似。更重要的是，与 LCAB-prestin 基因敲入小鼠相比，LCAP-prestin 基因敲入小鼠的高频听力明显下降。总之，该研究综合分子趋同分析、细胞功能实验、转基因小鼠听觉能力检测等多方面的证据，表明回声定位起源于蝙蝠共同祖先，并且在现生回声定位蝙蝠类群中经历了趋异演化。本研究不仅支持了回声定位在蝙蝠类群中“一次起源”的假说，为进一步揭示回声定位的分子遗传机制奠定了重要的基础，而且打破了仅通过化石记录推测适应性复杂性状起源和演化的局限性。



Evolutionary Developmental Biology

Prof. Zhen Liu, Principal Investigator. Evolutionary developmental biology is like a bridge to mediate the evolutionary biology and developmental biology for understanding the genetic basis of phenotypic changes macroevolutionarily. Using bats as a research model, we focus on the following major questions: (1) what are the roles of molecular variations on the developmental mechanisms for the origin and elaboration of adaptive phenotypes in evolutionary process? (2) what are the relative roles of chance and necessity in evolution for the developmental mechanisms of adaptive phenotypes?
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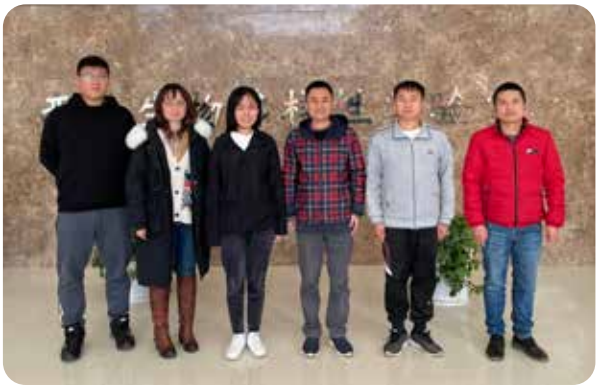
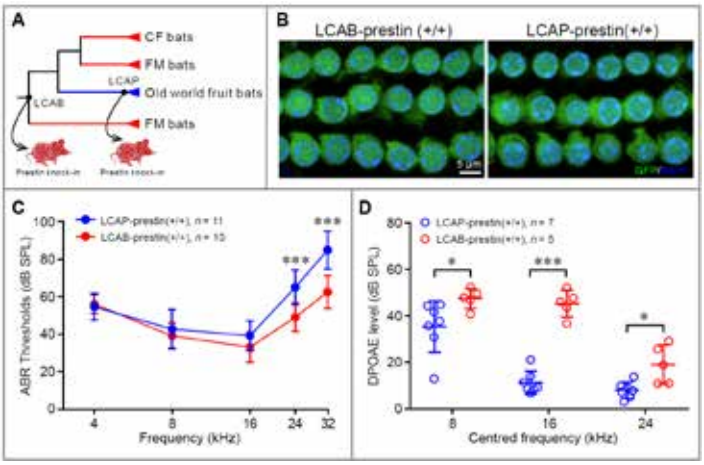


Molecular convergence and transgenic evidence suggest a single origin of laryngeal echolocation in bats

The laryngeal echolocation is regarded as one of the conspicuous traits that play major roles in flourishing bats. Whether the laryngeal echolocation in bats originated once, however, is still controversial. We address this question by performing molecular convergence analyses between ancestral branches of bats and toothed whales. Compared with controls, the molecular convergences were enriched in hearing-related genes for the last common ancestor of bats (LCAB) and extant echolocating bats, but not for the LCA of Old World fruit bats (LCAP). And the convergent hearing gene prestin of the LCAB and the extant echolocating bats functionally converged. More importantly, the high-frequency hearing of the LCAP-prestin knock-in mice decreased with lower cochlear outer hair cell function compared with the LCAB-prestin knock-in mice. Together, our findings provide multiple lines of evidence suggesting a single origin of laryngeal echolocation in the LCAB and the subsequent loss in the LCAP.



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刘明港 Ming-Gang Liu 2022

昆明野生动物细胞库

昆明野生动物细胞库（简称昆明细胞库）成立于 1986 年，是以保存动物的遗传资源和遗传多样性为主要目的的细胞库。现已保存有 380 种动物的细胞系 2625 株 20000 余份。 大多数为哺乳动物的细胞系，其中包括 61 种国家级重点保护动物的细胞系。目前，昆明细胞库是国家生物医学实验细胞资源库、中国科学院生物遗传资源库、中国西南野生生物种质库的成员单位之一，也是遗传资源与进化国家重点实验室的成员单位之一。

重要成果及产出：

Wang Jinhuan, **Su Weiting**, **Hu Yi**, Li Shengbin, O'Brien PCM, Ferguson-Smith MA, Yang Fengtang*, **Nie Wenhui***. Comparative chromosome maps between the stone curlew and three ciconiiform species (the grey heron, little egret and crested ibis). ***BMC Ecology and Evolution***, 2022, 22(1): 23.

