STATE KEY LABORATORY OF GENETIC RESOURCES AND EVOLUTION

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

2018年报
ANNUAL REPORT

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

目 录

主任致辞

砥砺奋进，春华秋实。2018 年是全面贯彻党的十九大精神的开局之年，也是全面落实国家“十三五”规划的关键一年。在各级主管部门的领导与关怀下，遗传资源与进化国家重点实验室在任务承担、科研成果、人才队伍建设、开放交流等各方面工作均取得了可喜进展，向成为“具有重要国际影响的遗传资源与进化研究中心”的目标又迈进了一步。

在科研项目承担方面，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。2018 年新增科研项目 63 项，包括主持国家重点研发计划重点专项 1 项，参与中国科学院 A 类战略性先导科技专项多个子课题，主持中国科学院国际合作局对外重点项目 1 项，获优秀青年科学基金资助 1 项等。目前在研省部级项目 190 项，横向协作项目 34 项，国际合作项目 7 项。年度到位科研经费 7687.89 万元。

在科研成果产出方面，实验室围绕三大研究方向，继续揭示生物多样性形成与演变的规律及其遗传机制，为遗传资源的保护和可持续利用提供理论依据。2018 年发表 SCI 论文 114 篇，其中以第一作者或通讯作者（含并列）发表论文 91 篇，一区论文共 33 篇，占总论文数的 28.9%。发表在 *Genome Research*，*Nature Communication*，*PNAS*，*Current Biology*，*Science Advances*，*Molecular Biology & Evolution* 等 $IF_{5\text{-}year}$>9 高影响力的论文共 31 篇。1 项成果获得云南省自然科学一等奖，1 项专利获得云南省专利二等奖。申请发明专利 7 项，其中 2 项获得授权。1 项水产新品种获得中国农业农村部认定。

在人才引进培养方面，实验室继续加强人才队伍建设，取得明显成效。在固定人员中，1 人新入选“欧洲科学院院士”，1 人荣获国家自然科学基金“优秀青年基金”资助，1 人新入选科技部“中青年科技创新领军人才”，1 人新入选云南省“万人计划科技领军人才”，5 人新入选云南省“万人计划”青年拔尖人才。此外，实验室还培养新增青年研究员 1 名（刘振）。依托于实验室主持的中科院先导 B 项目团队而组建的中科院动物进化与遗传前沿交叉卓越创新中心在获批筹建后，稳步运行，实验室参与人员共计 15 人。实验室毕业研究生 37 人，出站博士后 3 人。此外，还成功举办 2018 年“进化生物学”暑期班，吸引更多有志青年加入实验室。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。

在开放交流合作方面，实验室长期遵循“交流促进合作”的原则，在 2018 年开展了一系列学术活动。成功承办第 14 届全国野生动物生态与资源保护学术研讨会。邀请 27 名国内外知名专家来室进行学术交流。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 19 项，并将各科研平台开放共享。

不忘初心，创新前行！我们在学术委员会指导下，阔步迈入华章初展的 2019 年。让我们立足过去，满怀希冀，共创未来，力争为我国“十三五”科技创新工作做出更大贡献！在此，我谨代表实验室向给予实验室大力帮助的各级领导及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：施鹏

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，部署以下三个研究方向：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。并与依托单位中国科学院昆明动物研究所的“一三五”规划紧密结合，向成为具有重要国际影响的遗传资源与进化研究中心的目标不断前行。

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，为生物多样性和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、过程与机制方面做出了具有影响力的代表性成果。2011 年至今，实验室共发表 SCI 论文 977 篇，包括在 *Science*，*Nature Biotechnology*，*Nature Genetics*，*Cell Stem Cell* 等 $IF_{5\text{-}year}$（5 年平均影响因子）≥9 的国际顶级学术期刊上发表论文 137 篇。以第一完成单位荣获国家自然科学二等奖 2 项、云南省自然科学特等奖 1 项、一等奖 2 项、二等奖 2 项，三等奖 1 项，云南省科技进步三等奖 2 项，云南省专利二等奖 1 项、三等奖 1 项。

实验室拥有固定研究组 17 个，客座研究组 1 个，支撑部门 3 个。拥有国家自然科学基金委创新群体 1 个，中国科学院院士 1 人，百千万人才工程国家级人选 4 人，国家自然科学委“杰出青年基金”获得者 5 人，“优秀青年基金”获得者 3 人，青年千人计划 1 人，“万人计划”领军人才 3 人，中青年科技创新领军人才 3 人，中国科学院“百人计划”引进人才 9 人，中 - 德国马普学会青年科学家小组组长 2 人，何梁何利基金科学与技术进步奖获得者 1 人，教育部长江学者优秀奖一等奖获得者 1 人，云南省“万人计划”科技领军人才 1 人，云南省高端科技人才引进 5 人。现有科研工作人员 152 人，其中拥有博士学位 84 人。40 岁以下研究骨干占比为 75.3%，青年研究骨干承担了实验室大部分的科研任务，发挥着创新探索的不竭动力。目前，实验室在站博士后 6 名，在读研究生 150 名。

实验室目前拥有 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。拥有大型仪器设备共计 90 余台 / 套，设备总价值 8600 余万元。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。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，扩大了实验室与国内、国际同领域学术界的联系，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

进一步收集遗传资源，特别是我国西南地区丰富的少数民族和动物的遗传资源，研究遗传资源（多样性）的形成和演变的规律，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，为遗传资源的保护和合理利用提供科学依据。

2. 基因与基因组的进化

以不同关键进化地位的生物类群为研究对象，研究基因起源和进化的规律、基因适应性进化对环境适应的意义、基因功能途径和网络的进化模式、基因家族结构与功能演变的基础及其进化的模式和机制、基因组的起源与进化，探讨基因、基因家族和基因组的结构、功能在生物进化过程中的形成机制和进化规律。

3. 遗传发育与进化

通过对近缘物种和不同进化地位的代表类群（如昆虫、头索动物、两栖类和哺乳类等）发育调控机制的比较研究，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对物种形态演化与适应性的贡献。

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（按姓名拼音首字母排序）

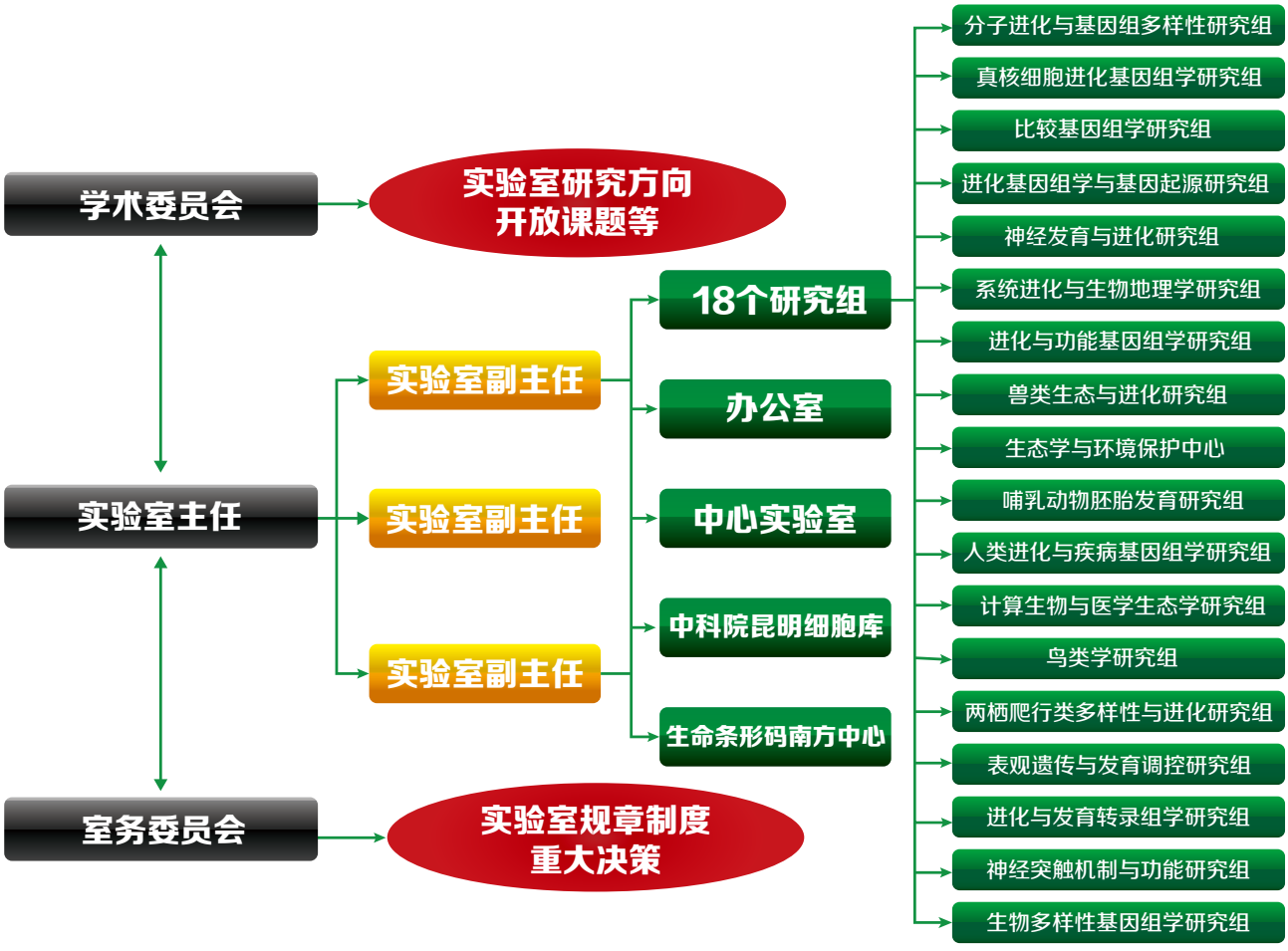
桂建芳　院　士，中国科学院水生生物学研究所

焦保卫　研究员，中国科学院昆明动物研究所

金　力　院　士，复旦大学

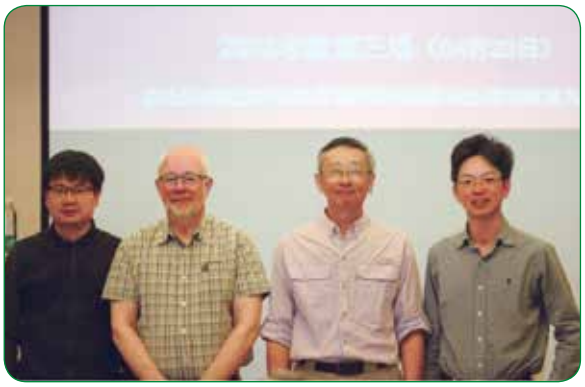
李德铢　研究员，中国科学院昆明植物研究所
施　鹏　研究员，中国科学院昆明动物研究所
汪小全　研究员，中国科学院植物研究所
王　文　研究员，中国科学院昆明动物研究所
魏辅文　院　士，中国科学院动物研究所
吴仲义　院　士，中山大学
杨　光　教　授，南京师范大学
张克勤　教　授，云南大学

3. 研究队伍



大事记

1 月 29 日，实验室第三届学术委员会第一次会议在西南生物多样性中心报告厅召开。会议由学术委员会主任张亚平院士主持，金力院士、桂建芳院士、魏辅文院士、汪小全研究员、杨光教授、张克勤教授等 9 位委员出席。研究所姚永刚所长、沈华书记以及重点实验室学术带头人和青年研究骨干参加会议。



从 1 月 29 日起，实验室不定期举办“遗传与进化前沿交叉论坛” 共计 7 场，邀请到桂建芳院士、吴仲义院士、David M. Hillis 院士、杨光教授、Jacobus Jan Boomsma 教授、Albert S. Feng 教授、Antonio Torroni 教授、Hans–J ü rgen Bandelt 教授等国内外知名学者到室进行学术报告，促进交流合作。

5 月 19–22 日 “第十四届公众科学日”活动期间，实验室在中科院昆明动物博物馆举办研究生科普海报比赛及展览。5 月 22 日国际生物多样性日，由昆明动物博物馆、实验室及其支撑部门生命条形码南方中心联合推出了“色彩的天空”世界蜻蜓展，并通过“央视新闻”新浪微博、“央视新闻”客户端等平台进行了直播。





从 6 月 29 日起，实验室定期举办 2018 年“遗传资源与进化青年学者论坛” 共计八场。每场邀请室内学术带头人及研究生或青年骨干进行学术报告，评选优秀报告，激发研究生以及青年学者的科研创新思维，促进室内人员学术交流，论坛同时也吸引了所内广大师生积极参与。




7 月 16–21 日，实验室与研究生部联合举办 2018 年“进化生物学” 暑期班，对 30 名国内高校的学生开放实习，讲授进化生物学方面的基础知识，组织学术专题研讨、座谈、参观、资源考察等活动，促进科教融合，吸引优质生源，并取得了良好的招生宣传效果。





11 月 21–24 日，第十四届全国野生动物生态与资源保护学术研讨会在昆明召开。会议由中国科学院昆明动物研究所、重点实验室、动物进化与遗传前沿交叉卓越创新中心及《动物学研究》编辑部联合承办。近 600 名学者参会，探讨我国动物生态、野生动物多样性、保护与管理等的发展战略，促进学术交流合作。

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

中国大鲵遗传多样性与保护研究取得重要进展

The Chinese giant salamander exemplifies the hidden extinction of cryptic species.

Yan F[1], Lü J[2], Zhang B[3], Yuan Z[1], Zhao H[4], Huang S[5], Wei G[6], Mi X[3], Zou D[5], Xu W[3], Chen S[7], Wang J[8], Xie F[8], Wu M[9], Xiao H[10], Liang Z[11], Jin J[1], Wu S[1], Xu C[12], Tapley B[7], Turvey ST[7], Papenfuss TJ[13], Cunningham AA[7], Murphy RW[14], Zhang Y[15], Che J[16].

Abstract

Overexploitation, habitat destruction, human-driven climate change and disease spread are resulting in the extinction of innumerable species, with amphibians being hit harder than most other groups [1]. Few species of amphibians are widespread, and those that are often represent complexes of multiple cryptic species. This is especially true for range-restricted salamanders [2]. Here, we used the widespread and critically endangered Chinese giant salamander (Andrias davidianus) to show how genetically uninformed management efforts can negatively affect species conservation. We find that this salamander consists of at least five species-level lineages. However, the extensive recent translocation of individuals between farms, where the vast majority of extant salamanders now live, has resulted in genetic homogenization. Mitochondrial DNA (mtDNA) haplotypes from northern China now predominate in farms. Unfortunately, hybrid offspring are being released back into the wild under well-intentioned, but misguided, conservation management. Our findings emphasize the necessity of genetic assessments for seemingly well-known, widespread species in conservation initiatives. Species serve as the primary unit for protection and management in conservation actions [3], so determining the taxonomic status of threatened species is a major concern, especially for amphibians. The level of threat to amphibians may be underestimated, and existing conservation strategies may be inadvertently harmful if conducted without genetic assessment.

Current Biology. 2018, 28(10): R590–R592.

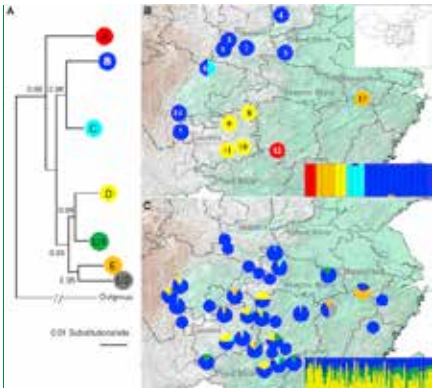


图 1. 基于线粒体片段、简化基因组 SNP、微卫星数据获得的中国大鲵系统发育关系和遗传结构

图 2. 中国大鲵生活照（Robert Murphy 摄）

车静研究团队及张亚平研究团队首次使用了简化基因组的方法，在基因组水平对中国大鲵的野生种群开展了群体遗传学分析。结合线粒体基因等的多项分析结果意外发现，中国大鲵并非单一物种，目前研究数据支持至少 5 个物种的划分。

该发现对于中国大鲵的保护具有非常重要的意义。物种是制定保护措施最基础的分类单元。基于过去的分类知识和常规的做法，在保护区划分、人工养殖、增殖放流等一系列的保护过程中，中国大鲵长期以来被当作一个物种对待，且没有区分不同地理种群。这隐藏巨大的风险。若不及时调整，不仅有的物种不能得到保护，还很容易使小种群物种受到其它物种的基因侵蚀，甚至被取代，造成巨大遗传资源损失甚至物种灭绝。该研究成果发表在 *Current Biology* 上，并在北京召开新闻发布会。

Current Biology
Magazine

研究方向一：遗传资源多样性的演化与保护

代表性成果二

张亚平等发文：与大自然共享发展空间，造福子孙后代

Space for nature

Jonathan Baillie[1,*], Ya-Ping Zhang[2,†]

How much of the planet should we leave for other forms of life? This is a question humanity must now grapple with. The global human population is 7.6 billion and anticipated to increase to around 10 billion by the middle of the century. Consumption is also projected to increase, with demands for food and water more than doubling by 2050. Simply put, there is finite space and energy on the planet, and we must decide how much of it we're willing to share. This question requires deep consideration as it will determine the fate of millions of species and the health and well-being of future generations.

Science. 2018, 361:1051-1051.

"Current levels of protection do not even come close to the required levels."

"人类应该为其它生命留出多大的生存空间？"这是摆在人类面前亟待解决的问题。目前，全球总人口为 76 亿，预计到本世纪中叶将会达到 100 亿。与此同时，人类的消耗也在不断增加，2050 年，人类对食品和水资源的需求将会翻倍。简单来说，地球上的空间和能源是有限的，人类愿意将多少生存空间与其它生命分享，我们必须给出确切的答案。这是一个值得人类深思的问题，因为它将决定地球上数以百万计的物种的命运，并影响人类未来的发展。

美国国家地理学会执行副主席兼首席科学家 Jonathan Baillie 与张亚平院士在 *Science* 上联合发表了题为《与大自然共享发展空间》的社论文章。文章以"人类应该为其它生命留出多大的生存空间？"这一摆在人类面前亟待解决的问题发端，通过列举一组组令人惊讶的数据，展示了目前人类和地球上其它生命形式所面临的严峻形势，提出人类应制定切实可行的未来生物多样性目标，实现人类与自然的和谐发展，造福子孙后代。

Science

研究方向一：遗传资源多样性的演化与保护

代表性成果三

家养动物基因交流方面取得重要进展

Pervasive introgression facilitated domestication and adaptation in the Bos species complex.