1. 细胞资源的收集和保藏

2022 年度，昆明野生动物细胞库利用从野外采集以及从其他途径获得的动物材料，共新建各类动物细胞系 197 株，其中包括青海湖裸鲤、黑颈鹤、少齿鼢鼠、侯氏猬、罗氏鼢鼠、北极狐、毛翼蝠等 13 个新物种的野生动物细胞系 86 株，建立家养动物、人和实验动物的正常细胞系和肿瘤细胞系 111 株。复苏和扩增各类动物细胞系 455 株次。

2. 对外服务

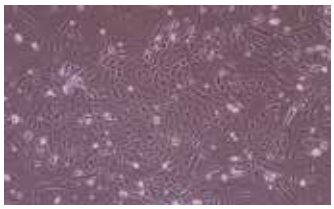
在 2022 年度，昆明野生动物细胞库为全国各地的 244 家单位，包括高等院校 108 家、科研院所 26 家、企业 110 家的研究人员提供各类野生和家养动物细胞系、人及常见实验动物的各类正常组织来源的细胞系、肿瘤细胞系及培养液共计 915 株次。除提供细胞服务外，昆明细胞库还提供了核型分析和 STR 检测等技术服务 168 株次，以及通过电话、邮件及现场指导等方式提供大量的细胞培养技术咨询。

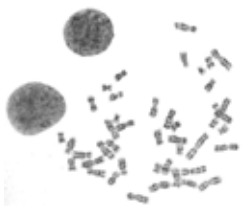
3. 小鼠细胞系分子鉴定方法的建立

小鼠细胞系是研究人类基因和疾病最常用的模型系统。已有的研究表明小鼠细胞系也和人源细胞一样存在着错误鉴定的情况。与人源细胞系不同，小鼠细胞系大多来源于数量有限的几个杂交品系，其基因位点的纯合度更高，使得小鼠细胞系身份鉴定更复杂和困难。现有的方法都有不足之处，有必要寻找新的方法进行小鼠细胞系的身份鉴定。昆明野生动物细胞库应用线粒体 DNA 突变位点作为分子标记开展了小鼠细胞系的身份鉴定，获得了常用小鼠细胞系的线粒体 DNA 序列及其变异位点，并建立了小鼠细胞系线粒体 DNA 变异位点比对数据库。这个方法的建立为开展小鼠细胞系质量控制检测提供了新的手段。

4. 猕猴皮肤鳞癌细胞系的建立

已成功建系的肿瘤细胞系大多来源于人类、大鼠和 小鼠的各类肿瘤组织，而来源于非人灵长类动物的肿瘤细胞系还未见报道。2022 年，昆明野生动物细胞库成功建立了一株猕猴皮肤鳞癌细胞系。这是第一株成功建系的非人灵长类动物的肿瘤细胞系。目前，这株猕猴皮肤鳞癌细胞系已在体外传代 20 余代次。核型分析结果表明，这株猕猴皮肤鳞癌细胞系的染色体数目为 43 条，而且有多条染色体的结构发生了变化。其他相关检测工作还在进行中。





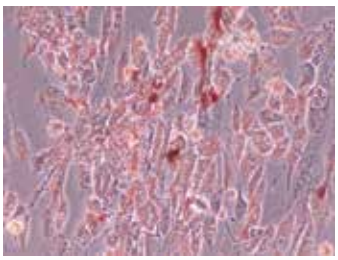
猕猴皮肤鳞癌细胞（左）及其中期染色体（右）

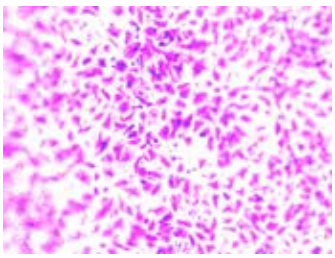
Kunming Wild Animal Cell Bank

In order to protect animal genetic resource and genetic diversity, Kunming wild animal cell bank was established in Kunming Institute of Zoology, Chinese Academy of Science in 1986. Up to now 2625 cell lines from 380 species have been preserved in our cell bank. Most cell lines are derived from mammals. Among the species, 61 species are national protected animals in China. Now it is one branch of National Biomedical Experimental Cell Resource Bank for Sci-Tech, Biological Genetic Resource Bank of CAS, the Germplasm Bank of Wild Species, and State Key Laboratory of Genetic Resources and Evolution.

1. The collection and preservation of cell lines

In 2022, 197 cell lines from various wild animals, domestic animals and humans had been established and frozen. Among these cell lines, 86 cell lines were derived from wild animals including 13 new species , such as Przewalski's naked carp , Black-necked Crane , Rothschild's Zokor , Hugh's hedgehog, and Arctic fox etc.; 111 normal cell lines and tumor cell lines of domestic animals, experimental animals and humans were established. Four hundred and fifty-five of frozen-stored cell lines were also resuscitated and subcultured.