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Abstract

Species of the Bos genus, including taurine cattle, zebu, gayal, gaur, banteng, yak, wisent and bison, have been domesticated at least four times and have been an important source of meat, milk and power for many human cultures. We sequence the genomes of gayal, gaur, banteng, wisent and bison, and provide population genomic sequencing of an additional 98 individuals. We use these data to determine the phylogeny and evolutionary history of these species and show that the threatened gayal is an independent species or subspecies. We show that there has been pronounced introgression among different members of this genus, and that it in many cases has involved genes of considerable adaptive importance. For example, genes under domestication selection in cattle (for example, MITF) were introgressed from domestic cattle to yak. Also, genes in the response-to-hypoxia pathway (for example, EGLN1, EGLN2 and HIF3a) have been introgressed from yak to Tibetan cattle, probably facilitating their adaptation to high altitude. We also validate that there is an association between the introgressed EGLN1 allele and haemoglobin and red blood cell concentration. Our results illustrate the importance of introgression as a source of adaptive variation and during domestication, and suggest that the Bos genus evolves as a complex of genetically interconnected species with shared evolutionary trajectories.

Nature Ecology & Evolution. 2018, 2(7): 1139-1145.

家养动物被人类成功驯化后，伴随着人类迁徙至世界各地。在这个过程中，家养动物会与当地各种野生近缘种相遇，从而发生杂交促使基因交流的发生。

牛属现存物种，包括普通牛、瘤牛、大额牛、印度野牛、爪哇野牛、牦牛、欧洲野牛和美洲野牛等等，它们在人类文明发展过程中占有重要的地位。但牛属中存在很多关键科学问题未得以解决。

张亚平研究团队及吴东东研究团队对大额牛、印度野牛、爪哇野牛、欧洲野牛和美洲野牛进行了全基因组高覆盖测序，同时包括多个物种的群体基因组测序。通过系统性地分析，确定了牛属之间的系统发育关系（图 1），得出大额牛不是印度野牛的驯化种，而是一个独立的物种或亚种的结论。进一步分析发现牛属之间存在广泛的基因交流，并挖掘出瘤牛与巴厘牛（爪哇野牛驯化种），瘤牛与大额牛发生基因交流的区域，发现许多神经系统基因、免疫系统基因从瘤牛扩散至巴厘牛以及大额牛中。同时，研究人员亦发现分布在青藏高原上的牦牛与藏黄牛之间存在显著的基因交流。这些研究结果表明基因交流是物种适应环境的重要方式之一，同时也是野生物种驯化的重要手段，阐明了基因交流在牛属动物的驯化以及环境适应中的重要作用，相关工作发表于 *Nature Ecology & Evolution*。

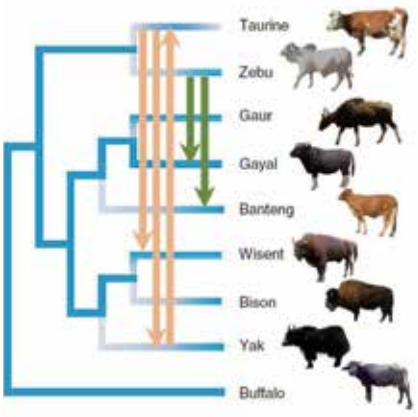

图 1. 牛属之间的系统发育关系

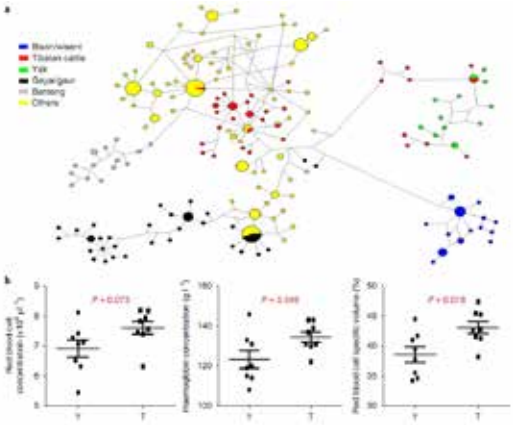

图 2. EGLN1 基因从牦牛向西藏牛的遗传渗入

研究方向一：遗传资源多样性的演化与保护

代表性成果四

揭示青藏高原高山倭蛙物种形成分化及适应进化机制

Selection and environmental adaptation along a path to speciation in the Tibetan frog *Nanorana parkeri*

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Abstract

Tibetan frogs, *Nanorana parkeri*, are differentiated genetically but not morphologically along geographical and elevational gradients in a challenging environment, presenting a unique opportunity to investigate processes leading to speciation. Analyses of whole genomes of 63 frogs reveal population structuring and historical demography, characterized by highly restricted gene flow in a narrow geographic zone lying between matrilines West (W) and East (E). A population found only along a single with adaptation to high eltributary of the Yalu Zangbu River has the mitogenome only of E, whereas nuclear genes of W comprise 89–95% of the nuclear genome. Selection accounts for 579 broadly scattered, highly divergent regions (HDRs) of the genome, which involve 365 genes. These genes fall into 51 gene ontology (GO) functional classes, 14 of which are likely to be important in driving reproductive isolation. GO enrichment analyses of E reveal many overrepresented functional categories associated evations, including blood circulation, response to hypoxia, and UV radiation. Four genes, including *DNAJC8* in the brain, *TNNC1* and *ADORA1* in the heart, and *LAMB3* in the lung, differ in levels of expression between low- and high-elevation populations. High-altitude adaptation plays an important role in maintaining and driving continuing divergence and reproductive isolation. Use of total genomes enabled recognition of selection and adaptation in and between populations, as well as documentation of evolution along a stepped cline toward speciation.

PNAS. 2018, 115: E5056-E5065.

图 1. 高山倭蛙生活照（王剑摄）

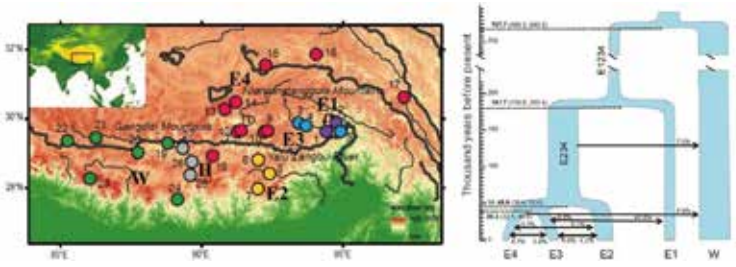


图 2. 高山倭蛙基因组重测序采样分布图（左）以及群体历史分析（右）。左图：绿色 W 为高山倭蛙西部居群；灰色 H 为杂交带个体；E 为东部居群，其中 E1 和 E3 为低海拔居群（2900m~3300m），E2（3900m~4900m）和 E4（3700m~4500m）为高海拔居群

车静研究团队与张亚平院士、加州大学伯克利分校 David Wake 院士等 7 个国内外团队合作，在前期基础上选取了高山倭蛙分布范围内 63 个居群样品进行了全基因组重测序，数据分析分析发现：(1) 东、西群体基因组中大部分区域已经出现明显隔离且不能发生基因渗透，高分化区域与生殖相关的基因存在显著富集，应为两个不同的物种。进一步分析提示选择作用在物种形成过程中扮演了重要角色；(2) 东部物种呈现明显的“低-高-低-高”海拔的遗传分化模式，与环境相关的基因，如血管循环，低氧应答，紫外应答等受到正选择和差异表达，提示高原适应在东部群体的分化过程中起了重要作用。

研究揭示了高原极端环境条件下物种形成、群体分化的遗传学基础，并探讨了选择和适应在物种形成过程中的重要作用。该研究成果发表在 *Proceedings of the National Academy of Sciences of the United States of America*。

研究方向二：基因与基因组的进化 ▶ 代表性成果一

发现藏族人群高原低氧生理适应的新机制

Blunted nitric oxide regulation in Tibetans under high-altitude hypoxia

ABSTRACT

Nitric oxide (NO) is an important molecule for vasomotor tone, and elevated NO signaling was previously hypothesized as a unique and adaptive physiological change in highland Tibetans. However, there has been lack of NO data from Tibetans living at low altitude and lowlander immigrants living at high altitude, which is crucial to test this hypothesis. Here, through cross-altitude (1990–5018 m) and cross-population (Tibetans and Han Chinese) analyses of serum NO metabolites (NOx) of 2086 individuals, we demonstrate that although Tibetans have a higher serum NOx level compared to lowlanders, Han Chinese immigrants living at high altitude show an even higher level than Tibetans. Consequently, our data contradict the previous proposal of increased NO signaling as the unique adaptive strategy in Tibetans. Instead, Tibetans have a relatively lower circulating NOx level at high altitude.This observation is further supported by data from the hypoxic experiments using human umbilical vein endothelial cells and gene knockout mice. No difference is detected between Tibetans and Han Chinese for endothelial nitric oxide synthase (eNOS), the key enzyme for circulating NO synthesis, suggesting that eNOS itself is unlikely to be the cause. We show that other NO synthesis-related genes (e.g. *GCH1*) carry Tibetan-enriched mutations significantly associated with the level of circulating NOx in Tibetans. Furthermore, gene network analysis revealed that the downregulation and upregulation of NOx is possibly achieved through distinct pathways. Collectively, our findings provide novel insights into the physiological and genetic mechanisms of the evolutionary adaptation of Tibetans to high-altitude hypoxia.

National Science Review. 2018, 5: 516-529.

宿兵研究团队通过多个单位合作，测定了 2000 多个长期生活在不同海拔地区的藏族和汉族个体的血清 NO 水平。研究结果表明，相比于低海拔汉族，虽然高海拔藏族表现出更高的 NO 水平，但长期生活在高海拔的汉族表现出了比同海拔藏族更高的 NO 水平。因此，研究结果否定了西方学者提出的 NO 升高是藏族特有的生理适应特征的假说。并根据研究结果，提出了 “NO 钝化调节 ” 的新假说。

该假说认为，藏族血液 NO 水平的调控类似于其血红蛋白的调控。世居高海拔的藏族与生活在平原地区的人群相比有较高的血红蛋白水平，这有利于在高原低氧环境下机体更有效的运输氧。但高原藏族血红蛋白的升高是有限度的，这源于机体对高原低氧的钝化反应，从而可以避免红细胞过度增殖导致的慢性高原病。前期研究表明，参与藏族血红蛋白钝化调节的主要是 *EPAS1* 和 *EGLN1* 两个重要的低氧代谢通路基因。同样的，藏族血液 NO 水平的 “ 温和上升 ” 有利于舒张血管从而促进氧的运输，但由于 NO 的钝化调节使得上升幅度得到控制，避免 NO 过度升高可能带来的负效应。该研究成果发表在 *National Science Review* 上。

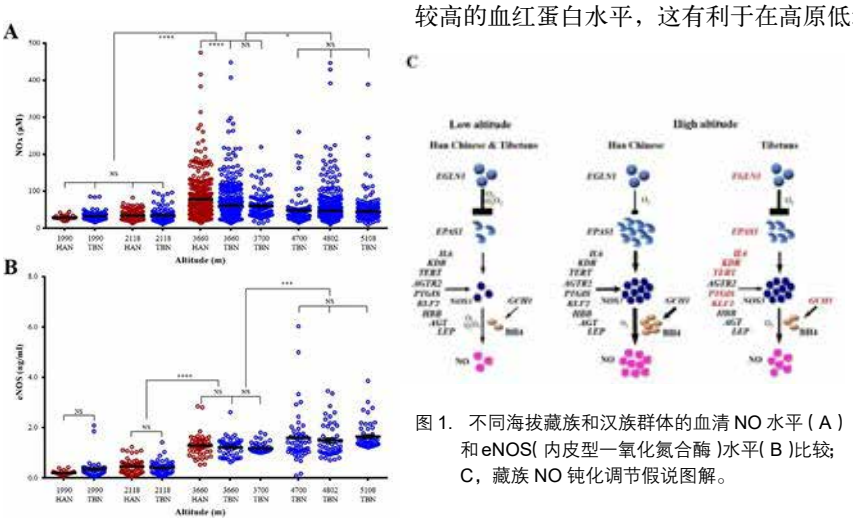


图 1. 不同海拔藏族和汉族群体的血清 NO 水平 (A) 和 eNOS(内皮型一氧化氮合酶)水平(B)比较; C，藏族 NO 钝化调节假说图解。

研究方向二：基因与基因组的进化

代表性成果二

人群环境适应遗传机制方面取得新进展

Darwinian Positive Selection on the Pleiotropic Effects of *KITLG* Explain Skin Pigmentation and Winter Temperature Adaptation in Eurasians

Zhaohui Yang,[†,1,2,4] Hong Shi,[†,1,4] Pengcheng Ma,[†,2] Shilei Zhao,[3] Qinghong Kong,[5] Tianhao Bian,[1,4] Chao Gong,[1,4] Qi Zhao,[1,4] Yuan Liu,[5] Xuebin Qi,[2] Xiaoming Zhang,[2] Yinglun Han,[6] Jiewei Liu,[2] Qingwei Li,[6] Hua Chen,[*,3] and Bing Su[*,2,7]

Abstract

Human skin color diversity is considered an adaptation to environmental conditions such as UV radiation. Investigations into the genetic bases of such adaptation have identified a group of pigmentation genes contributing to skin color diversity in African and non-African populations. Here, we present a population analysis of the pigmentation gene *KITLG* with previously reported signal of Darwinian positive selection in both European and East Asian populations. We demonstrated that there had been recurrent selective events in the upstream and the downstream regions of *KITLG* in Eurasian populations. More importantly, besides the expected selection on the *KITLG* variants favoring light skin in coping with the weak UV radiation at high latitude, we observed a *KITLG* variant showing adaptation to winter temperature. In particular, compared with UV radiation, winter temperature showed a much stronger correlation with the prevalence of the presumably adaptive *KITLG* allele in Asian populations. This observation was further supported by the in vitro functional test at low temperature. Consequently, the pleiotropic effects of *KITLG*, that is, pigmentation and thermogenesis were both targeted by natural selection that acted on different *KITLG* sequence variants, contributing to the adaptation of Eurasians to both UV radiation and winter temperature at high latitude areas.

Molecular Biology and Evolution. 2018, 35: 2272-2283.

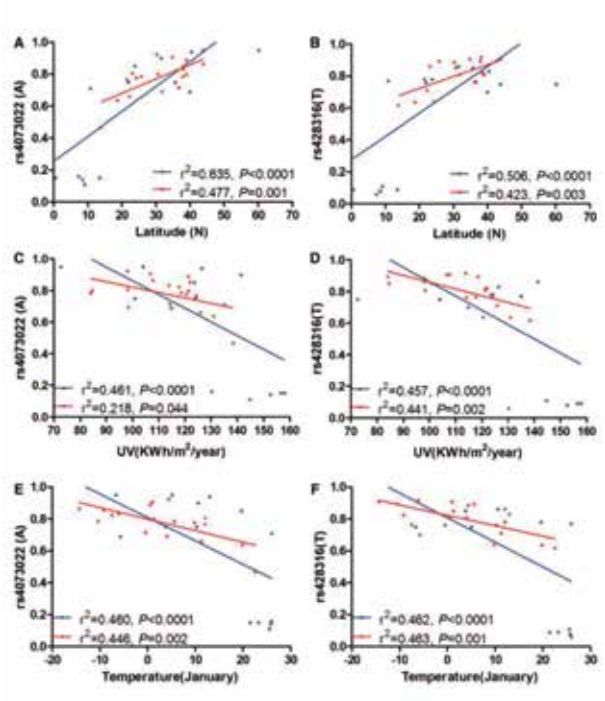


图 1. 不同海拔藏族和汉族群体的血清 NO 水平（A）和 eNOS（内皮型一氧化氮合酶）水平（B）比较；C，藏族 NO 钝化调节假说图解。

人群肤色的差异是对紫外辐射强弱变化最有代表性的适应表型。总体来看，生活在赤道附近的人群肤色较深，而生活在高纬度地区的人群肤色较浅。然而，纬度的变化除了导致紫外辐射强度的改变还会导致温度的变化，特别是冬季气候的变化。紫外辐射与气温是随纬度变化同时变化的环境因子，在遗传上是否存在同时导致对这两种环境因子变化适应的基因呢？

宿兵研究团队与昆明理工大学和中科院北京基因组所合作，通过群体遗传和细胞功能实验的分析发现 *KITLG* 基因在欧洲和东亚群体中均存在显著的达尔文正选择信号，且选择信号出现在基因的不同区域，包括基因上游和下游的调控区。他们推测，*KITLG* 在现代人走出非洲向高纬度地区扩散的过程中可能经历了不止一次的选择事件。他们发现 *KITLG* 基因上不仅存在欧亚群体中富集的导致肤色变浅的突变，还在基因的其它区域富集了对寒冷适应的突变，并通过细胞低温培养实验进行了验证。这是一个基因的多种功能（基因多效性）在人群中同时受到选择并影响表型的例证，对了解人类环境适应和表型多样性的遗传基础具有重要的启示。研究成果发表在 *Molecular Biology and Evolution*。

MOLECULAR BIOLOGY AND EVOLUTION

研究方向二：基因与基因组的进化 代表性成果三

等位基因特异的 RNA 编辑研究取得新进展

Genome wide analyses uncover allele-specific RNA editing in human and mouse

Zhong-Yin Zhou[1,†], Yue Hu[2,†], Aimin Li[3,†], Ying-Ju Li[4,5,†], Hui Zhao[4,†], Si-Qi Wang[4,5], Newton O. Otecko[1,6], Dejiu Zhang[7], Jin-Huan Wang[1], Yajun Liu[8], David M. Irwin[9], Yan Qin[7] and Ya-Ping Zhang[1,10,*]

Abstract

RNA editing is one of the most common RNA level modifications that potentially generate amino acid changes similar to those resulting from genomic nonsynonymous mutations. However, unlike DNA level allele-specific modifications such as DNA methylation, it is currently unknown whether RNA editing displays allele-specificity across tissues and species. Here, we analyzed allele-specific RNA editing in human tissues and from brain tissues of heterozygous mice generated by crosses between divergent mouse strains and found a high proportion of overlap of allele-specific RNA editing sites between different samples. We identified three allele-specific RNA editing sites cause amino acid changes in coding regions of human and mouse genes, whereas their associated SNPs yielded synonymous differences. *In vitro* cellular experiments confirmed that sequences differing at a synonymous SNP can have differences in a linked allele-specific RNA editing site with nonsynonymous implications. Further, we demonstrate that allele-specific RNA editing is influenced by differences in local RNA secondary structure generated by SNPs. Our study provides new insights towards a better comprehension of the molecular mechanism that link SNPs with human diseases and traits.