2. Cell lines service and technical service

In 2022, Kunming Cell Bank have provided cell services 915 times, such as wild and domestic animal cell lines, tumor cell lines and culture medium for researchers from 244 units across the country, including 108 universities, 26 research institutes and 110 enterprises. In addition to providing cell services, we also have provided technical services like karyotype analysis and STR test for 168 times, as well as a large number of cell culture technical advices through telephone, email and on-site guidance.

3. A molecular method for mouse cell line identification

Mouse cell lines are widely used in studying human genes and diseases. It has been shown that mouse cell lines are subject to misidentification as well as human-derived cell lines. Unlike human-derived cell lines, mouse cell lines are mostly derived from a limited number of inbred strains with a higher degree of gene site purity, making the identification of mouse cell lines more complex and difficult. It is necessary to find a new method for the identification of mouse cell lines. Mitochondrial DNA mutation sites were used as molecular markers to identify mouse cell lines in Kunming cell Bank. Mitochondrial DNA sequence and variation sites of commonly used mouse cell lines were obtained, and a comparison database of mitochondrial DNA variation sites of mouse cell lines was established. The establishment of this method provides a new tool for the quality control of mouse cell lines.

4. Establishing a skin squamous carcinoma cell line from Rhesus macaque

Most of the tumor cell lines that have been successfully constructed are derived from tumor tissues of human, rat and mouse, while the tumor cell lines from non-human primates have not been reported. In 2022, a macaque squamous carcinoma cell line was successfully established in the Kunming cell Bank. This is the first tumor cell line from a non-human primate. At present, this macaque squamous carcinoma cell line has been subcultured for more than 20 generations in vitro. Karyotype analysis showed that the number of chromosomes in this macaque squamous cell line was 43, and the structure of several chromosomes had changed. Other related tests are still in progress.

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重要在研项目

序号	项目名称	项目来源	项目类别	负责人	执行期	总经费（万元）	参与类型
1	第二次青藏高原综合科学考察研究任务五（生物多样性保护与可持续利用）	科技部	科技基础资源调查专项	施　鹏	2019-2024	18993	主持
2	社交障碍的神经环路机制与干预研究	科技部	科技创新 2030 重大项目	张亚平	2021-2026	4000	主持
3	“猕猴介观神经联接图谱”项目课题二：《猕猴全脑空间转录组图谱绘制和细胞类型鉴定》	科技部	科技创新 2030 重大项目	罗　鑫	2021-2026	1004.3	参与
4	中国健康长寿人群多队列的系统研究	科技部	国家重点研发计划	孔庆鹏	2018-2022	2820	主持
5	灵长类多能干细胞基因组稳态调控网络及增强策略	科技部	国家重点研发计划	郑　萍	2021-2026	2329	主持
6	高黎贡地区野生动物全景动态监测体系建设与安全评估示范	科技部	国家重点研发计划	车　静	2022-2025	2480	主持
7	高黎贡地区野生动物全景动态监测体系建设与安全评估示范	科技部	国家重点研发计划	张晓明	2022-2025	600	主持
8	新冠病毒基因组进化规律与动态演变研究技术体系创建与应用	科技部	国家重点研发计划	吕雪梅	2020-2022	450	主持
9	生猪高产优质高效性状形成的分子调控网络	科技部	国家重点研发计划	谢海兵	2021-2026	1140	参与
10	中国长寿家系人群健康老龄调控因子甄别研究	科技部	国家重点研发计划	李功华	2019-2022	530	参与
11	病原变异及其跨物种传播的回溯和演进方法体系构建	科技部	国家重点研发计划	吕雪梅	2021-2024	513	参与
12	利用多组学技术解析社交与情感的遗传基础和调控网络	科技部	国家重点研发计划	王国栋	2019-2024	438	参与
13	非人灵长类与树鼩脑疾病模型创建与关键技术研究	科技部	国家重点研发计划	毛炳宇	2021-2024	300	主持
14	基础科学中心	基金委	基础科学中心项目	宿　兵	2023-2027	1200	参与
15	两栖爬行动物多样性与进化	基金委	杰出青年科学基金	车　静	2023-2027	400	主持
16	东亚早期人类的表型演化分子机制与群体历史	基金委	优秀青年科学基金	张晓明	2023-2025	200	主持
17	多能干细胞高效调控 DNA 复制压力反应的关键 lncRNA 鉴定与功能分析	基金委	重点项目	郑　萍	2020-2024	312	主持