Nucleic Acids Research. 2018, 46: 8888-8897.

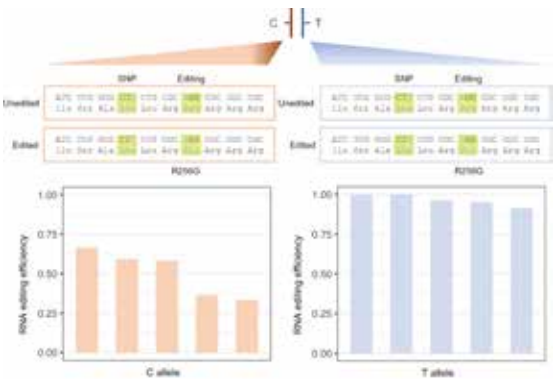


图 1. Allele-specific RNA editing causes an amino acid change in the product of the Dact3 gene in the mouse

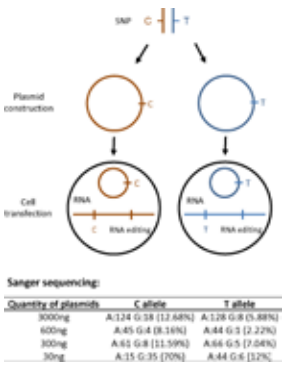


图 2. 细胞实验证实 SNP 会引起等位基因特异的 RNA 编辑

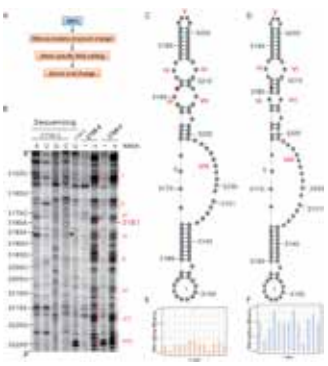


图 3. RNA secondary structure and allele-specific RNA editing.

RNA 编辑是 RNA 水平一种常见的修饰，是增加基因转录和功能多样性的重要形式。张亚平研究团队研究了人类和小鼠各种组织中等位基因特异的 RNA 编辑情况。在人中鉴定出 315 个等位基因特异的 RNA 编辑位点，且这些位点在不同组织中有相当比例的重叠。同时，利用远源杂交的小鼠，鉴定到 184 个等位基因特异的 RNA 编辑位点，并发现在不同的杂交组合中有相当比例的重叠，这提示这个鉴定方法是可信的，并证明等位基因特异的 RNA 编辑是广泛存在的。有意思的是，在鉴定的等位基因特异的 RNA 编辑位点中有部分位点引起了氨基酸的改变，然而，与之临近的 SNP 却为同义突变。细胞水平的突变实验揭示这些同义突变的位点会影响 RNA 编辑的编辑效率（图 2），也就是，同义突变的 SNP 会导致引起氨基酸改变的 RNA 编辑表现为等位基因特异的修饰。进一步的 SHAPE 实验揭示，SNP 通过影响 RNA 二级结构从而产生等位基因特异的 RNA 编辑。该工作为等位基因特异的 RNA 编辑研究提供了一个成功的范例，也为解释和疾病以及性状改变相关的同义突变提供了新的思路。该研究工作发表在 *Nucleic Acids Research*。

Nucleic Acids Research

研究方向二：基因与基因组的进化

代表性成果四

比较基因组学研究揭示结构变异和新基因在家犬驯化中的作用

Structural variation during dog domestication: insights from gray wolf and dhole genomes

Guo-Dong Wang[1,2,†], Xiu-Juan Shao[3,†], Bing Bai[4,5,†], Junlong Wang[6,7], Xiaobo Wang[3], Xue Cao[8], Yan-Hu Liu[9], Xuan Wang[1,10], Ting-Ting Yin[1,10], Shao-Jie Zhang[9], Yan Lu[11], Zechong Wang[11], Lu Wang[9], Wenming Zhao[12], Bing Zhang[12], Jue Ruan[3,*] and Ya-Ping Zhang[1,2,*]

Abstract

Several processes like phenotypic evolution, disease susceptibility and environmental adaptations, which fashion the domestication of animals, are largely attributable to structural variations (SVs) in the genome. Here, we present high-quality draft genomes of the gray wolf (*Canis lupus*) and dhole (*Cuon alpinus*) with scaffold N50 of 6.04 Mb and 3.96 Mb, respectively. Sequence alignment comprising genomes of three canid species reveals SVs specific to the dog, particularly 16 315 insertions, 2565 deletions, 443 repeats, 16 inversions and 15 translocations. Functional annotation of the dog SVs associated with genes indicates their enrichments in energy metabolisms, neurological processes and immune systems. Interestingly, we identify and verify at population level an insertion fully covering a copy of the *AKR1B1* (Aldo-Keto Reductase Family 1 Member B) transcript. Transcriptome analysis reveals a high level of expression of the new *AKR1B1* copy in the small intestine and liver, implying an increase in *de novo* fatty acid synthesis and antioxidant ability in dog compared to gray wolf, likely in response to dietary shifts during the agricultural revolution. For the first time, we report a comprehensive analysis of the evolutionary dynamics of SVs during the domestication step of dogs. Our findings demonstrate that retroposition can birth new genes to facilitate domestication, and affirm the importance of large-scale genomic variants in domestication studies.

National Science Review. 2018, doi:10.1093/nsr/nwy076.

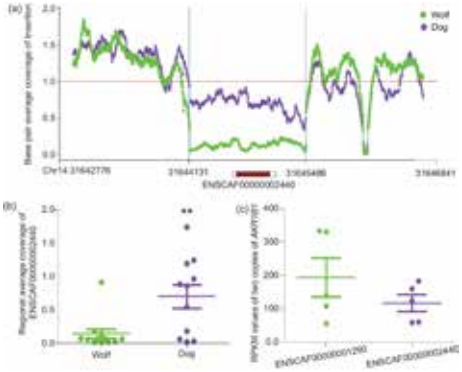


图 1. *AKR1B1* (ENSCAFG00000001290) and the dog-specific insertion (chromosome 14:31642776–31646841) in detail.

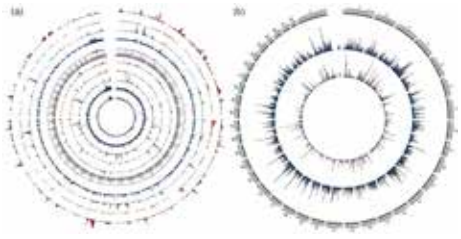


图 2. Structural variation in the dog genome.

张亚平研究团队长期致力于家养动物的起源和驯化研究。因为缺乏家犬的野生近缘种和外群的基因组，前期研究大都集中在单核苷酸多态位点（SNPs）上，而对结构变异这一类大尺度基因组变异研究甚少。结构变异包括大的插入缺失、重复、倒位、易位等，在表型多样性、疾病易感性、环境适应中扮演了重要的作用。研究人员通过二代测序和基因组从头组装的方法，获得了灰狼（*Canis lupus*）和豺狗（*Cuonalpinus*）的基因组，scaffold N50 分别为 6.04 Mb 和 3.96 Mb。通过对家犬、灰狼、豺狗三个犬科物种的基因组比较分析，得到家犬驯化特异的结构变异，包括 16,315 个插入，2,565 个缺失，443 个重复，16 个倒位，和个 15 易位。这些结构变异显著的影响到能量代谢、神经处理过程、和免疫系统相关的基因。更有意思的是，研究发现家犬基因组中一个通过逆转录转座（retroposition）产生的新基因 ENSCAFG00000002440，它作为 AKR1B1 的新拷贝在小肠和肝脏中高表达，参与脂肪的从头合成和降低高淀粉饮食带来的毒性等功能。这一发现不仅阐明了家犬从肉食性到杂食性的遗传机制，而且展示了新基因在家养动物驯化过程中的作用。本研究为家养动物的驯化研究提供了新的思路和视角。该研究成果发表在 *National Science Review* 上。

研究方向三：遗传、发育与进化

代表性成果一

揭示百岁老人长寿重要的健康保护机制

Transcriptome evidence reveals enhanced autophagy-lysosomal function in centenarians

Fu-Hui Xiao,[1,2,4,7,12] Xiao-Qiong Chen,[1,2,4,7,12] Qin Yu,[1,2,4,5,7,12] Yunshuang Ye,[5,6,12] Yao-Wen Liu,[1,2,4,5,7] Dongjing Yan,[3] Li-Qin Yang,[1,2,4,7] Guijun Chen,[6] Rong Lin,[8] Liping Yang,[6] Xiaoping Liao,[9] Wen Zhang,[3] Wei Zhang,[5,6] Nelson Leung-Sang Tang,[4,10] Xiao-Fan Wang,[11] Jumin Zhou,[6] Wang-Wei Cai,[3] Yong-Han He,[1,2,4,7] and Qing-Peng Kong[1,2,4,7]

Abstract

Centenarians (CENs) are excellent subjects to study the mechanisms of human longevity and healthy aging. Here, we analyzed the transcriptomes of 76 centenarians, 54 centenarian-children, and 41 spouses of centenarian-children by RNA sequencing and found that, among the significantly differentially expressed genes (SDEGs) exhibited by CENs, the autophagy-lysosomal pathway is significantly up-regulated. Overexpression of several genes from this pathway, *CTSB*, *ATP6V0C*, *ATG4D*, and *WIPI1*, could promote autophagy and delay senescence in cultured IMR-90 cells, while overexpression of the *Drosophila*homolog of *WIPI1*, *Atg18a*, extended the life span in transgenic flies. Interestingly, the enhanced autophagy-lysosomal activity could be partially passed on to their offspring, as manifested by their higher levels of both autophagy-encoding genes and serum beclin 1 (BECN1). In light of the normal age-related decline of autophagy-lysosomal functions, these findings provide a compelling explanation for achieving longevity in, at least, female CENs, given the gender bias in our collected samples, and suggest that the enhanced waste-cleaning activity via autophagy may serve as a conserved mechanism to prolong the life span from *Drosophila* to humans.

Genome Research. 2018, 28: 1601-1610.

作为人类健康老龄典范的长寿老人（尤其是百岁老人），不但具有显著延长的寿命，而且还能延缓甚至规避一些重大老年性疾病的发生。揭示其健康衰老保护机制，将为延缓衰老、改善老年人健康提供新视角和新策略。

孔庆鹏研究团队与周巨民课题组及海南医学院蔡望伟教授团队合作，获得并分析海南长寿家系 171 例样本（百岁老人、百岁老人 F1 后代和 F1 后代配偶）外周血白细胞转录组数据（RNA-seq）。基于组学分析及细胞、果蝇等功能实验，提示自噬-溶酶体信号通路功能增强可能有助于人类健康寿命延长。该研究成果发表于 *Genome Research*，并被遴选为该杂志第 11 期的封面文章。

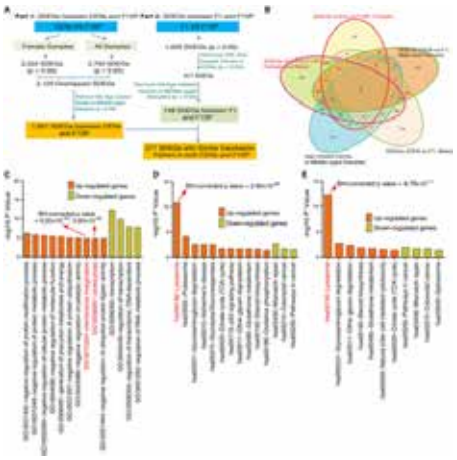


图 1. Significantly differentially expressed genes (SDEGs) between the CEN and F1SP groups.

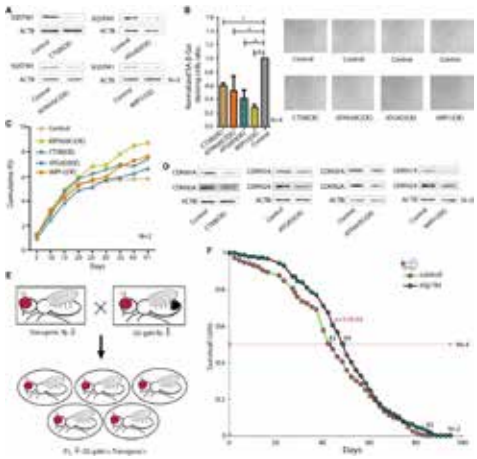


图2. Functional studies of up-regulated autophagy-lysosomal genes in IMR-90 cells and transgenic flies

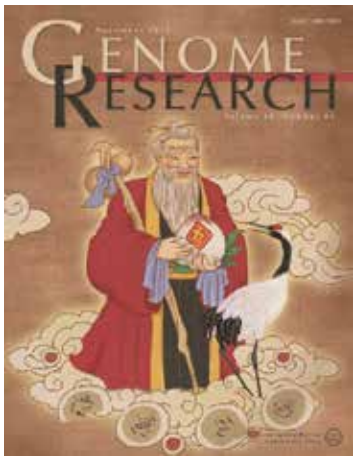


图 3. Genome Research 杂志 2018 年第 11 期封面

研究方向三： 遗传、发育与进化

代表性成果二

揭示突触可塑性长时程增强（LTP）的突触后分子机制

LTP requires postsynaptic PDZ-domain interactions with glutamate receptor/auxiliary protein complexes

Nengyin Sheng[a,b,c,1], Michael A. Bemben[c], Javier Díaz-Alonso[c], Wucheng Tao[c], Yun Stone Shi[c,d], and Roger A. Nicoll[c,e,1]

Abstract

Long-term potentiation (LTP) is a persistent strengthening of synaptic transmission in the brain and is arguably the most compelling cellular and molecular model for learning and memory. Previous work found that both AMPA receptors and exogenously expressed kainate receptors are equally capable of expressing LTP, despite their limited homology and their association with distinct auxiliary subunits, indicating that LTP is far more promiscuous than previously thought. What might these two subtypes of glutamate receptor have in common? Using a single-cell molecular replacement strategy, we demonstrate that the AMPA receptor auxiliary subunit TARP γ-8, via its PDZ-binding motif, is indispensable for both basal synaptic transmission and LTP. Remarkably, kainate receptors and their auxiliary subunits Neto proteins share the same requirement of PDZ-binding domains for synaptic trafficking and LTP. Together, these results suggest that a minimal postsynaptic requirement for LTP is the PDZ binding of glutamate receptors/auxiliary subunits to PSD scaffolding proteins.

PNAS. 2018, 115: 3948-3953.

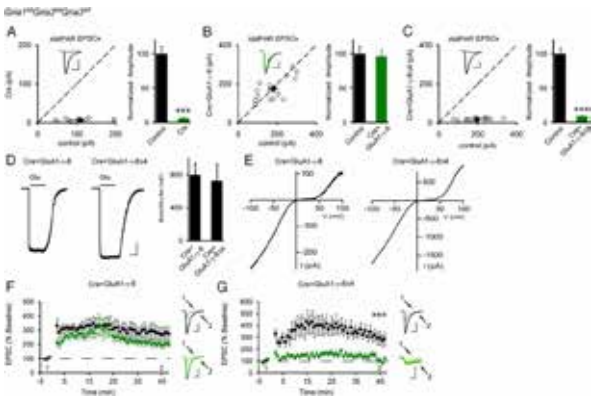


图 1. 在 Gria1fl/fl Gria2 fl/fl Gria3 fl/fl 条件性敲除小鼠海马 CA1 神经元中敲除 AMPA 受体、将其替换为 GluA-g-8 融合受体或 PDZ 结构位点缺失的 GluA-g-8D4 突变受体后，神经电生理分别考察其对突触传递（A-C）和突触可塑性 LTP（D-E）的影响。PDZ-binding motif-mediated interaction is required for basal synaptic trafficking and LTP of AMPARs.

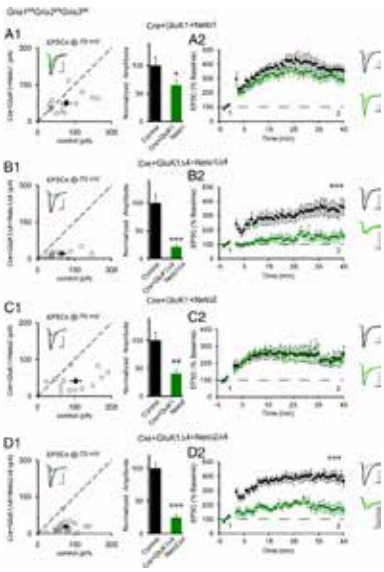


图 2. PDZ-binding motif-mediated interaction is required for synaptic trafficking and plasticity of KARs

盛能印研究团队与美国加州大学旧金山分校 Roger Nicoll 实验室合作，以 AMPA 受体基因条件性敲除小鼠为研究系统，研究谷氨酸受体复合物与突触后 PDZ 支架蛋白的相互作用在长时程增强 (LTP) 中的功能和机制。结合海马脑片和神经电生理等手段，研究结果表明，无论是由何种谷氨酸受体所介导，LTP 表达的突触后机制很保守且由共同的机制所调控；在 LTP 过程中，突触后 PDZ 支架蛋白是主要功能靶点，而谷氨酸受体的突触转运则可能为被动协同过程。

该项研究工作揭示了突触可塑性长时程增强的突触后分子机制，为进一步阐明学习记忆的分子机制以及相关神经精神疾病的发病机理提供了重要理论基础。成果发表于 *Proceedings of the National Academy of Sciences*。

研究方向三： 遗传、发育与进化

代表性成果三

揭示灵长类早期胚胎发育多能性的变化模式

Single-cell RNA-sequencing reveals the existence of naive and primed pluripotency in pre-implantation rhesus monkey embryos

Denghui Liu,[2,5,7] Xinyi Wang,[1,3,7] Dajian He,[1,3,5,7] Chunli Sun,[1,3,5,7] Xiechao He,[4] Lanzhen Yan,[4] Yizhou Li,[2] Jing-Dong J. Han,[2] and Ping Zheng[1,3,4,6]

Abstract

Naive pluripotency exists in epiblast cells of mouse pre-implantation embryos. However, whether the naive pluripotency is transient or nonexistent in primate embryos remains unclear. Using RNA-seq in single blastomeres from 16-cell embryos through to hatched blastocysts of rhesusmonkey, we constructed the lineage segregation roadmap in which the specification of trophectoderm, epiblast, and primitive endoderm is initiated simultaneously at the early blastocyst stage. Importantly, we uncovered the existence of distinct pluripotent states in monkey pre-implantation embryos. At the early- and middle-blastocyst stages, the epiblast cells have the transcriptome features of naive pluripotency, whereas they display a continuum of primed pluripotency characteristics at the late and hatched blastocyst stages. Moreover, we identified potential regulators that might play roles in the transition from naive to primed pluripotency. Thus, our study suggests the transient existence of naive pluripotency in primates and proposes an ideal time window for derivation of primate embryonic stem cells with naive pluripotency.

Genome Research. 2018, 28:1481-1493.

郑萍研究团队通过单细胞转录组方法，分析了猕猴着床前胚胎发育过程中，早期细胞命运分化调控，并重点研究了四个囊胚发育阶段（早期囊胚，中期囊胚，晚期囊胚，孵化囊胚），上胚层细胞多能性的动态变化。发现猕猴早期胚胎细胞命运决定模式和调控与人类胚胎极其相似，并首次揭示了灵长类着床前胚胎中存在发育多能性由原始态向始发态的转变过程。

该研究揭示了灵长类和啮齿类早期胚胎细胞多能性变化模式的差异，发现了灵长类原始多能性存在的时间窗口，为体外建立原始多能性灵长类胚胎干细胞奠定了重要基础。研究成果发表于 *Genome Research*，并被遴选为该杂志第 10 期的封面文章。

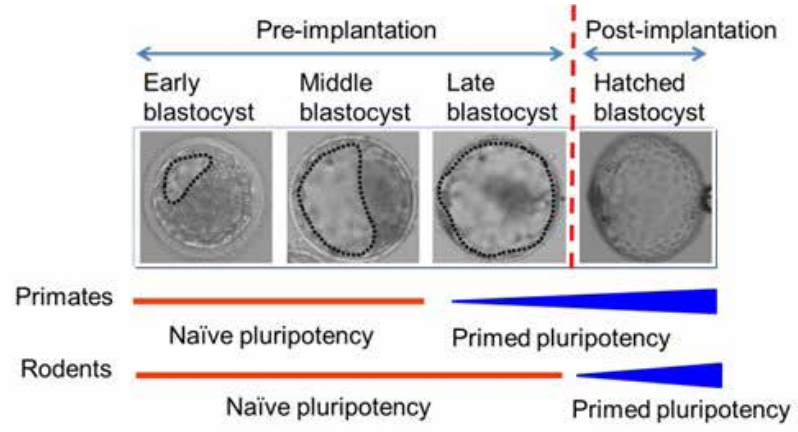


图 1. 灵长类和啮齿类早期胚胎具不同的多能态变化特征。

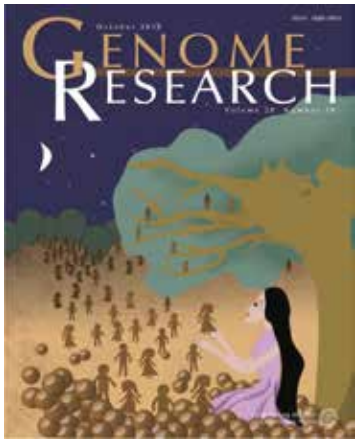


图 2. Genome Research 杂志 2018 年第 10 期封面

研究方向三： 遗传、发育与进化

代表性成果四

选择性剪接在三阴性乳腺癌进程中的调控作用

Loss of TDP43 inhibits progression of triple-negative breast cancer in coordination with SRSF3

Hao Ke[a,b,1], Limin Zhao[a,b,1], Honglei Zhang[a,1], Xu Feng[a,c], Haibo Xu[a,b], Junjun Hao[a], Shaowei Wang[a,d], Qin Yang[a], Li Zou[a], Xiaosan Su[e], Liqiong Wang[f], Chunlian Wu[d], Yang Wang[g], Jianyun Nie[h], and Baowei Jiao[a,2]

Abstract

Aberrant alternative splicing has been highlighted as a potential hallmark of cancer. Here, we identify TDP43 (TAR DNA-binding protein 43) as an important splicing regulator responsible for the unique splicing profile in triple-negative breast cancer (TNBC). Clinical data demonstrate that TDP43 is highly expressed in TNBC with poor prognosis. Knockdown of TDP43 inhibits tumor progression, including proliferation and metastasis, and overexpression of TDP43 promotes proliferation and malignancy of mammary epithelial cells. Deep sequencing analysis and functional experiments indicate that TDP43 alters most splicing events with splicing factor SRSF3 (serine/arginine-rich splicing factor 3), in the regulation of TNBC progression. The TDP43/SRSF3 complex controls specific splicing events, including downstream genes *PAR3* and *NUMB*. The effect of reduced metastasis and proliferation upon the knockdown of TDP43 or SRSF3 is mediated by the splicing regulation of *PAR3* and *NUMB* exon 12, respectively. The TDP43/SRSF3 complex and downstream PAR3 isoform are potential therapeutic targets for TNBC.

PNAS. 2018, 10, 115(15): E3426-E3435.

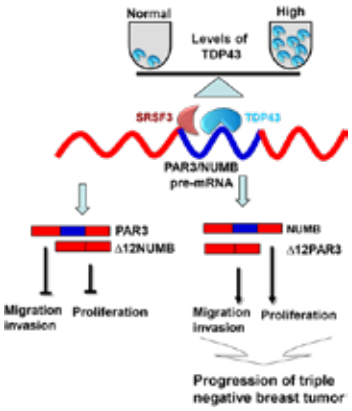


图 1. TDP43 在剪接事件中的调控作用

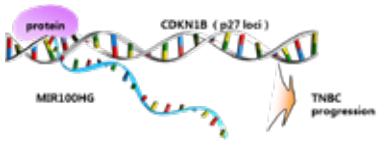


图 2.16 种肿瘤原发实体瘤标本与正常组织标本 X:AA 比值

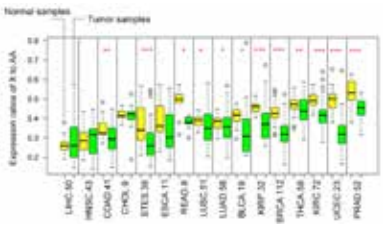


图 3. MIR100HG 与 CDKN1B 形成三螺旋结构调控 TNBC 进程

三阴性乳腺癌（TNBC）是一类恶性程度较高的乳腺癌分型。相对于其他类型的乳腺癌，三阴性乳腺癌表现出转移率高、细胞增殖快和预后差等特征。而目前缺乏三阴型乳腺癌的成功靶向药物。

焦保卫研究团队首先利用生物信息学分析发现：相比于其他乳腺癌亚型，三阴性乳腺癌存在独特的选择性剪接谱。这种独特剪接模式的调控因子可能做为三阴性乳腺癌潜在的药物靶点。因此，该课题组沿着这个研究思路发现：剪接因子 TDP43 在三阴性乳腺癌的选择剪接谱中发挥主导功能。TDP43 在三阴性乳腺癌中高表达，且高表达对应预后差；在三阴性乳腺癌细胞系中敲降 TDP43 表达抑制了细胞增殖、促进细胞凋亡、抑制细胞转移侵袭能力。反之 TDP43 高表达则促进肿瘤细胞的恶性生长。通过蛋白质谱、转录组分析与功能实验验证等，课题组进一步发现 TDP43 与另一个剪接因子 SRSF3 形成剪接复合物，协同调控三阴性乳腺癌的选择性剪接事件。最后，通过功能回补实验，确定该复合物通过调控下游基因 PAR3 与 NUMB 的选择性剪接，进而影响三阴性乳腺癌增殖与转移能力。上述结果表明 TDP43 可以作为三阴性乳腺癌治疗的潜在靶标，该项研究将为从三阴性乳腺癌的独特剪接谱角度为治疗靶点提供新的研究方向。

该研究工作发表在 *Proceedings of the National Academy of Sciences*。

系统进化与生物地理学

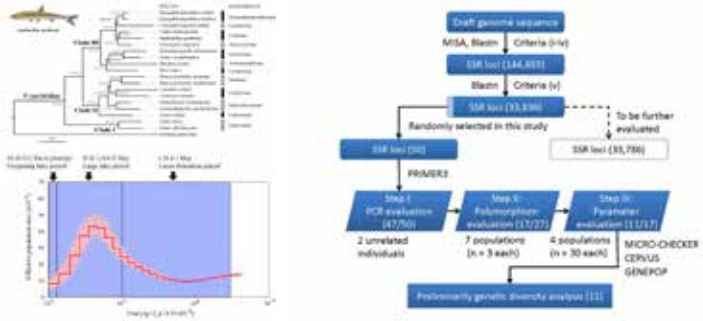
杨君兴，博士，研究员，博士生导师。研究方向包括：生物多样的考察监测及评价、系统分类、系统发育与生物地理学；珍稀特有物种的生态学研究和保育；湿地生态系统的恢复研究。本年度共有在研课题 22 项，其中新申请批准的项目 6 项。获得滇池金线鲃“鲃优 1 号”水产新品种。发表论文 11 篇，其中 SCI 论文 10 篇，获授权国家发明专利 2 项，云南省专利二等奖 1 项。

重要成果及产出：

1. **Jiang WS, Yang JX*.** et al. 2018. Genome Assembly for a Yunnan-Guizhou Plateau “3E” Fish, Anabarilius grahami (Regan), and Its Evolutionary and Genetic Applications. Frontiers in Genetics, 9: 264. Doi: 10.3389/fgene.2018.00614.
2. **Endruweit M*.** 2018. Description of four new species of freshwater gobies from the Black River drainage in China and Vietnam (Teleostei: Gobiidae). Zootaxa, 4486 : 284–310.
3. Ren Q, **Yang JX***, and Chen XY*. 2018. Phylogeographical and morphological analyses of *Triplophysa stenura* (Cypriniformes: Nemacheilidae) from the three parallel rivers region, China. Zoological Studies, 57: 26-39.
4. **Yu GH**, Hui H, Rao DQ*, **Yang JX*. 2018**. A new species of Kurixalus from western Yunnan, China (Anura, Rhacophoridae). Zookeys, 770: 211-226.
5. **Zheng LP**, He Y, **Yang JX***, Wu LB. 2018. A new genus and species of Labeonini (Teleostei: Cyprinidae) from the Pearl River in China. PLoS ONE, 13(7): e0199973.
6. **Zheng LP***, Qin T, Chen XY*. 2018. *Altigena malihkaia*, a new species of Labeonini (Teleostei: Cyprinidae) from the Irrawaddy River basin in Myanmar. Zootaxa, 4476 : 87–93.
7. **潘晓赋，王晓爱，杨君兴，刘倩，杨坤凤**. 一种短须裂腹鱼人工繁殖方法. 专利号：201510863420.7
8. **潘晓赋，王晓爱，杨君兴，刘倩**. 一种暗色唇鱼肝脏细胞系的构建方法. 专利号：201510204441.8
9. **杨君兴，潘晓赋，李再云，** 陈小勇. 一种暗色唇鱼的人工繁殖方法. 云南省专利奖二等奖

1. “3E”鱼类——鳡鮈白鱼全基因组测序与进化遗传应用

云南四大名鱼之一鳡鮈白鱼是云贵高原一种典型的“3E”鱼类，即具有濒危（Endangered）、特有（Endemic）和经济价值（Economic）三重特点。为了推动其物种保护和可持续利用，我们对其开展了全基因组测序组装等分析。组装获得的该物种基因组大小为 1.006 Gb，共注释到 25,250 个蛋白编码基因。基于组装注释的鳡鮈白鱼全基因组，我们开展了三个方面的进化遗传分析。首先，我们下载了现今公共数据库中 18 种鲤科鱼类的基因组或转录组数据，通过比对获得了 4,580 单拷贝同源基因，基于这些基因构建了首个基于组学数据规模的鲤科鱼类各亚科之间的系统发育关系。其次，构建鳡鮈白鱼的种群历史表明，其种群动态与抚仙湖湖泊形成演化的三个周期具有非常密切的联系。再次，基于组装的基因组，我们开发获得了 33,836 个微卫星位点。随机选取 50 个位点，经过三重筛选，最终选择 11 条对鳡鮈白鱼 4 个种群进行了遗传多样性评估。本次鳡鮈白鱼全基因组测序为其后续物种保护与开发利用提供了重要的基因资源。



2. 野鲮亚科、原指树蛙属等类群分类取得综合进展

本年度课题组成员对野鲮亚科、原指树蛙属等类群进行了分类学研究，发现了 3 新种，分别是靖西左江鱼、迈立开高鲮和杨氏原指树蛙。分类学研究共发表 SCI 论文 3 篇。

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

滇池金线鲃“鲃优 1 号”正式获得农业农村部认定，获得水产新品种证书。

2018 年繁殖滇池金线鲃鱼苗 200 余万尾，抚仙金线鲃鱼苗 3 万余尾。突破后背鲈鲤和大理裂腹鱼的人工繁殖，繁殖后背鲈鲤 500 余尾、大理裂腹鱼 3000 余尾、程海白鱼 3 万余尾、宽鳍鱲 1000 余尾、桥街结鱼 1000 余尾、大眼圆吻鲴 50 万余尾。繁殖西畴金线鲃 2 万余尾，繁殖鳡鱼良白鱼 20 万余尾，繁殖软鳍新光唇鱼 50 万余尾（其中昆明 1 万余尾，西畴 50 万余尾）。繁殖短须裂腹鱼 30 万余尾（其中昆明 3000 余尾，会泽 30 万余尾）。

目前，珍稀鱼类保育基地饲养有土著鱼类 50 余种，40 万余尾，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、会泽、通海、芒市、保山、丽江、大理等养殖基地定期进行技术指导。

2018 年度在昆明晋宁古滇艺码头放流滇池金线鲃 10 万余尾，在杞麓湖放流杞麓鲤 1 万余尾。支持西畴、会泽三个水产公司滇池金线鲃鱼苗 30 余万尾，裂腹鱼、光唇鱼等种鱼 100 余千克。

Phylogenetics and Biogeography

Prof. Junxing Yang, Professor. 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. In 2018, total 22 research programs have been implementing with 6 programs newly approved. Certification of *Sinocyclocheilus grahami* breeding line has been awarded. A total of 11 papers have been published which 10 of them are SCI papers. Two national invention patent licensing and one patent second prize of Yunnan Province .

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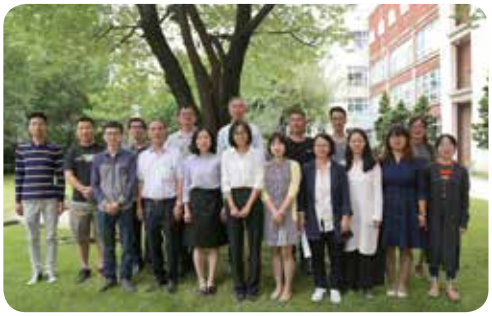
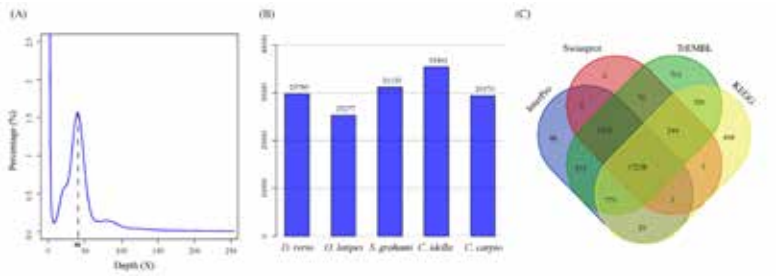


1. Genome assembly for a Yunnan-Guizhou Plateau "3E" fish, Anabarilius grahami (Regan), and its evolutionary and genetic applications

Kanglang white minnow (Anabarilius grahami), is a typical "3E" (Endangered, Endemic, and Economic) species in Yunnan-Guizhou Plateau of China. To promote the conservation and sustainable utilization of this fish, we initiated its whole genome sequencing project using an Illumina Hiseq2500 platform. The assembled genome size of A. grahami is 1.006 Gb, and a total of 25,520 protein-coding genes were subsequently predicted. A phylogenetic tree based on 4,580 single-copy genes from A. grahami and 18 other cyprinids revealed three well-supported subclades within the Cyprinidae. This is the first inter-subfamily relationship of cyprinids at genome level, providing a simple yet useful framework for understanding the traditional but popular subfamily classification systems. A further population demography of A. grahami uncovered a historical relationship between this fish and Fuxian Lake, suggesting that range expansion or shrinkage of the habitat has had a remarkable impact on the population size of endemic plateau fishes. Additionally, a total of 33,836 simple sequence repeats (SSR) markers were identified, and 11 loci were evaluated for a preliminary genetic diversity analysis in this study, thus providing another useful genetic resource for studying this "3E" species.



2. The taxonomy of *Kurixalus* and *Exostoma*

In this year, we described three new species (*Zuojiangia jingxiensis* sp. nov., *Altigena malihkaia* sp. nov. and *Kurixalus yangi* sp. nov.) from Guangxi, Myanmar and Yunnan province. These three new species is distinguished from their congeneric species by a combination of morphological evidence.