序号	项目名称	项目来源	项目类别	负责人	执行期	总经费（万元）	参与类型
18	回声定位蝙蝠高频听力适应性进化的遗传发育机制	基金委	重点项目	施　鹏	2020-2024	303	主持
19	基于七鳃鳗脑发育多组学图谱研究脊椎动物脑起源的遗传机制	基金委	重点项目	宿　兵	2023-2027	280	主持
20	高原湖泊水质变化过程中鲫鱼复合体种群体多样性变化及其生态适应性	基金委	联合基金项目	吕雪梅	2020-2023	231	主持
21	全球视角下全基因组数据解析家鸡的起源和扩散	基金委	联合基金项目	吴东东	2020-2023	230	主持
22	猕猴大脑发育调控的三维基因组解析与灵长类脑进化的遗传机制研究	基金委	联合基金项目	宿　兵	2021-2024	227	主持
23	猴精原干细胞系的建立及基于精原干细胞研发猴高效基因敲入新技术	基金委	联合基金项目	郑　萍	2022-2025	279.6	主持
24	动物复杂性状的进化创新与重塑	中科院	B 类先导专项培育项目	施　鹏	2021-2022	800	主持
25	驯化动植物对高寒环境的适应及基因资源利用	中科院	A 类先导专项	彭旻晟	2018-2022	1160	参与
26	高原湿地垫脚石式廊道生态修复技术与示范（子课题 2）	中科院	A 类先导专项	杨君兴	2019-2023	1145	参与
27	猪育种示范基地建设与完善	中科院	A 类先导专项	张亚平	2019-2024	1130	参与
28	关键区域的高通量、连续覆盖生物多样性监测与评估	中科院	A 类先导专项	Douglas W Yu	2018-2023	1094.2	参与
29	气候环境变化对典型动物及种群的影响	中科院	A 类先导专项	车　静	2018-2023	1060.3	参与
30	高原人群适应高寒环境的遗传资源发掘	中科院	A 类先导专项	孔庆鹏	2018-2022	686.3	参与
31	西南山地旗舰动物生态廊道设计技术与示范	中科院	A 类先导专项	蒋学龙	2019-2023	621.5	参与
32	两栖类生物多样性格局及其与季风气候的关系	中科院	B 类先导专项	柴　静	2018-2023	398.7	参与
33	鸟类不同类群间及与病毒间的协同演化机制研究	中科院	B 类先导专项	张国捷	2018-2023	300	参与
34	建立哀牢山自然保护区快速生物多样性监测方法	中科院	重点项目	Douglas W Yu	2017-2022	400	主持
35	家犬强迫症疾病模型初探	中科院	前沿重点项目	王国栋	2019-2023	300	主持

序号	项目名称	项目来源	项目类别	负责人	执行期	总经费（万元）	参与类型
36	江西鄱阳湖流域山区水系分布的大鲵种质资源调查及保护创新研究	中科院	科技服务网络计划（STS 计划）区域重点项目	车　静	2021-2023	990	主持
37	非洲动物多样性格局及动物资源研究与利用课题 -3	中科院	中非联合研究中心项目	蒋学龙	2021-2023	200	主持
38	现生鸟类多样性演化历史及机制研究	中科院	国际合作项目	张国捷	2019-2022	270	主持
39	非洲猪科动物种质和遗传资源	中科院	国际合作项目	彭旻晟	2021-2024	240	主持
40	云南跨境生物监测预警技术体系研究及应用	云南省	重大科技专项计划	施　鹏	2021-2024	2000	主持
41	云南地方特色畜禽资源高效精准定向选育技术体系构建与示范	云南省	重大科技专项计划	吴东东	2022-2024	800	参与
42	分子检测和基因编辑技术的研发与应用	云南省	重点研发计划	张亚平	2022-2025	1000	主持
43	云南高原湖泊特有四大名鱼的保育及其深度发掘利用研究	云南省	对外科技合作专项	杨君兴	2020-2023	300	主持
44	云南省领军人才项目 —— 宿兵	云南省	领军人才项目	宿　兵	2020-2024	920	主持
45	云南省云岭学者（2020）—— 孔庆鹏	云南省	高层次人才培养支持计划	孔庆鹏	2020-2025	200	主持
46	云南省云岭学者（2019）—— 施鹏	云南省	高层次人才培养支持计划	施　鹏	2019-2024	200	主持
47	科学家工作室	云南省	兴滇英才支持计划	宿　兵	2023-2028	992	主持
48	昆明市高层次创新创业团队项目	云南省	昆明市“春城计划”	张亚平	2022-2027	3000	主持
49	春城科技领军人才专项 —— 孔庆鹏	昆明市	春城科技领军人才专项	孔庆鹏	2021-2024	1000	主持
50	云南水富港扩能工程一期对长江上游珍稀特有鱼类国家级自然保护区（云南段）生态补偿项目	云南省	横向项目	潘晓赋	2021-2027	305	主持