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

Certification of *Sinocyclocheilus grahami* breeding line has been awarded. In this year, we cultivated and produced more than 3 million fish fry of these fishes, including *Sinocyclocheilus grahami*, *Sinocyclocheilus tingi*, *Percocypris retrodorslis*, *Schizothorax taliensis*, *Anabarilius liui chenghaiensis*, *Zacco platypus*, *Anabarilius grahami*, *Tor qiaojiensis* and *Distoechodon macrophthalmus*. More than 0.1 million individuals were released in wild to rebuilt and restore the wild population of these fishes.


水产新品种
证书

Certification of *Sinocyclocheilus grahami* breeding line

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工作人员 (Staff)

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彭　云　学士　研究实习员
Yun Peng, Research assistant

研究生 (Graduate Students)

Marco Endruweit 2014
牛诚祎 Chengyi Niu 2015
杜丽娜 Lina Du 2016
孙　超 Chao Sun 2017
殷艳慧 Yanhui Yin 2017
吴安丽 Anli Wu 2017
潘晓赋 Xiaofu Pan 2018
黄新迪 Xindi Huang 2018

兽类生态与进化

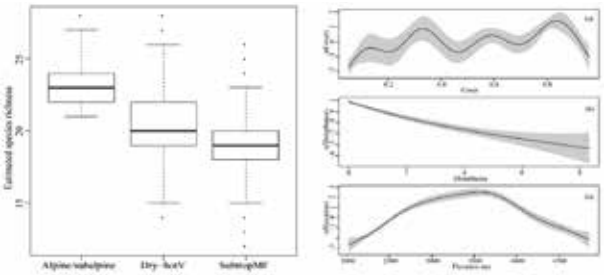
蒋学龙，博士，研究员。立足于东喜马拉雅－横断山地区开展哺乳动物生态与进化研究，主要研究内容包括哺乳动物分类、系统演化与生物地理，灵长类动物的生态行为，兽类资源考察、监测与保护，以揭示横断山地区哺乳动物多样性的形成机制及在特殊生态条件下的适应性进化与保护。近年来，主要以东喜马拉雅－横断山地区特有与常见小型哺乳动物、灵长类及地栖大中型兽类为研究对象，重点研究横断山区哺乳动物分布格局及其演化机制、西黑冠长臂猿的生态行为与适应性，并全面布局横断山区兽类资源监测网络与数据库建设，开展亚洲象生态学研究，为人象冲突防范与亚洲象保护提供科学对策。

重要成果及产出：

1. **Li, XY.**, W. V. Bleisch, **XL. Jiang***. 2018. Using large spatial scale camera trap data and hierarchical occupancy models to evaluate species richness and occupancy of rare and elusive wildlife communities in southwest China. Diversity and Distributions 24:1560-1572.
2. **Wan T**, He K, Jin W, Liu SY, Chen ZZ, Zhang B, Murphy RW, **Jiang XL***. 2018. Climate niche conservatism and complex topography illuminate the cryptic diversification of Asian shrew-like moles. Journal of Biogeography 45:2400-2414.
3. **Khanal, L.**, M. K. Chalise, K. He, B. K. Acharya, Y. Kawamoto, **XL. Jiang *.** 2018. Mitochondrial DNA analyses and ecological niche modeling reveal post-LGM expansion of the Assam macaque (*Macaca assamensis*) in the foothills of Nepal Himalaya. **American Journal of Primatology** 80:e22748.
4. **Khanal, L.**, Mukesh Kumar Chalise ,Tao Wan , **XL. Jiang** *. Riverine barrier effects on population genetic structure of the Hanuman langur (*Semnopithecus entellus*) in the Nepal Himalaya. **BMC Evolutionary Biology**,2018,18:159
5. **Li, XY.,** W. V. Bleisch, **XL. Jiang*.** 2018. Unveiling a wildlife haven: occupancy and activity patterns of mammals at a Tibetan sacred mountain. **European Journal of Wildlife Research** 64:53.
6. **Huang, C.,** XY. Li, L. Shi, **XL. Jiang*.** 2018. Patterns of human-wildlife conflict and compensation practices around Daxueshan Nature Reserve, China. **Zoological Research** 39:406-412.
7. **He K**, Chen X, Chen P, He SW, Cheng F, **Jiang XL***, Campbell K*. A new genus of Asiatic short-tailed shrew (Soricidae, Eulipotyphla) based on molecular and morphological comparisons. **Zoological Research**, 2018, 39(5): 321-334.
8. **Ai HS**, He K, Chen ZZ, Li JQ, Wan T, Li Q, Nie WH, Wang JH, Su WT, **Jiang XL*.** Taxonomic revision of the genus Mesechinus (Mammalia: Erinaceidae) with description of a new species. **Zoological Research**, 2018, 39(5): 335-347.
9. **Nie WH**, Wang JH, Su WT, Hu Y, He SW, **Jiang XL***, He K. Species identification of crested gibbons (*Nomascus*) in captivity in China using karyotyping- and PCR-based approaches. Zoological Research, 2018, 39(5): 356-363.

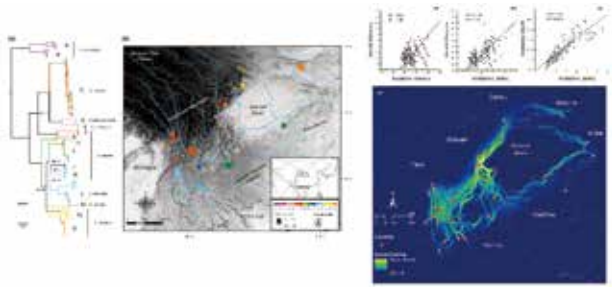
1. 西南高山峡谷区珍稀野生动物物种多样性与分布格局及其保护意义

地栖珍稀野生动物由于数量稀少、行踪隐秘而难以开展物种多样性与分布格局研究。兽类生态与进化课题组利用红外相机技术和层次占有率模型分析中国西南高山峡谷区地栖 3 类典型景观中珍稀野生动物物种多样性与分布格局，通过构建状态变量（latent variable），分层解析物种分布的生态过程（是否有分布）和调查过程（是否观察到）中的相关参数，利用随机混合效应模型预测各类景观中的物种多样性与垂直分布格局，并分层分析物种、类群以及类群集合对环境变量的响应。研究结果出乎意料的揭示干热河谷区地栖珍稀野生动物物种多样性高于亚热带山地森林，且岩羊、斑羚等偶蹄类动物对该类景观具有显著的正选择；人类活动改变了地栖珍稀野生动物的生境适宜度，表现在物种多样性随人类活动强度的增加而单调递减，方差（生境适宜性不确定性）随人类活动强度而增加。

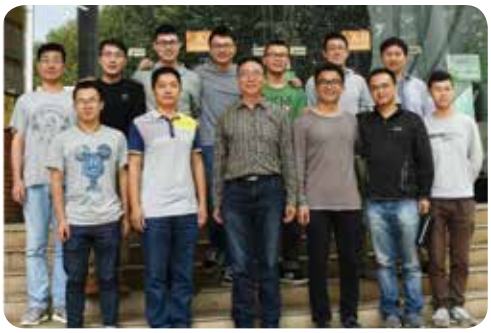


2. 亚洲鼩鼱的隐存种多样性形成机制

中国西南山地是世界上最为重要的山地生物多样性热点区域。喜马拉雅和青藏高原的隆起以及其自身的构造运动形成了以“三江并流”为代表的复杂地貌。然而，一个有趣的科学问题始终没有进行深入探讨，即为何景观复杂度高的地区利于形成遗传上高度分化但形态上却难以区分的新物种（即，隐存种现象）。为了回答这个问题，我们以亚洲鼩鼱为研究对象，通过谱系地理分析发现：（1）亚洲鼩鼱的支系主要呈异域分布，且支系之间的气候生态位显著保守，提示它们对特定环境的依赖是彼此之间隔离分化的重要因素；（2）空间距离－遗传距离的相关性结果提示，亚洲鼩鼱的遗传格局由“天空之岛”的空间分布所决定；（3）而生态位模型显示西南山地中长期稳定地存在这样的“天空之岛”，提示不同支系在彼此隔离的环境中仍然受到相似的环境压力，因此导致形态上缺乏变异，最终形成隐存种。该研究为复杂景观环境中的多样性形成提供了一套合理的解释和检测方案，对中国西南山地的动物多样性与保护具有一定启示。



Mammal Ecology and Evolution



Prof. Xuelong Jiang, 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 Henduanshan Region, and also in spatial ecology of rare and cryptic mammal faunas, behavior and conservation of black crested gibbon, as well as conservation biology of Asian elephant and other large mammals.

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1. Riverine barrier effects on population genetic structure of the Hanuman langur (*Semnopithecus entellus*) in the Nepal Himalaya

The Himalayan region, frequently referred to as the third pole of the Earth, has experienced large-scale climatic oscillations and bears geographical barriers such as rivers but their effects in shaping the demographic history and population genetic structure of organisms were documented. We examined the effects of late-Quaternary glacial-interglacial cycles and riverine barriers on the genetic composition of Hanuman langurs (Semnopithecus entellus), using the mitochondrial DNA control region (CR,1090 bp) and cytochrome B (CYTB,1140 bp) sequences combined with paleodistribution modeling. mtDNA sequences (2230 bp) successfully retrieved from 67 non-invasively collected fecal samples belonging to 18 wild Hanuman langur troops identified 37 haplotypes with haplotype and nucleotide diversities of 0.958 ± 0.015 and 0.0237 ± 0.0008, respectively. The troops were clustered into six major clades corresponding to their river-isolated spatial distribution, with the significantly high genetic variation among these clades confirming the barrier effects of the snow-fed Himalayan rivers on genetic structuring. Analysis of demographic history projected a decrease in population size with the onset of the last glacial maximum (LGM); and, in accordance with the molecular analyses, paleodistribution modeling revealed a range shift in its suitable habitat downward/southward during the LGM.

2. A new genus of Asiatic short-tailed shrew (Soricidae, Eulipotyphla) based on molecular and morphological comparisons

Blarinellini is a tribe of soricine shrews comprised of nine fossil genera and one extant genus. Blarinelline shrews were once widely distributed throughout Eurasia and North America, though only members of the Asiatic short-tailed shrew genus Blarinella currently persist . Only three forms of Blarinella have been recognized as either species or subspecies. However, recent molecular studies indicated a strikingly deep divergence within the genus, implying the existence of a distinct genus-level lineage. We sequenced the complete mitochondrial genomes and one nuclear gene of three Asiatic short-tailed and two North American shrews and analyzed them morphometrically and morphologically. Our molecular analyses revealed that specimens ascribed to B. griselda formed two deeply diverged lineages, one a close relative to B. quadraticauda, whereas the other—comprised of topotype specimens from southern Gansu—diverged from other Blarinella in the middle Miocene. Although the skulls were similarly shaped in both lineages, we observed several diagnostic characteristics, including the shape of the upper P4. In consideration of the molecular and morphological evidence, we recognize B. griselda as the sole species of a new genus, namely, Pantherina gen. nov. Interestingly, some characteristics of Pantherina griselda are more similar to fossil genera, suggesting it represents an evolutionarily more primitive form than Blarinella. Recognition of this new genus sheds light on the systematics and evolutionary history of the tribe Blarinellini throughout Eurasia and North America.

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Hong Hui, Senior Worker

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成　市 Shi Cheng　硕士生 2017 级
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Alois Wambua Mweu　硕士生 2018 级

鸟类学

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. Kong DJ, Wu F, Shan PF, Gao JY, Yan D, Luo WQ, Yang XJ*. Status and distribution changes of the endangered Green Peafowl (Pavo muticus) in China over the past three decades (1990s–2017). Avian Res. 2018, 9:18.
2. Kong DJ, Luo WQ, Liu Q, Li ZQ, Huan GY, Zhang JJ, Yang XJ*. Habitat use, preference, and utilization distribution of two crane species (Genus: Grus) in Huize National Nature Reserve, Yunnan-Guizhou Plateau, China . PeerJ.2018 6:e5105;DOI 10.7717/peerj.5105.
3. Jiang L, Wang QQ, Yu J,Vinita G, Gabriel J, Yang JK, Kan XZ, Yang XJ*. miRNAome expression profiles in the gonads of adult Melopsittacus undulatus. PeerJ.2018 6:e4615;DOI 10.7717/peerj.4615.
4. Wang QQ, Lu WK, Yang JK, Jiang L, Zhang Q, Kan XZ*, Yang XJ*. Comparative transcriptomics in three Passerida species provides insights into the evolution of avian mitochondrial complex I. CBP.2018 6:e4615;DOI 10.1016/j.cbd.2018.06.002.
5. 税玉民，武素公，王应祥，陈文红，李艳春，黄素华，杨晓君，熊江，黄顺友，张开平，莫明忠，等 . 云南大围山国家级自然保护区综合科学研究 . 昆明：云南科技出版社 , 2018. ISBN 978-7-5587-1192-3.

1. 中国濒危绿孔雀（*Pavo muticus*）在过去三十年（20 世纪 90 年代至 2017 年）的现状和分布变化

绿孔雀曾在中国 54 个县分布。在过去的三十年中，近 60%的分布县散失，仅剩的 22 个县分布在中国西南部的中部，南部和西部。除双柏县和新平县外，所有分布区域均检测到种群数量减少；双柏县和新平县的绿孔雀数量占总种群数量的 60%以上。与 20 年前相同的采访方法，此次调查仅记录到约原种群数量的 30%。865 公里的样线仅记录到 3 只绿孔雀个体，一个绿孔雀残骸，6 声鸣叫 12 处脚印，表明绿孔雀在田间的遭遇率极低。还检测到绿孔雀种群大小急剧减少，从 20 世纪 90 年代的每群 8–20 只到目前的 3–5 只。偷猎和栖息地转换是两种普遍而持久的威胁，而中毒导致过去死亡，水电建设影响了绿孔雀的生存。

2. 中国云南绿孔雀资源调查（2018 年）

2018 年 3–7 月，进行了全省 54 县绿孔雀调查，仅 19 县现存绿孔雀，且全省绿孔雀数量仅在 500 只左右。

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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1. Status and distribution changesof the endangered Green Peafowl (*Pavo muticus*) in China over the past three decades(1990s–2017)

The Green Peafowl once habituated in 54 counties in China. Nearly 60% of the distribution counties were lost in the past three decades, with the left 22 counties distributed in central, southern and western Yunnan, SW China. Population decrease detected in all distribution areas except for Shuangbai and Xinping county where more than 60% of the total population is located. Only about 30% of the former bird population were recorded with the same interviewing method as 20 years ago. Three birds, 1 carcass, 6 calls and 12 footprints were detected along the 865 km line transects, indicating extremely low encounter rate of Green Peafowl in field. Sharp decreases in flock sizes were also detected, from 8–20 birds per flock in the 1990s to 3–5 birds at present. Poaching and habitat conversion are two widespread and long-lasting threats, while poisoning caused mortality in the past and hydropower construction affect regional population's survival. Large flocks of 18–27 birds were discovered in the field, which increases our confidence of population recovery of this endangered pheasant in China.

Time period	Number of locations with presence		Total counties recorded
	Counties	Towns	
Pre-2000	34	120	41
2001–2010	40	–	50
2011–2017	22	33	52

	2011–2017	2001–2010	1991–2000	Pre-1991
Average flock size (birds/flock)	3.36–4.84	3.59–5.5	8.58–10.42	8.5–20
Range of flock size	1–27	1–20	1–30	7–30
Sample size (*n*)	25	22	12	2

2. Survey on Green Peafowl (Pavo muticus) in Yunnan, China (2018)

From march to July in 2018, a survey was conducted on Green Peafowl (Pavo muticus) in 54 counties in Yunnan. The Green Peafowl is only found in 19 counties, and the population of Green Peafowl in the province is just about 500.

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Dr. Fei Wu, Assistant Prof
伍和启　博士　助理研究员
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GLADYS NYAKERU KUNG'U
赵　岩　Zhao Y
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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 90 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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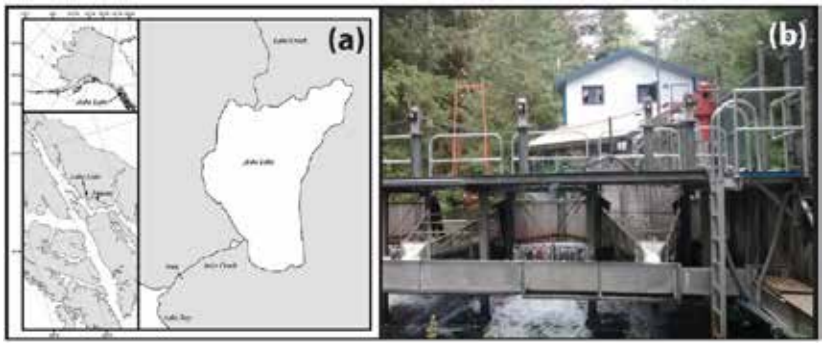
重要成果及产出：

1. Levi T, Allen JM, Bell D, Joyce J, Russell JR, Tallmon DA, Vulstek SC, **Yang CY, Yu, DW*** Environmental DNA for the enumeration and management of Pacific salmon. Molecular Ecology Resources. 2018. bioRiv: https://doi.org/10.1101/394445.
2. Kocher SD, Mallarino R, Rubin BER., **Yu DW**, Hoekstra HE, Pierce NE. The genetic basis of a social polymorphism in halictid bees. Nature Communications. 2018,9:4338.
3. Andújar C, Arribas P, **Yu DW**, Vogler AP, and Emerson BC. Why the COI barcode should be the community DNA metabarcode for the metazoa. Molecular Ecology. 2018,27:3968-3975. doi:10.1111/mec.14844.
4. Heine D, Holmes N, Worsley S, Alves dos Santos A, Innocent T, Scherlach K, Patrick E, **Yu DW**. Murrell JC, Viera P, Boomsma J, Hertweck C, Hutchings M, Wilkinson B. Chemical warfare between leafcutter ant symbionts and a co-evolved pathogen. Nature Communications. 2018, 9:2208.
5. Hua FY, **Wang L**, Fisher B, Zheng XL, **Wang XY, Yu DW**, Tang Y, **Zhu JG***, Wilcove, D.S. Plantations replacing native forest and abandoned cropland: the nature of apparent forest recovery in southwestern China. Biological Conservation. 2018, 222:113-124.
6. Tessler M, Weiskopf SR, Berniker L, Hersch R, Mccarthy KP, Yu DW, Siddall ME. Bloodlines: mammals, leeches, and conservation in southern Asia. Systematics and Biodiversity. 2018:1-9 .