发表论文

（蓝色标注：实验室是文章第一完成单位；加粗：标注实验室的人员；通讯作者 *；共同第一作者 [1]）

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授权专利

专利号	专利名称	类别	授权日期	完成人
17204302	HYBRIDIZATION METHOD OF SINOCYCLOCHEILUS GRAHAMI AND CARP	美国发明专利	2022-10-12	Yuanwei Zhang, Xiaoai Wang, Xiaofu Pan, Junxing Yang
ZL202010976166.2	一种犬脐带来源的间充质干细胞培养基和培养方法	发明专利	2022.05.13	王国栋、张树润、李欣懿
ZL202011411917.2	一种软鳍新光唇鱼人工繁殖方法	发明专利	2022.06.07	王晓爱、潘晓赋、张源伟、杨君兴、范　伟、王云峰
ZL202011410487.2	一种犀角金线鲃人工繁殖方法	发明专利	2022.06.07	潘晓赋、王晓爱、张源伟、杨君兴、卢泊霖
ZL202110154107.1	一种滇池金线鲃和鲫鱼杂交的方法	发明专利	2022.06.07	王晓爱、张源伟、潘晓赋、杨君兴
ZL202011410270.1	一种滇池金线鲃和鲤鱼杂交方法	发明专利	2022.06.07	张源伟、王晓爱、潘晓赋、杨君兴

获　奖

科技奖励

序号	成果名称	类型	等级	完成人	完成情况
1	新冠病毒谱系划分及进化动态分析体系的建立及应用	北京市科学技奖——科技进步奖	二等奖	陆　剑、吕雪梅、吴仲义、崔　杰、钱朝晖、唐小鹿、应若晨、阮永森	非第一完成人(非独立完成)

荣誉称号

姓名	年度	奖项	类型
施　鹏	2022	谈家桢生命科学创新奖	国家级
车　静	2022	第十八届中国青年女科学家奖	国家级

第二章 开放合作交流

开放课题

序号	课题编号	申请人	职 称	申请人所在单位	项目名称	资助经费（万元）
1	GREKF22-01	Robert Ward Murphy	教授	加拿大多伦多大学	基于 DNA 条形码研究中国蛇类物种多样性	7.5
2	GREKF22-02	张　鹏	教授	中山大学	基于系统发育基因组学探讨广义水蛙属的多样性及其演化	7.5
3	GREKF22-03	宋文宇	助理研究员	大理大学	三江并流区高山小型兽类群落构建过程及其影响因素研究	7.5
4	GREKF22-04	李建真	教授	西北师范大学	新型升糖激素 Placensin 在脊椎动物中的演化分析	7.5
5	GREKF22-05	申　秋	主治医师	昆明市第一人民医院	基于代谢模拟技术研究刻画泛肿瘤 (Pan-Cancer) 共有代谢模式及规律	7.5
6	GREKF22-06	马怡诚	副研究员	云南大学	基于单细胞测序技术研究番茄巨细胞形成机制	7.5
7	GREKF22-07	寸玉鹏	研究员	重庆医科大学附属儿童医院	表观遗传介导的细胞类型特异性转录因子调控	7.5
8	GREKF22-08	邹　权	教授	电子科技大学	炎性肠病肠道菌群宏基因组学研究	7.5
9	GREKF22-09	李　艳	研究员	中国科学院昆明植物研究所	筛选靶向 RNF220 的药物及其机制研究	7.5
10	GREKF22-10	王　勇	研究员	中国科学院数学与系统科学研究院	大脑皮层胼胝体进化起源中 Satb2 基因表达调控网络的进化机制研究	7.5
11	GREKF22-11	张　勇	研究员	中国科学院动物研究所	灵长类特有嗜乳脂蛋白 BTN 家族成员在神经突触进化中的作用机制研究	7.5
12	GREKF22-12	郝五零	副教授	云南师范大学	胎盘哺乳类动物出生前后分子调控网络的动力学分析	7.5
13	GREKF22-13	王　晨	畜牧师	广州动物园	亚洲象新发突变及速率研究	7.5

序号	课题编号	申请人	职 称	申请人所在单位	项目名称	资助经费（万元）
14	GREKF22-14	逄　越	教授	辽宁师范大学	基于雷氏七鳃鳗重要发育时期转录组数据的基因组重注释研究	7.5
15	GREKF22-15	张　慧	副研究员	昆明理工大学	汉藏人群脐静脉内皮细胞的多组学研究	7.5
16	GREKF22-16	刘　阳	教授	中山大学	高原雉类的比较基因组学研究	7.5

参加学术会议

序号	会议名称	会议时间	会议地点	报告人（参会人）
1	浙江大学双脑中心大讲堂	2022.03.18	浙江杭州	张国捷
2	第十六届中国鸟类学大会	2022.04.08-10	广东珠海	吴　飞、彭旻晟
3	第八届全国计算生物学与生物信息学学术会议	2022.07.27	广州市	宿　兵
4	进化之光云论坛	2022.07.27	线上	张国捷
5	集智同行第八次会议	2022.08.05-07	西安	刘薇薇
6	2022 年中国生物化学与分子生物学会学术会议	2022.10.20-22	线上	刘　霈、缪佳雨
7	昆明医科大学学术交流会	2022.11.02	云南昆明	文建凡
8	首届黑颈鹤保护国际网络会议	2022.11.07-15	不丹	杨晓君、伍和启
9	2022 年水产养殖技术培训会	2022.11.08	云南丽江	吴安丽、殷艳慧
10	高黎贡山区域生物多样性专题会暨《云南 KJSW 监测预警技术体系研究及应用》重大专项工作研讨会	2022.11.13-16	云南保山	王国栋