1. 太平洋鲑鱼计数和管理的环境 DNA 研究

太平洋鲑鱼是美国阿拉斯加的重要资源，每年的经济效益超过 5 亿美元。由于它们的溯河产卵的习性，成年产卵鱼分布在成千上万的河流中，这给管理带来了巨大的挑战。目前，由于依赖于人工计数和声波定位，成熟的雌鲑鱼只在少数几条流中被计数。利用脱落组织（eDNA，即环境 DNA）检测生物的能力有望提供一种更有效的计数方法。然而，虽然 eDNA 与当地鱼类的丰度普遍相关，但我们不知道 eDNA 是否能准确地计数鲑鱼。在这里，我们的研究表明，基本上每天，跟踪洄游红鲑（sockeye）和银鲑鱼（coho）的雌鱼，以及每日流出的红鲑鱼的数量，与经水流数据校正后的 eDNA 率密切相关。eDNA 保证了准确性和效率，但为了提供更可靠的数据，还需要更准确的水流数据，因为鲑鱼的雄鱼、幼鱼和成熟鱼之间的脱落率是不同的，因此至少需要每天进行采样，并且要关注具有简单生命历史的物种。



2. 取代天然林的人工林：2000 年至 2015 年中国西南部原耕地森林明显恢复的能力和驱动力

中国在保护和恢复森林方面实施了一些强大的支持政策，这些政策可以作为其他国家的榜样。然而，这些政策的实际环境效果却鲜为人知。在这里，我们将遥感分析与家庭访谈相结合，评估 2000–2015 年中国主要森林保护和再造林政策实施后，西南地区土地覆盖变化的能力和驱动因素。我们发现，尽管该地区的总树木覆盖率增长了 32%，但这一增长完全是由于农田变成了树木种植园，尤其是单一栽培。而本土森林则遭受了 6.6% 的净损失。因此，该区域明显的森林恢复并没有真正恢复森林景观和产生相应的环境效益，反而有效地取代了原生森林，包括那些本来可以在摆脱农业的土地上自然再生的森林。另一个驱动因素是许多家庭希望遵守邻居的土地使用决定。我们的结论是，为了实现真正的森林恢复以及由此带来的环境效益，中国的政策必须更加有力地保护现有的原生森林，促进原生森林的恢复。在中国的森林政策中，自然更新一直被严重忽视，自然更新应该被视为一种合法的森林恢复手段。此外，应利用家庭一级的社会因素，特别是追求利润和符合社会规范，促进更好的土地覆盖、生物多样性和环境成果。更广泛地说，中国和其他国家要想成功地恢复森林，政策必须明确区分原生森林和植树造林。

Ecology, Conservation, & Environment Center (ECEC)

Prof. 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 90 publications, including in Nature, Science, PNAS, PLoS Biology, Ecology Letters, Ecological Monographs, Ecology.

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1. Environmental DNA for the enumeration and management of Pacific salmon

Pacific salmon are a keystone resource in Alaska, with an economic impact of well over ~US$500 million/yr. Due to their anadromous life history, adult spawners distribute amongst thousands of streams, posing a huge management challenge. Currently, spawners are enumerated at just a few streams because of reliance on human counters and, rarely, sonar. The ability to detect organisms by shed tissue (environmental DNA, eDNA) promises a more efficient counting method. However, although eDNA correlates generally with local fish abundances, we do not know if eDNA can accurately enumerate salmon. Here we show that daily, and near-daily, flow-corrected eDNA rate closely tracks daily numbers of immigrant sockeye and coho spawners and emigrant sockeye smolts. eDNA promises accuracy and efficiency, but to deliver the most robust numbers will need higher-resolution stream-flow data, at-least-daily sampling, and to focus on species with simple life histories, since shedding rate varies amongst jacks, juveniles, and adults.

2. Tree plantations displacing native forests: The nature and drivers of apparent forest recovery on former croplands in Southwestern China from 2000 to 2015

China is credited with undertaking some of the world's most ambitious policies to protect and restore forests, which could serve as a role model for other countries. However, the actual environmental consequences of these policies are poorly known. Here, we combine remote-sensing analysis with household interviews to assess the nature and drivers of land-cover change in southwestern China between 2000–2015, after China's major forest protection and reforestation policies came into effect. We found that while the region's gross tree cover grew by 32%, this increase was entirely due to the conversion of croplands to tree plantations, particularly monocultures. An additional driver was the desire of many households to conform with the land-use decisions of their neighbors. We conclude that to achieve genuine forest recovery along with the resulting environmental benefits, China's policies must more strongly protect existing native forests and facilitate native forest restoration. More generally, for China and other countries to succeed in recovering forests, policies must clearly distinguish between native forests and tree plantations.

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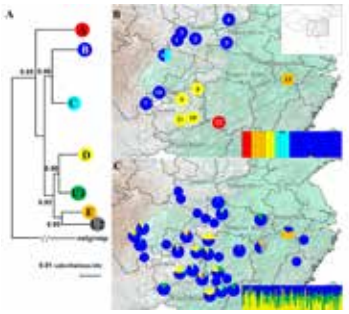
两栖爬行类多样性与进化

车静，博士，研究员。“中国两栖类”信息系统负责人。中国动物学会两爬分会副理事长。国家基金委优秀青年基金获得者。入选 2017 年度科技部中青年科技创新领军人才；2015 年首批入选“中国科学院青年创新促进会优秀会员”人才项目；2014 年荣获中科院“朱李月华优秀教师奖”；2011 年荣获中科院“卢嘉锡青年人才奖”。云南省中青年学术和技术带头人后备人才。本课题组以两栖爬行动物为研究对象，致力于生物多样性的形成、演化、物种适应及保护工作。目前已在 *Syst Biol*、*PNAS*、*Curr Biol*、*Mol Ecol* 等一系列国际刊物发表近 60 篇 SCI 论文。

重要成果及产出：

1. **Chen JM**[1], Poyarkov Jr NA, **Suwannapoom C**, Lathrop A, **Wu YH**, **Zhou WW**, **Yuan ZY**, **Jin JQ**, **Chen HM**, Liu HQ, Nguyen TQ, Nguyen SN, Duong TV, Eto K, Nishikawa K, Matsui M, Orlov NL, Stuart BL, Brown RM, Rowley JJL*, **Murphy RW***, Wang YY*, **Che J***. 2018. Large-scale phylogenetic analyses provide insights into unrecognized diversity and historical biogeography of Asian leaf-litter frogs, genus *Leptolalax* (Anura: Megophryidae). ***Mol Phylogenet Evol*** 124, 162–171.
2. **Sun YB**[1], **Fu TT**[1], **Jin JQ**, **Murphy RW**, Hillis DM*, Zhang YP*, **Che J***. 2018. Species groups distributed across elevational gradients reveal convergent and continuous genetic adaptation to high elevations. ***Proc Natl Acad Sci U S A***, 115(45), E10634-E10641.
3. **Sun YB**[1,*]. 2018. FasParser2: a graphical platform for batch manipulation of tremendous amount of sequence data. ***Bioinformatics***, 34(14):2493-2495.
4. Wang GD[1], **Zhang BL**[1], **Zhou WW**, Li YX, **Jin JQ**, Shao Y, Yang H, Liu YH, **Yan F**, **Chen HM**, Jin L, Gao F, Zhang Y, Li HP, Mao BY, **Murphy RW**, Wake DB*, Zhang YP*, **Che J***. 2018. Selection and environmental adaptation along a path to speciation in the Tibetan frog *Nanorana parkeri*. ***Proc Natl Acad Sci U S A***, 115(22):E5056-E5065.
5. **Yan F**[1], Lü JC, **Zhang BL**, **Yuan ZY**, Zhao HP, Huang S, Wei G, Mi X, Zou DH, **Xu W**, Chen S, Wang J, Xie F, Wu MY, Xiao HB, Liang ZQ, **Jin JQ**, Wu SF, Xu CS, Tapley B, Turvey ST, Papenfuss TJ, Cunningham AA, **Murphy RW***, Zhang YP*, **Che J***. 2018. The Chinese giant salamander exemplifies the hidden extinction of cryptic species. ***Curr Biol***, 28(10): R590–R592.
6. Turvey ST[1], Chen S, Tapley B, Wei G, Xie F, **Yan F**, Yang J, Liang ZQ, Tian HF, Wu MY, Okada S, Wang J, Lü JC, Zhou F, Papworth S K, Redbond J, Brown T, **Che J**, and Cunningham AA*. Imminent extinction in the wild of the world's largest amphibian. 2018. ***Curr Biol*** 28(10):R592-R594.

1. 中国大鲵（*Andrias davidianus*）隐存物种正悄然灭绝



中国大鲵为中国特有珍稀野生动物，曾广泛分布于我国长江、黄河及珠江流域的 18 个省份。由于栖息地破坏和人为过度捕捉，野生资源迅速减少，被列为极度濒危物种（CE），并收录入 CITES 公约附录 I。为保护中国大鲵提出针对性的指导意见，该团队基于 10 余年的考察，在全国范围内展开了对中国大鲵的群体研究。基于简化基因组学和群体遗传学揭示：中国大鲵至少存在 5 个隐存支系物种（简称为：陕西种，四川种，广西种，贵州种，安徽种），它们的分化时间保守估计约为 4.71-10.25 百万年以前，属于有较长分化历史的典型物种。研究表明现有保护措施（人工养殖、增殖放流等）导致全国养殖场大约有 78.82% 的个体都是“陕西种”，在此情况下，小种群物种极易受到其它物种的基因侵蚀，甚至被取代灭绝的风险。以贵州省为例，通过微卫星数据分析显示，随机取样的 100 份养殖个体虽然有不同的母系来源，但是核基因水平已经混杂为一个物种。换言之，不当的保护还可能加速物种的灭绝。

该成果发表后，国内 20 余家媒体杂志（中央电视台、人民日版、新华社等）对此进行了报道；*Science* 杂志、纽约时报等国际期刊杂志也相继作了报道。（**Yan F, et al. 2018 *Current* Biology; Turvey, et al. 2018 *Current Biology***）

2. 动物的高原适应及其动态进化历程

探讨动物的高原适应是研究物种对极端环境适应机制的理想模型。以往研究中通过比较高海拔物种与低海拔近缘种，在分子及表型层面鉴定了很多高原物种的适应特征。然而，已有研究多侧重于高、低两物种的比较，而高原环境存在很大的异质性，物种在什么海拔范围就已经进化出了高原适应？不同海拔的物种在分子适应上有哪些异同、以及不同类群的物种在相似的海拔是否会进化出趋同的分子适应等一系列问题在前期的研究中还没有得到解答。该团队对两个呈现海拔梯度分布的类群（倭蛙属和沙蜥属）展开了进化分析，揭示动物的高原适应可能在 2000 米左右就已出现，部分功能（尤其是 DNA 损伤修复和能量代谢相关通路）持续经历快速进化，暗示它们在高原适应中的重要作用；此外，该研究还发现不同类群在面临相似环境压力时会产生分子水平的趋同性，而趋同性更多地体现在功能上。（**Sun YB, et al. 2018 *PNAS***）

3. 高山倭蛙物种形成分化及适应进化机制

该团队在前期基础上选取了高山倭蛙分布范围内 63 个居群样品进行了全基因组重测序，数据分析分析发现：(1) 东、西群体基因组中大部分区域已经出现明显隔离且不能发生基因渗透，高分化区域与生殖相关的基因存在显著富集，应为两个不同的物种。进一步分析提示选择作用在物种形成过程中扮演了重要角色；(2) 东部物种呈现明显的“低 - 高 - 低 - 高”海拔的遗传分化模式，与环境相关的基因，如血管循环，低氧应答，紫外应答等受到正选择和差异表达，提示高原适应在东部群体的分化过程中起了重要作用。（**Wang GD, et al. 2018 *PNAS***）

Herpetological Diversity and Evolution

Prof. Jing Che, Principal Investigator. Using amphibian and reptile as model, we often explore the biodiversity issue 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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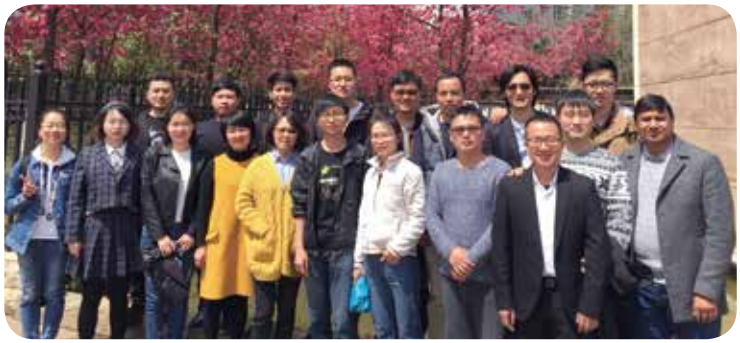


1. Hidden extinction of cryptic species in Chinese giant salamander

The Chinese Giant Salamander (*Andrias davidianus*) is a "living fossil" among amphibians. Due to the damage of their habitat and overhunting since the 1950s, the densities of populations have decreased rapidly to the extent that some wild populations may have been extirpated.

Previously, the Chinese Giant Salamander had a wide distribution covering 17 provinces, while, it was assumed to be "one species" and, currently, its protection is based on this. Considering the suitable habits often isolate amphibians, we ask: did the wide distribution and the long history of evolution result in any significant distinctions among the populations from different places? Is the current policy of protection appropriate or effective? To answer these questions and better protect the iconic salamander, we analyzed its population genetic structure based on 70 wild samples and 1034 samples from the farms (mostly tissues from the shed skin and mouth).

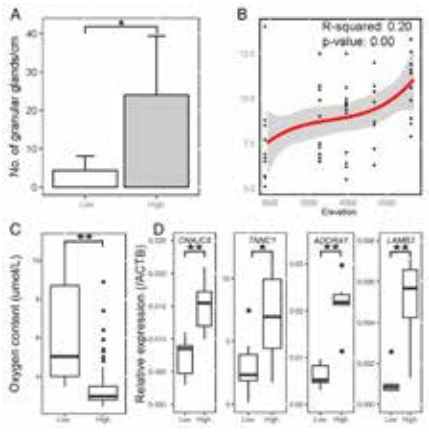
The genome-level data discovered that the Chinese Giant Salamander consists of 5 clade-species. The distributions of these species closely associate with aquatic systems. Conservative estimations suggest that speciation occurred about 4.71 to 10.25 million years ago; each species has a long evolutionary history. A random sampling of the farm population found that 78.82% of the individuals originated from Shaanxi. In another words, genetically uninformed efforts to protect the species may have accelerated extinction via genetic homogenization (**Yan F, et al. 2018 *Current* Biology; Turvey, et al. 2018 *Current Biology* **).

2. High-elevation adaptation and its dynamic evolutionary pattern

Although many cases of genetic adaptations to high elevations have been reported, the processes driving these modifications and the pace of their evolution remain unclear. Many high-elevation adaptations (HEAs) are thought to have arisen in situ as populations rose with growing mountains. In contrast, most high-elevation lineages of the Qinghai-Tibetan Plateau appear to have colonized from low-elevation areas. These lineages provide an opportunity for studying recent HEAs and comparing them to ancestral low-elevation alternatives. We studied two distantly related groups that are distributed across a broad elevational gradient on and near the Qinghai-Tibetan Plateau and identified molecular adaptations to increasing elevations. We show that high-elevation adaptation emerged soon after a split from low-elevation lineages, and adaptations (e.g. DNA repair and energy metabolism) continue to evolve in species that inhabit increasingly high elevations (**Sun YB, et al. 2018 *PNAS***).

3. Speciation and environment adaptations in *Nanorana parkeri*

Tibetan frogs, *Nanorana parkeri*, are differentiated genetically but not morphologically along geographical and elevational gradients in a challenging environment, presenting a unique opportunity to investigate processes leading to speciation. A cohort of whole-genome sequences of 63 individuals of *N. parkeri* from across its entire range opens avenues for incorporating population genomics into studies of speciation. Natural selection plays an important role in maintaining and driving the continuing divergence and reproductive isolation of populations of the species. This study highlights that the QTP is a natural laboratory for studying how selection drives adaptation, how environments influence evolutionary history, and how these factors can interact to provide insight into speciation (**Wang GD, et al. 2018 *PNAS***).



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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，哥本哈根大学生物系终身教授，中国国家基因库副主任。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, Nature Genetics*, *Nature Communication*, *PNAS*, *Current Biology* 等国际高影响力杂志发表论文 100 余篇（其中第一作者及通讯作者 40 多篇）。2018 年，课题组利用群体遗传学研究揭示了赤狐驯化中行为快速改变的遗传机制，通过转录组研究揭示了源于蚂蚁共同祖先的基因调控网络在现存蚂蚁中起着调节等级繁殖分工的作用，通过基因组学研究揭示了吸血蝙蝠特殊食性的演化适应机制，发起并启动了地球生物基因组计划，成功主办了第一届亚洲演化生物学大会。2018 年，在 *Nature Ecology & Evolution* (3), *PNAS* (1), *Molecular Biology & Evolution* (1) 等国际刊物发表 SCI 文章 9 篇。 http://zhanggjlab.cn/en/index.html

重要成果及产出：

1. Lewin HA[1]*, Robinsone GE, Kressf WJ, Bakerg WJ, Coddingtonf J, Crandallh KA, Durbini R, Edwardsk SV, Forestg F, Gilbertm MTP, Goldsteino MM, Grigorievp IV, Hackettr KJ, Haussslers D, Jarvisu ED, Johnsonv WE, Patrinosw A, Richardsx S, Castilla-Rubioy JC, van Sluys MA, Soltiscc PS, Xu X, Yang HM, **Zhang GJ**. Earth BioGenome Project: Sequencing life for the future of life. ***PNAS***. 2018, 115(17): p. 4325-4333.
2. Mendoza MLZ[1]*, **Xiong ZJ**[1], Escalera-Zamudio M, Runge AK, Thézé J, Streicker D, Frank HK, Loza-Rubio E, Liu SM, Ryder OA, Castruita JAS, Katzourakis A, Pacheco G, Taboada B, Löber U, Pybus OG, Li Y, Rojas-Anaya E, Bohmann K, Baez AC, Arias CF, Liu SP, Greenwood AD, Bertelsen MF, White NE, Bunce M, **Zhang GJ**, Sicheritz-Pontén F，Gilbert MPT*. Hologenomic adaptations underlying the evolution of sanguivory in the common vampire bat. ***Nature Ecology & Evolution.*** 2018, 2(4): p. 659-668.
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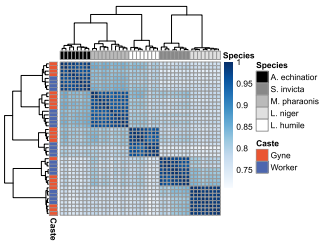
5. Rogers RL[1], Zhou L[1], Chu C, Márquez R, Corl A, Linderoth T, Freeborn L, MacManes MD, **Xiong ZJ**, Zheng J, Guo CX, Xun X, Kronforst MR, Summers K, Wu YF, Yang HM, Richards-Zawacki CL, **Zhang GJ***, Nielsen R*. Genomic Takeover by Transposable Elements in the Strawberry Poison Frog. ***Molecular Biology & Evolution***. 2018, 35(12):2913-2927.
6. **Zhang GJ**[1]*. The first AsiaEvo conference, connecting Asian evolutionary biologists to the world. ***National Science Review***. 2018, 5(5): p. 614-616.