序号	会议名称	会议时间	会议地点	报告人（参会人）
11	2022 年生物科学前沿系列学术讲座	2022.11.19	线上	李学燕
12	中国神经科学学会第十五届全国学术会	2022.11.27-29	线上	盛能印
13	2022 年第三届国际动物遗传育种前沿科技论坛	2022.12.02	武汉	彭旻晟
14	中国动物学会两栖爬行学分会 - 首届承钊青年学术论坛	2022.12.10	线上	车　静
15	中国动物学会两栖爬行学分会 - 首届承钊青年学术论坛	2022.12.10	线上	王　剀
16	2022 年云南省水产学会学术年会	2022.12.10	云南昆明	王晓爱、吴安丽
17	“ 国际山岳日 ” 山地科学论坛	2022.12.11	云南昆明	董　锋
18	COP15 第二阶段会议 “ 极小种群物种和生物多样性保护边会 ”	2022.12.15	加拿大	蒋学龙
19	中国动物学会原生动物学分会学术论坛	2022.12.18	线上	文建凡、吕章夏、白慧掀、程姣妮、邓　琪、沈　洁
20	第十届国际疾病基因组变异研讨会	2022.12.23	线上	彭旻晟

邀请专家报告

序号	专家姓名	单位	职称	报告题目	报告时间
1	周　斌	中国科学院分子细胞科学卓越创新中心	研究员	细胞谱系示踪技术与器官修复再生研究	2022.02.27
2	彭广敦	中国科学院广州生物医药与健康研究院	研究员	Integrative spatial transcriptome analysis for molecular architecture of embryo development	2022.02.25
3	李天晴	昆明理工大学	教　授	灵长类早期胚胎发育和干细胞	2022.03.25

序号	专家姓名	单位	职称	报告题目	报告时间
4	史际帆	东京大学国际高等研究所	研究员	Dynamics-based data science in biology —— Three examples	2022.04.25
5	蔚鹏飞	中国科学院深圳先进技术研究院	研究员	计算神经行为学技术与在神经系统疾病研究中的应用	2022.04.26
6	张世华	中国科学院数学与系统科学研究院	研究员	Deciphering spatial domains from spatially resolved transcriptomics	2022.04.29
7	袁　晶	厦门大学	教　授	寄生原虫细胞形态控制 --- 以疟原虫为例	2022.05.16
8	李　光	厦门大学	教　授	文昌鱼 Nodal 和 N-β-catanin 信号胚胎发育功能解析及其对脊索和背神经管起源的启示	2022.05.16
9	胡　政	中科院深圳先进技术研究院	研究员	解码细胞的前世今生：一种动态细胞分化图谱构建新方法	2022.05.23
10	陶　勇	云南大学	研究员	细胞命运决定与肿瘤发生发展	2022.05.27
11	毛亚飞	上海交通大学	教　授	结构变异和基因树不一致性在灵长类演化和疾病中的机制	2022.06.08
12	刘　宣	中国科学院动物研究所	研究员	外来入侵陆生脊椎动物的生态危害和风险预警	2022.06.24
13	张　锐	中山大学	教　授	mRNA m5C 的调控、进化和功能	2022.07.29
14	赵小阳	南方医科大学	教　授	男性不育与精子再生	2022.08.15
15	汪　胜	中国科学院分子细胞科学卓越创新中心	研究员	以结构为导向的药物设计	2022.09.27
16	星耀武	中国科学院西双版纳热带植物园	研究员	山地植物多样性演化和高山植物适应性研究	2022.12.30

第三章 人才队伍培养

新增人才称号

姓名	荣誉称号	项目来源	获得年份
车　静	杰出青年基金	基金委	2022
张晓明	优秀青年基金	基金委	2022
吴东东	西部交叉团队	中科院	2022
许东明、张伟道、邵　永	青年创新促进会会员	中科院	2022
吴　飞	区域发展青年学者	中科院	2022
周中银、刘薇薇、王　林	西部之光青年学者	中科院	2022
张亚平	“动物模型与转化医学应用”创新创业团队	云南省	2022
宿　兵	科学家工作室	云南省	2022
施　鹏	“兴滇英才支持计划”科技领军人才	云南省	2022
车　静、郑　萍	“兴滇英才支持计划”云岭学者	云南省	2022
Douglas Yu	“兴滇英才支持计划” 高端外国专家	云南省	2022
李功华、和耀喜、罗　鑫、李　权、蔡　星、柳延虎、周中银、王　林、许东明	“兴滇英才支持计划”青年人才	云南省	2022
焦保卫	云南省政府特殊津贴专家	云南省	2022
王国栋	云南省杰出青年基金	云南省	2022
马鹏程、李玉春	云南省优秀青年基金	云南省	2022
尹婷婷、邵　永、肖富辉	中青年学术和技术带头人后备人才	云南省	2022