1. 赤狐全基因组研究揭示对其行为快速驯化的遗传机制



对狐狸行为的人工驯化在过去的几十年中取得了显著的成功，但是对该过程中行为改变的遗传机制知之甚少。为探究赤狐人工驯化后攻击行为快速改变的遗传机制，本项目基于构建的赤狐全基因组对三个群体（温顺、攻击型和未被驯化农场饲养的群体）的行为受选择情况开展了群体遗传学研究。研究发现温顺型群体与其它两个群体在遗传组成上具有明显的差异，提示了人工驯化在几十代的时间内导致了群体遗传基础的变化。对不同行为类型的群体比较鉴定出了 100 多个在驯化过程中收到强烈人工选择的基因，这些基因明显富集于与狐狸的行为数量性状基因座相关的区域。此外，我们还发现这些受选择基因与人类基因组的同源序列大量的参与了人类神经系统疾病致病过程。这表明赤狐不仅是研究驯化过程中攻击和温顺行为变化很好的模型，同时对人类行为演化方面的研究也有着重要意义。【Kukekova et al. 2018 ***Nature Ecology & Evolution***】

2. 蚂蚁大脑转录组研究揭示了源于蚂蚁共同祖先的基因调控网络在现存蚂蚁中起着调节繁殖分工的作用

在蚂蚁群体里，蚁后与工蚁在形态与行为上有着明确的繁殖分工，这种分工在大约 1.5 亿年前起源于各蚂蚁的共同祖先。由于蚂蚁物种的等级系统属于同源性状，因此从发育演化生物学角度，我们预测这些同源性状是由蚂蚁祖先状态的基因网络所调控。通过对五种蚂蚁的转录组研究，我们筛选出一批在各蚂蚁中都参与等级调控并存在相同表达谱的基因，间接证明了祖先状态基因调控网络在蚂蚁等级系统的重要性。通过与其它物种转录组的比较，证实了在演化上丢失了等级系统的蚂蚁里，该批基因依然存在但其调控网络关系已丢失；而在趋同演化出等级系统的蜜蜂里，虽有部分蚂蚁等级调控网络的基因参与了蜜蜂的等级调控，但它们的调控方式却不相同，意味着趋同演化有着独立的基因调控。此外我们寻找到 40 多个在不同蚂蚁之间非常保守同时在不同等级中存在相同表达差异的基因，这些基因可能对蚂蚁社会等级的起源至关重要【Qiu et al. 2018 ***Nature Ecology & Evolution***】

3. 启动地球生物基因组计划（EBP）

2018 年 11 月 1 日，地球生物基因组计划（Earth Biogenome Project，EBP）在英国伦敦正式启动。地球生物基因组计划（EBP）是一项旨在对地球上所有已知的动植物、真菌和原生生物基因组进行测序的全球合作计划，最终将为推动生物多样性保护和人类社会可持续发展创造新的基础。其目标是在十年时间里对地球所有真核生物的基因组进行测序、编目和分类。该项目将推动全新计算算法、分析方法和模型的创立，革新我们对生物学的理解，有望极大改善物种保护工作，并为农业、医药和生态系统服务创造新的基因资源。本课题组是 EBP 计划的重要理事成员【Lewin et al. 2018 PNAS】

4、第一届亚洲演化生物学会议顺利召开，促进亚洲演化生物学交流与发展

2018 年 4 月，由深圳国家基因库、遗传资源与进化国家重点实验室等共同主办的第一届亚洲演化生物学大会（http://asianevo.org/）在中国深圳举行，大会吸引了来自 34 个国家和地区的 812 名参会者，包括 126 名特邀专家学者，13 位国内外院士。本次会议促进了亚洲国家在演化生物学领域的学术交流和学科交叉，加强了演化生物学不同研究分支的科学家之间的积极沟通，将对亚洲的演化生物学学术发展产生重要的影响。第二届亚洲演化生物学大会将于 2020 年在日本东京召开。【Zhang G. 2018 ***National Science Review***】

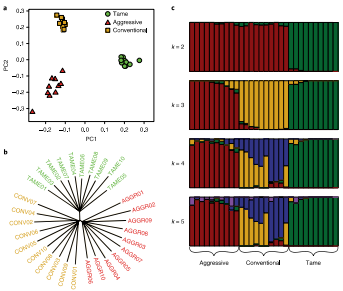
Biodiversity Genomics Lab

Prof. Guojie Zhang, visiting professor, head of Biodiversity Genomics Group, Kunming Institute of Zoology, CAS; full professor in University of Copenhagen and Associate Director of the China National GeneBank. He has been served as peer reviewer for ***Nature***, ***Science***, ***Genome Research***, ***Current Biology*** and several grant-giving agencies. He has more than 100 publications, including ***Science***, ***Nature***, ***Cell***, ***Nature Genetics, Nature Communication***, ***PNAS***, ***Current Biology***.

In 2018, we identified genomic regions associated with tame and aggressive behaviours in red fox genome; reconstructed the ancestral brain gene-network regulating caste differentiation in ants, and revealed the mechanism of adaptation to specialized diets in vampire bat. We launched The Earth BioGenome Project (EBP) and successfully held The First AsiaEvo Conference. In 2018, we published 9 high impact factor SCI papers, including ***Nature Ecology and Evolution*** (3), ***PNAS*** (1), ***Molecular Biology & Evolution*** (1). Email: zhanggjconi@gmail.com

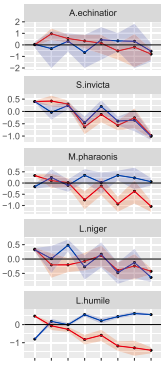
1. Red fox genome assembly identifies genomic regions associated with tame and aggressive behaviours

Fox domestication experiments have been remarkably successful over the past few decades, but little is known about the genetic mechanisms of the behavior changes during this process. In order to explore the genetic mech-anism of the rapid change of aggression behavior of red fox, we performed the population genetics study for tame, aggressive, and conventional farm-bred populations. We identified over 100 loci that under strong artificial selection for behavior and most of these are overlapping with behavioral QTL loci in red fox.In addition, we found many neural-function genes under strong artificial selection within such short-term domestication program, and are also associated with human brain disorders. These results suggest that fox is not only a powerful model for the genetic analysis of affiliative and aggressive behaviors, but also of great significance to the research on the evolution of human behavior.



2. Towards reconstructing the ancestral brain gene-network regulating caste differentiation in ant

Caste system with permanent reproductive division of labour origin- ated in the last common ancestor of ants and represents homologous characters. However, whether these homologous characters are reg -ulated by a core-set of ancestral genes or being lineage specific is largely unknown. To address this question, we sequenced and com- pared the brain transcriptome of queen and worker castes from five ant species across three lineages, and identified a core-set of genes consistently involved in caste regulation, representing the ancestral genetic regulatory network (GRN) for caste system in ants. Further comparison with ants that lost queen caste and honeybee that inde- pendently evolved caste system suggests that losing ancestral caste system (queenless ants) also lost ancestral GRN, whereas conver- gent evolution (honeybee) used distinct GRN for caste regulation. Finally, we reported over 40 genes showing consistently caste-bias expression across all detected species that might hold the important mechanisms for the evolution of caste differentiation in ants.



3. Earth BioGenome Project: Sequencing life for the future of life

The Earth BioGenome Project (EBP) has been launched on 1 November 2018 in London. It aims to sequence and annotate~1.5 million known eukaryotic species in three phases over a 10-year period using a phylogenomic approach, which will revise and reinvigorate our under-standing of biology, ecosystems, and evolution, enable the conservation, protection, and rege- neration of biodiversity and maximize returns to society and human welfare. Our group is one of the key players in EBP project and has contributed significantly amount of works for EBP.

4. The first AsiaEvo conference, connecting Asian evolutionary biologists to the world

In April 2018, The First AsiaEvo Conference (http://asianevo.org/) was held in Shenzhen, China. Prof. Guojie Zhang served as the chairman of this conference. The conference attracted 812 participants from 34 countries and regions, including 126 invited experts. The conference aims to promote evolutionary biology in Asia and encourages more biological researchers to participate in research related to evolutionary biology. The 2nd AsiaEvo conference will be held in Tokyo in 2020.

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Mr. Guo Ding, Research Assistant

博士后（Postdoctoral Fellow）

高琼华　Dr. Qionghua Gao, 2016

研究生（Graduate Student）

李　冀　Ji Li, 2018

实习生（Internship）

应昊良　Mr. Haoliang Ying, Intern
卢麒玥　Ms. Qiyue Lu, Intern

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，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，*Genome Biol Evol* 副主编，*Hum Mol Genet* 编委。近几年重点开展高原适应的分子机制、家养动物起源与驯化机制及动物复杂性状形成的遗传机制等方面的研究，2018 年揭示了高山倭蛙、温泉蛇、沙蜥属等两栖爬行动物不同类群高原适应的进化机制；阐明了新基因在家犬驯化过程中食性转变的遗传机制，首次证实了等位基因特异的 RNA 编辑在人和动物中广泛存在，在国际权威杂志上发表了 SCI 论文 23 篇，其中 IF>10 的有 8 篇，包括 ***Science*** **(1)**, ***PNAS*** **(3)**, ***Mol Biol Evol*** **(2)**, ***Nucl Acids Res*** **(1)**, ***Nat Sci Rev*** **(1)** 等。张亚平院士在 *Science* 上联合发表了题为《与大自然共享发展空间》的社论文章，展示了目前人类和地球上其它生命形式所面临的严峻形势，提出人类应制定切实可行的未来生物多样性目标，实现人类与自然的和谐发展 。

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1. Baillie J, **Zhang YP**. Space for nature. ***Science***, 2018, 361:1051-1051. IF40.627
2. **Guo X**[1], Li YQ[1], **Wang MS**[1], Wang ZB[1], Zhang Q, **Shao Y**, Jiang RS, Wang S, Ma CD, **Murphy RW**, Wang GQ, Dong J, Zhang L, **Wu DD***, Du BW*, **Peng MS***, **Zhang YP***. A parallel mechanism underlying frizzle in domestic chickens. ***J Mol Cell Biol***, 2018, doi:10.1093/ jmcb/mjy037. IF6.825
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4. **Wang GD**[1], **Zhang BL**[1], **Zhou WW**, **Li YX**, **Jin JQ**, **Shao Y**, Yang HC, Liu YH, **Yan F**, **Chen HM**, Jing L, Gao F, Zhang YG, Li HP, **Mao BY**, **Murphy RW**, Wake DB*, **Zhang YP***, **Che J***. Selection and environmental adaptation along a path to speciation in the Tibetan frog Nanorana parkeri. ***PNAS***, 2018, 115:E5056-E5065. IF10.359
5. **Wang GD**[1], Shao XJ[1], Bai B[1], Wang JL, Wang XB, Cao X, Liu YH, **Wang X**, **YinTT**, Zhang SJ, Lu Y, Wang ZC, Wang L, Zhao WM, Zhang B, Ruan J*, **Zhang YP***. Structural variation during dog domestication: insightsfrom grey wolf and dhole genomes. ***Nat Sci Rev***, 2018, doi:10.1093/ nsr/nwy076. IF10.973
6. **Wu DD***, Ding XD, **Wang S,** Wójcik JM, Zhang Y, Tokarska M, Li Y, **Wang MS**, Faruque O, Nielsen R*, Zhang Q* and **Zhang YP***. Pervasive introgression facilitated domestication and adaptation in the Bos species complex. ***Nat Ecol Evol*** 2018,2(7):1139-1145
7. **Zhou ZY**[1], Hu Y[1], Li AM[1], Li YJ[1], Zhao H[1], Wang SQ, **Otecko NO**, Zhang DJ, **Wang JH**, Liu YJ, Irwin DM, Qin Y, **Zhang YP***. Genome wide analyses uncover allele-specific RNA editing in human and mouse. ***Nucl Acids Res***, 2018, 46:8888-8897. IF10.235

1. 基因交流在牛属动物的驯化及环境适应中的作用

对多种牛属动物进行了全基因组高覆盖测序以及群体基因组测序，分析确定了牛属之间的系统发育关系，得出大额牛是一个独立的物种或亚种的结论。分析发现牛属之间存在广泛的基因交流，并挖掘出瘤牛与巴厘牛（爪哇野牛驯化种），瘤牛与大额牛发生基因交流的区域，发现许多神经系统基因、免疫系统基因从瘤牛扩散至巴厘牛以及大额牛中。推测基因交流在促进动物被成功驯化的过程中起到重要的作用；发现分布在青藏高原上的牦牛与藏黄牛之间存在显著的基因交流。在家牛中受到选择作用的与毛色相关的 MITF 基因通过基因交流被导入到了牦牛基因组中，部分藏黄牛基因组中的低氧诱导通路基因 *EGLN1*、*EGLN2*、*HIF3a* 从牦牛中获得，这也提示，藏黄牛通过“拿来主义”从牦牛中快速获得适应高原低氧环境的遗传变异。

【Wu DD et al. 2018 ***Nataure Ecoloy & Evolotion***】

2. 家犬食性转变的遗传机制

通过对家犬、灰狼、豺狗三个犬科物种的基因组比较分析，发现家犬基因组中一个通过逆转录转座产生的新基因，作为 AKR1B1 的新拷贝在小肠和肝脏中高表达，参与脂肪的从头合成和降低高淀粉饮食带来的毒性等功能。这一发现不仅阐明了家犬从肉食性到杂食性的遗传机制，而且展示了新基因在家养动物驯化过程中的作用。

【Wang GD et al. 2018 ***National Science Review***， IF=10.973】

3. 等位基因特异的 RNA 编辑

RNA 编辑是增加基因转录和功能多样性的重要形式。DNA 层面等位基因特异表达和修饰的现象非常普遍。然而，生物体内在 RNA 层面是否存在等位基因特异的修饰还没有相关的研究。我们在人和小鼠中分别鉴定出 315 个和 184 个等位基因特异的 RNA 编辑位点，这提示等位基因特异的 RNA 编辑是广泛存在的。细胞水平的突变实验和 SHAPE 实验还发现，同义突变的 SNP 可以通过影响 RNA 二级结构从而产生等位基因特异的 RNA 编辑，进而引起了氨基酸的改变。该研究为解释与疾病以及性状改变相关的同义突变提供了新的思路。

【Zhou ZY et al. 2018 ***Nucleic Acids Research***, IF= 10.235】

Molecular Evolution and Genome Diversity

Prof. Ya-Ping Zhang, Academician & Vice-President, Chinese Academy of Sciences. He is an associate editor of ***Genome Biol Evol***, and the editorial board of ***Hum Mol Genet.*** Recently year we focused on genomic evolution of artificial selection and molecular machenism of the comlex traits and high-altitude adaptation in animals. Within 2018, They revealed evolutionary mechanisms of high-altitude adaptation in different groups of amphibian reptiles.The genetic basis of the diet change during domestication of dogs was elucidated. They also demostrated the likelihood of synonymous SNPs leading to amino acid changes through allele-specific RNA editing, which is ubiquitous in human and animals. The above research progresses were published in 23 SCI-indexed papers, including ***Science*** **(1),** ***PNAS*** **(3),** ***Mol Biol Evol*** **(2),** ***Nucl Acids Res*** **(1),** ***Nat Sci Rev*** **(1).** Email: zhangyp@mail.kiz.ac.cn

1. Pervasive introgression facilitated domestication and adaptation in the Bos species complex

We sequence the genomes of gayal, gaur, banteng, wisent and bison, and an additional 98 individuals.The phylogeny and evolutionary history of these species was inferred. It shows that the threatened gayal is an inde-pendent species or subspecies. We show genes under domestication selection in cattle (for example, *MITF*) were introgressed from domestic cattle to yak and genes in the response-to-hypoxia pathway (for example, *EGLN1, EGLN2* and *HIF3a*) were introgressed from yak to Tibetan cattle, probably facilitating their adaptation to high altitude. Our results illustrate the importance of introgression as a source of adaptive variation and during domestication.

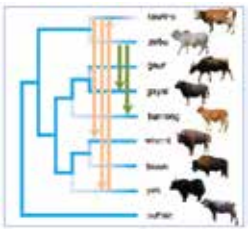

Fig.2 Phylogeny of Species of the Bos genus

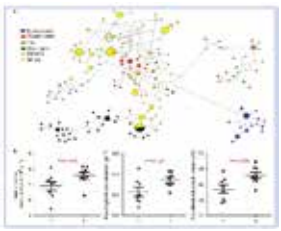

Fig.3 *EGLN1* was introgressed from yak to Tibetan cattle.