在读研究生及博士后

序号	导师	硕士生	博士生	博士后
1	Douglas W Yu		李宗煦、罗明洁	
2	车　静	余传鑫、荀　皓、万　涵、刘逸涵、牟皓楠	侯绍兵、易木荣、董文捷、卢宸祺、冯小刚、Alex Plimo Karuno、Felista Kasyoka Kilunda	
3	佴文惠	王浩博、陆　琼		
4	和耀喜	张伟杰		
5	蒋学龙	牛晓炜、于秋鹏、胡文强、何水旺、朱中旭、Sambaya Brian Anoto	陈春妮、汪思远、李弈仙、Samson Mabeya Ouru	
6	李学友	王金宇、白　如		
7	焦保卫	黄吉鹏、缪佳雨、杨　超、王　毯、张　溪、陈　欢	杨　旭、邹　丽、刘　霈、邵海莉	
8	孔庆鹏	翁崇峻、王霞燕、张润峰、薛婷月	葛明侠、尹藩乾、苏　倩、敖鸿舜、郜宗亮、赵　龙、夏天睿	
9	李功华	周青青		
10	刘　振	国天曰、刘明港	蒋继滨、孙长杰	
11	吕雪梅	李丰邑、廖思洁、张　蕾、何　昊、刘　灿	闫　凯、魏昀旸、张　昕、李梓锋、赵师磊	
12	马占山		肖琬蒙、陈红菊、乔玉亭、MD Motiur Rahman	
13	毛炳宇	马玉竹、陈锦芳、李　伟、张致标、杨陈成	朱　良、李雨薇、魏　姝、茶靖美、徐建林	
14	盛能印	李　熹、杨　锐、张　浩、李榆蓉、蔡灏漾	叶雅馨、刘娅敏、万　梨、金博星	
15	施　鹏	周　豪、陈施培、饶　琦、智浩宇	白　婧、陈　杰、蔡婉芷、华　绒、周　鑫、陈　鹏、姚晓晴、杨　陆、华秦杨、马苑硕	
16	王国栋	冯馨瑶、曾　敏、程　欣、钱辰畅、字鑫楠、黄鑫豫	张少杰、周其俊	

序号	导师	硕士生	博士生	博士后
17	王　文	李　俊、范正广	毛初阳、关　晴、吴雨瀚	万雯婷、胡　平、余甜甜
18	李学燕	覃宝连		
19	文建凡	罗宇鹏	程姣妮、邓　琪	
20	吴东东	甘　爽、骆阿云、陆一铮	张佳进、张锦锦、庄晓琳、涂小龙、陈勇璇、刘宁雅文	王　胜、王　坤
21	宿　兵	罗文皓、陈凯敏、陈勇杰	郑王山、郭永博、孟晓宇、岳　天、周　斌、曾雪芮、张凤云、吴海旭、张　悦	
22	罗　鑫	徐嘉浩		
23	杨君兴	吴可心、施　敏、吴　睿	孙　超、潘晓赋、殷艳慧、车星锦、龙　静、刀　微、韦建福	
24	潘晓赋	朱　龙		
25	杨晓君		王　洁、高建云	
26	吴　飞	何　林、陆　源		
27	张国捷	钟文江、王　娇	戴学勤、张霞芳、左大双、杞燕梅	
28	张晓明	赵银辉、周　慧		
29	张亚平	王凤娟、吴然燃、岑道机、刘利生	戴珊珊、颜　晨、许明敏、张越东、周博闻、汪　轩、李应菊、刘　行、王　蓉、李　婕、孙伟杰、施　贤、陶　林、石田赔、秦婉婷、杨云丽、蒋雪雁、肖玉焕、童奕博、冯馨瑶、丁梦婷、Lameck Ajuma Odongo	刘　凤、张月苗
30	高　云	曹学娜、宋修成、黄爱如		
31	尹婷婷	陈　星		
32	郑　萍	董玉萍、孟夏朵、李羿霏、谢谰萍	姜方洁、龚道华、李　聪、宁雨琪、金　洁、唐　敏、谢　恒	

研究生优秀论文奖

序号	姓名	获奖等级	期刊	IF	作者排序
1	戴珊珊	一等奖	*Molecular Biology and Evolution*	20.074	第一作者
2	万　梨	二等奖	*Science Advances*	16.9	并列第一作者
3	李雨薇	三等奖	*Journal of Molecular Cell Biology*	6.688	第一作者
4	伍胤桥	三等奖	*J Animal Sci Biotechnol*	6.851	第一作者

毕业研究生一览表

序号	姓名	学位	攻读专业	导师姓名	毕业日期
1	徐　伟	博士	遗传学	车　静	2022.01
2	曹如君	硕士	动物学	车　静	2022.01
3	于中斌	硕士	动物学	车　静	2022.06
4	张　毅	博士	动物学	车　静、Douglas w Yu	2022.06
5	高简奥	硕士	生物工程	佴文惠	2022.06
6	牛文静	硕士	生物工程	高　云	2022.06
7	Kenneth Otieno Onditi	博士	动物学	蒋学龙	2022.06
8	Samson Mabeya Ouru	硕士	动物学	蒋学龙	2022.06
9	胡文豪	硕士	动物学	蒋学龙	2022.06
10	郭　璐	博士	细胞生物学	焦保卫	2022.06
11	王昊天	博士	遗传学	孔庆鹏	2022.01
12	陈泽宇	博士	遗传学	吕雪梅	2022.06
13	冯　璇	博士	遗传学	吕雪梅	2022.06
14	魏婉宜	硕士	动物学	吕雪梅	2022.06

序号	姓名	学位	攻读专业	导师姓名	毕业日期
15	李文迪	博士	遗传学	马占山	2022.06
16	杨　旭	硕士	遗传学	马占山	2022.06
17	杨陈成	硕士	细胞生物学	毛炳宇	2022.06
18	姜香香	硕士	遗传学	彭旻晟	2022.06
19	何圆圆	硕士	动物学	饶定齐	2022.06
20	吴月春	硕士	神经生物学	盛能印	2022.06
21	易琳昀	硕士	神经生物学	盛能印	2022.06
22	吕颜洁	硕士	生物工程	施　鹏	2022.01
23	刘　奇	博士	遗传学	施　鹏	2022.06
24	郭媛婷	博士	遗传学	施　鹏	2022.06
25	李雪凤	硕士	药学	施　鹏	2022.06
26	吴青琴	硕士	动物学	王国栋	2022.06
27	田航宇	博士	遗传学	吴东东	2022.01
28	李彦旭	硕士	遗传学	吴东东	2022.06
29	Violet Magoma Onsongo	硕士	遗传学	吴东东	2022.06
30	姚舜禹	硕士	动物学	杨晓君	2022.06
31	赵　岩	硕士	动物学	杨晓君	2022.06
32	沈全宽	博士	遗传学	张亚平	2022.01
33	母昌概	硕士	遗传学	张亚平	2022.06
34	耿伟航	博士	遗传学	张亚平、于　黎	2022.06
35	孙春丽	博士	细胞生物学	郑　萍	2022.01
36	谢　恒	硕士	细胞生物学	郑　萍	2022.06
37	陶慧玲	硕士	细胞生物学	郑　萍	2022.06

工作人员名单

（按姓名拼音首字母排序）

学术带头人

Douglas W Yu	车　静	蒋学龙	焦保卫	孔庆鹏	刘　振
吕雪梅	马占山	毛炳宇	盛能印	施　鹏	王国栋
王　文	文建凡	吴东东	宿　兵	杨君兴	杨晓君
张国捷	张亚平	郑　萍			

工作人员

Adeniyi Charles Adeola	Jamal Muhammad Ameen	Kenneth Otieno Onditi	Zia Ur Rahman	白慧掀	鲍万冬
蔡　星	曹如君	曾　琳	柴　静	常云艳	常　洲
陈思梦	崔　宁	戴红娟	邓家坤	董　锋	董志巍
佴文惠	高建云	高　伟	高　云	谷丽娇	郭　彦
郝军军	何水旺	何文彬	和耀喜	胡远芳	胡哲畅
辉　洪	季吟秋	金洁琼	雷孟龙	李朝翠	李功华
李桂梅	李建波	李锦秀	李连伟	李梦成	李梦雯
李　权	李欣然	李学燕	李学友	李玉春	李玉宏
李毓劲	廖爱文	刘贵春	刘　奇	刘　倩	刘薇薇
柳延虎	罗　杰	罗荣松	罗　鑫	吕　雪	吕章夏
马怀孝	马鹏程	马思雨	潘晓赋	彭旻晟	浦绍艳
饶定齐	邵　永	沈文菁	施禄也	苏伟婷	孙长杰
谭玉莲	田航宇	涂小龙	王昊天	王洪娇	王绘山
王　慧	王　洁	王金焕	王　剴	王　林	王识之
王晓爱	王运梅	韦建福	吴安丽	吴春莹	吴　飞
吴汝念	吴云鹤	伍和启	肖富辉	谢国丽	谢海兵
谢林哲	徐　沙	徐　伟	薛宪词	岩　道	杨春燕
杨　晖	杨利琴	杨敏敏	杨　钦	杨　虓	杨　星
姚舜禹	殷利夺	尹婷婷	于中斌	余　琴	喻　运
张宝林	张栋儒	张海林	张　琴	张树润	张　涛
张伟道	张晓明	张源伟	张　越	张云春	赵　洁
赵丽娜	赵明茹	赵若苹	赵士萍	郑俊娟	周　通
周　鑫	周中银	朱春玲	邹　丽		

遗传资源与进化国家重点实验室 2022年报

2022年度报告
ANNUAL REPORT

遗传资源与进化国家重点实验室
中国科学院昆明动物研究所

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