2. Genomic basis of diet change of domestic dogs

Here, we present high-quality genomes of the gray wolf (*Canis lupus*) and dhole (*Cuon alpinus*), respectively. We identify and verify at population level an insertion fully covering a copy of the *AKR1B1* transcript. High level of expression of the new AKR1B1 copy in the small intestine and liver, implying an increase in de novo fatty acid synthesis and antioxidant ability in dog compared to gray wolf, likely in response to dietary shifts during the agricultural revolution. Our findings demonstrate that retroposition can birth new genes to facilitate domestication.

3. Allele-specific RNA editing

RNA editing has important implications on the organism's genetic diversity. A large class of genes displayed allele-specific expression and modification at the DNA level. However, whether allele-specific modifications occurring at the RNA level is unknown. Here, we documented 315 and 184 allele-specific RNA editing sites in human and mouse. These findings indicate that allele-specific RNA editing is ubiquitous. Interestingly, cellular and SHAPE experiments highlighted the likelihood of synonymous SNPs leading to amino acid changes through allele-specific RNA editing. The study provides a new understanding about connection between synonymous mutations and both diseases and complex traits.

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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。长期以来一直进行进化基因组学研究。目前已经在 *Science*、*Nature Biotechnology*、*Nature Communications* 等重要学术杂志上发表论文 150 余篇，论文被各类 SCI 刊物累计引用 10868 余次，H 指数 48。 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）。

实验室主页：http://159.226.149.45/wangw2013/WenWang_Labweb_2013-3-22.htm

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2. **Hu JH**[1], Zeng T[1], Xia QM, Qian Q, Yang CD, Ding Y*, Chen LN* & **Wang W***. Unravelling miRNA regulation in yield of rice (Oryza sativa) based on diferential network model. ***Scientific Reports***. 2018, 8(1):8498.
3. **Wang X**[1], Zhang JJ[1], He SM[1], Gao YN, Ma XQ, Gao Y, Zhang GH, **Kui L**, **Wang W**, Wang Y*, Yang SC* and Dong Y*. HMOD: An Omics Database for Herbal Medicine Plants. ***Molecular Plant***. 2018, 11(5): 757-759.
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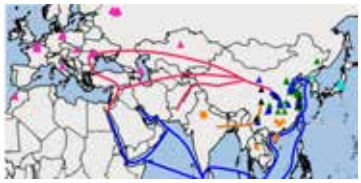
1. 家蚕规模化重测序分析阐明家蚕驯化历史及重要驯化性状的分子机制



中国以蚕丝贸易为代表开辟了古老丝绸之路，孕育了东西方文明的交流与传播。与华南农大、上海植生所科学家合作，通过系统的群体遗传学、群体动态分析，阐明了家蚕自野蚕驯化及驯化后的进化历程。研究证实了家蚕起源于中国野蚕的单一起源事件，同时发现家蚕在连接中国、南亚和欧洲的古丝绸之路沿路上曾出现过多次扩散，并随后在中国和日本形成了特有的优良品种。通过人工选择信号分析，发现氮营养尤其是氨基酸代谢对于家蚕进化过程中茧丝量的提升发挥着重要作用；生物钟节律基因对于家蚕驯化及地方适应性具有一定的作用。利用大规模基因组数据资源，该研究还首次将全基因组联合分析（GWAS）应用于家蚕重要性状的定位，证实了该方法的可行性和科学性，并对一些重要抗性位点进行了定位。该成果发表为家蚕育种及功能基因组学研究提供了全面系统的数据资源和参考依据。

2. 基于差异网络模型系统揭示 miRNA 在水稻产量中的调控作用

水稻是重要的粮食作物，而分蘖、穗分枝和灌浆是决定水稻产量的三个重要因素。本研究中，我们发展了一种新的算法：基于差异变换的共表达调控网络 (GRN-DET), 对植物发育中 miRNA 进行系统分析，并鉴定出关键调控 miRNA。利用该算法，结合现有大量水稻产量相关的 small RNA 和 RNA-seq 测序数据，我们初步构建了影响水稻产量的 miRNA- 基因调控网络。鉴定出常规差异表达方法未能发现的水稻产量调控关键 miRNA：osa-miR171 和 osa-miR1432。进一步分析了生长素和油菜素内脂等植物激素在调控水稻产量中的交互作用网络。该工作为系统鉴定植物重要性状关键调控 miRNA 提供了范例，也为进一步了解水稻产量调控网络提供了分子基础。

3. 中草药组学数据库——HMOD

中国是中草药的发源地。为了进一步整合现有的药用植物组学数据资源，我们对近 20 年的组学数据进行地毯式搜索和统计，整合了 23 个药用植物基因组数据、172 个药用植物转录组数据、55 个药用植物代谢组数据以及 18 个代谢通路信息，涵盖了目前为止已发表的基因组、转录组、代谢组以及代谢通路数据，初步实现百种中草药数据的共享、利用，满足合成生物学对有效成分、关键合成酶的查找、定位功能，搭建了 Herbal Medicine Omics Database 数据库 (HMOD, http://www.herbal-genome.cn/)。 该数据库极大地提升了相关研究的工作效率，实现了数据纵向系统贯穿、横向分享分析，达到了提高药用植物研究交流水平和数据共享的目的。该成果由博士研究生王筱与云南农业大学、华南植物园、武汉植物园共同完成。

4. 亚洲首次发现的发光叩甲的线粒体基因组的解析

叩甲是鞘翅目叩甲科的统称，该科包含 1 万多种，广布全世界。但过去报道的发光种类（200 多种）仅分布在新热带地区和大洋洲。最近我们在滇西采集到一种发光叩甲，这是亚洲首次记录的发光叩甲。我们解析了其近完整的线粒体基因组，基于线粒体基因组的系统发育分析证实其在叩甲科的分类地位。相关研究发表在 *Mitochondrial DNA Part B: Resources*。形态研究很难确定该种的亚科分类地位，进一步的分子系统发育分析表明该种与其它发光叩甲一样，隶属于槽缝叩甲亚科 (Agrypninae)，该种将作为新属新种发表。该种的发现对探讨生物荧光的起源和进化具有重要意义，其它相关的研究正在进行中。

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 150 papers in such scientific journals as *Science, Nature Biotechnology*, *Nature Communications* etc, which are totally cited more than 10868 times with a H-index of 48. 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 and two second prize in Yunnan Natural Science Award in 2017.

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1. The evolutionary road from wild moth to domestic silkworm

The Silk Road, which derives its name from the trade of silk produced by the domestic silkworm *Bombyx mori*, was an important episode in the development and interaction of human civilizations. However, the detailed history behind silkworm domestication remains ambiguous, and little is known about the underlying genetics with respect to important aspects of its domestication. Here, we reconstruct the domestication processes and identify selective sweeps by sequencing 137 representative silkworm strains. The results present an evolutionary scenario in which silkworms may have been initially domesticated in China as trimoulting lines, then subjected to independent spreads along the Silk Road that gave rise to the development of most local strains, and further improved for modern silk production in Japan and China, having descended from diverse ancestral sources. We find that genes with key roles in nitrogen and amino acid metabolism may have contributed to the promotion of silk production, and that circadian-related genes are generally selected for their adaptation. We additionally identify associations between several candidate genes and important breeding traits, thereby advancing the applicable value of our resources.

2. Unravelling miRNA regulation in yield of rice (*Oryza sativa*) based on differential network model

Rice (*Oryza sativa L.*) is one of the essential staple food crops and tillering, panicle branching and grain filling are three important traits determining the grain yields. We here present a novel algorithm, Gene Co-expression Network differential edge-like transformation (GRN-DET), which can identify key regulatory miRNAs in plant development. Based on the small RNA and RNA-seq data, miRNA-gene-TF co-regulation networks were constructed for yield of rice. Using GRN-DET, the key regulatory miRNAs for rice yield were characterized by the differential expression variances of miRNAs and co-variances of miRNA-mRNA, including osa-miR171 and osa-miR1432. Phytohormone cross-talks (auxin and brassinosteroid) were also revealed by these co-expression networks for the yield of rice. This efficient algorithm provides an example for systematically identifying the key regulatory microRNAs for plant important agronomic traits, and also provides a molecular basis for further understanding the rice yield regulation network.

3. HMOD: An Omics Database for Herbal Medicine

We have established the Herbal Medicine Omics Database (HMOD, http://www.herbal-genome.cn/) to provide all published herbal omics data and key enzymes involved in active component synthesis, collected 23 publicly available herbal medicine genomic data and 171 transcriptome data (48 de novo sequenced and assembled in this project, 124 public data), 18 plant KEGG pathway information and metabolome data for 55 species. Tools of generic genome browser (Gbrowse), Blast and Download are provided for all these data. The HMOD collects and provides comprehensive new data from omics data and pathway information, and will be a valuable resource for scientists studying comparative genomics, transcriptomes, and synthesis biology.

4. The mitochondrial genome of the first luminous click-beetle (*Coleoptera*: Elateridae)

The cosmopolitan family Elateridae (click beetle) contains almost 10,000 species, but its luminous taxa including about 200 species previously found exclusively in Neotropical region and Oceania. Surprisingly, a luminous click beetle, *Sinopyrophorus schimmeli* Bi et Li., was recently recorded from Dian Xi, China (Asia). We assembled its nearly complete mitochondrial genome. The phylogenetic analyses of 13 PCGs confirm the position of *S. schimmeli* in Elateridae. The discovery of this luminous click beetle is important for exploring the origin and evolution of bioluminescence.

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比较基因组学

宿兵，研究员、博士生导师，中国科学院知识创新工程学科带头人，中科院“百人计划”引进人才、国家基金委杰出青年基金获得者、“新世纪百千万人才工程”国家级人选，从事灵长类大脑演化的遗传学机制以及现代人类起源、迁徙与适应性进化的遗传学研究。已在《*Science*》、《*Nature*》、《*Nat Rev Genet*》、《*PNAS*》、《*Am J Hum Genet*》、《*Genome Res*》、《*Mol Biol Evol*》、《*Hum Mol Genet*》等国际核心刊物上发表研究论文 150 余篇。实验室主页：http://159.226.149.45/compgenegroup/compgenegroup.htm

重要成果及产出：

1. **He, Y.[1], Qi, X.[1]**, Ouzhuluobu[1], Liu, S.[1], Li, J.[1], **Zhang, H.**, Baimakangzhuo, Bai, C., **Zheng, W., Guo, Y.**, Duojizhuoma, Baimayangji, Dejiquzong, Bianba, Gonggalanzi, Pan, Y., Qula, Kangmin, Cirenyangji, Guo, W., Yangla, **Peng, Y., Zhang, X., Xiang, K., Yang, Z.**, Wang, L., Gengdeng, Zhang, Y., Wu, T., **Su, B.*** & Cui, C.* Blunted nitric oxide regulation in Tibetans under high-altitude hypoxia. ***National Science Review* 5**, 516-529 (2018).
2. **Qi, X.[1]**, Zhang, Q.[1], **He, Y.[1], Yang, L.[1], Zhang, X., Shi, P.**, Yang, L., Liu, Z., Zhang, F., Liu, F., Liu, S., Wu, T., Cui, C., Ouzhuluobu, Bai, C., Baimakangzhuo, Han, J., Zhao, S., Liang, C. & **Su, B.*** The transcriptomic landscape of yaks reveals molecular pathways for high altitude adaptation. ***Genome Biol Evol*** (2018). Doi: 10.1093/gbe/evy264
3. **Yang, Z.[1]**, Shi, H.[1], Ma, P.[1], Zhao, S.[1], Kong, Q.[1], Bian, T., Gong, C., Zhao, Q., Liu, Y., **Qi, X., Zhang, X.**, Han, Y., Liu, J., Li, Q., Chen, H.* & **Su, B.*** Darwinian positive selection on the pleiotropic effects of KITLG explain skin pigmentation and winter temperature adaptation in Eurasians. ***Mol Biol Evol* 35, 2272-2283** (2018).
4. **Yang, L.[1], Yang, Y.[1], Yuan, J.[1]**, Sun, Y., Dai, J. & **Su, B.*** Transcriptomic Landscape of von Economo Neurons in Human Anterior Cingulate Cortex Revealed by Microdissected-Cell RNA Sequencing. ***Cereb Cortex*** (2018). Doi: 10.1093/cercor/bhy286

1. 揭示了一氧化氮在藏族人群对高原低氧环境适应的生理调节机制：

提到青藏高原，人们首先想到的便是高寒缺氧的极端环境，然而在这片高寒之地上，目前有 500 多万藏族居民世代居住。平原人一上高原就容易出现高原反应，但世代定居在青藏高原的藏族居民却已经对高原低氧环境产生了最佳的生理适应。为什么会有这种适应性，这种生理适应又是通过什么样的基因组水平的精细调控过程实现对心、肺等关键低氧敏感器官的生理功能的适应性改变的？高原适应是一种复杂的生理性状，各种与氧吸收、氧运输，氧代谢相关的器官都参与其中。其中，一氧化氮（NO）是重要的血管舒张因子，在心血管和呼吸等重要生理功能中发挥着重要作用。西方学者 10 年前通过比较高原藏族与平原人群之间的血液 NO 浓度发现，高原藏族血液 NO 水平要比平原人群血液 NO 水平高出 10 倍以上，因此，国际生理学和高山医学界一直认为 NO 升高可能是藏族特有的对高原低氧环境的生理适应特征。然而，由于西方学者的数据缺乏长期生活在高原低氧环境中的平原人群和长期生活在平原地区的藏族人群的血液 NO 数据，因此，该假说存在许多不足之处。为了系统阐明高原藏族人群与移居高原的平原汉族人群中血液 NO 的变异模式，我们测定了在不同海拔藏族人群与汉族人群的血液 NO 浓度，以期揭示 NO 在藏族人群对高原低氧环境适应中的调控机制。通过系统比较常居不同海拔环境中的藏族与汉族人群血液 NO 浓度，我们发现，汉族人群在高原低氧环境中表现出了比同海拔藏族人群更高的 NO 水平。这一结果否定了西方学者提出的 NO 升高是藏族特有的高原生理适应特征的假说，并首次提出“藏族人群在高原低氧环境中 NO 的钝化调节”假说，即藏族血液 NO 水平的‘温和上升’有利于舒张血管从而促进氧的运输，但由于 NO 的钝化调节使得上升幅度得到控制，避免 NO 过度升高带来的负效应。这一调控与世居高海拔藏族的血红蛋白的调控类似。该成果为一氧化氮用于慢性高原病治疗打下了坚实的理论基础，同时对于利用一氧化氮对血管的舒张效应治疗其它内外环境缺氧性疾病时的剂量问题提供了第一手的科学数据，有重要的科学意义和广阔的医学应用前景。该原创性成果发表于中国科学院创办的首份英文版自然科学综合性学术期刊《国家科学评论》（*National Science Review*，5:516-529，2018），SCI 五年影响因子 10.973。

2. 东亚人群对紫外线辐射与寒冷适应的分子机制

现代人在 20-30 万年前起源于非洲，大约于 7.5 万年前左右走出非洲并随后扩散到世界各地。我们的非洲祖先从一个靠近赤道的热带环境迁徙到高纬度的亚热带及寒带环境会面临多种新的环境条件，例如紫外辐射的减弱及冬季气候变冷等等。这些环境条件的变化会对人类的基因组产生新的选择压力从而导致新的生理和表型适应。

人群肤色的差异是对紫外辐射强弱变化最有代表性的适应表型。总体来看，生活在赤道附近的人群肤色较深，而生活在高纬度地区的人群肤色较浅。以前的研究已经发现了多个控制人群肤色变化的基因及其适应性的突变。例如，宿兵实验室在 2016 年报道了色素调控基因 OCA2 在东亚人群中导致肤色变浅的一个适应性突变（Yang 等，*Molecular Biology and Evolution* 2016 33(5):1177-1187）。然而，纬度的变化除了导致紫外辐射强度的改变还会导致温度的变化，特别是冬季气候的变化。宿兵实验室在 2009 年曾经报道了 P53 基因的一个功能性突变导致人群对高纬度冬季寒冷气候的适应（Shi 等，*American Journal of Human Genetics* 2009 84:1-8）。紫外辐射与气温是随纬度变化同时变化的环境因子，在遗传上是否存在同时导致对这两种环境因子变化适应的基因呢？

宿兵实验室与昆明理工大学和中科院北京基因组所合作，通过群体遗传和细胞功能实验的分析发现 KITLG 基因在欧洲和东亚群体中均存在显著的达尔文正选择信号，且选择信号出现在基因的不同区域，包括基因上游和下游的调控区。他们推测，*KITLG* 在现代人走出非洲向高纬度地区扩散的过程中可能经历了不止一次的选择事件。他们发现 *KITLG* 基因上不仅存在欧亚群体中富集的导致肤色变浅的突变，还在基因的其它区域富集了对寒冷适应的突变，并通过细胞低温培养实验进行了验证。研究论文 2018 年 6 月 29 日在线发表于进化遗传学国际知名期刊 *Molecular Biology and Evolution* 35, 2272-2283 (2018)。这是一个基因的多种功能（基因多效性）在人群中同时受到选择并影响表型的例证，对了解人类环境适应和表型多样性的遗传基础具有重要的启示。

Comparative Genomics

Prof.Bing Su, principal investigator, The enlarged brain and highly developed cognitive skills are the most significant characteristics that set us apart from our relatives, the non-human primates. This evolutionary expansion is believed to be crucial to the highly developed cognitive abilities in humans, yet its genetic basis remains unsolved. our laboratory focuses on (1) the genetic mechanism underlying the dramatic enlargement of human brain and its highly developed cognitive skills during human evolution; (2) Origins and migration of modern human populations in East Asia and its adaptation to environmental stress.

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1. Blunted Nitric Oxide Regulation in Tibetans under High Altitude Hypoxia

Nitric oxide (NO) is an important molecule for vasomotor tone, and an elevated NO signaling was previously hypothesized as a unique and adaptive physiological change in highland Tibetans. However, there has been lack of NO data from Tibetans living at low altitude and lowlander immigrants living at high altitude, which are crucial to test this hypothesis. Here through cross-altitude (1,990m-5,018m) and cross-population (Tibetans and Han Chinese) analyses of serum NO metabolites (NOx) of 2,086 individuals, we demonstrate that although Tibetans have a higher serum NOx level compared to lowlanders, Han Chinese immigrants living at high altitude show an even higher level than Tibetans. Consequently, our data contradict the previous proposal of an increased NO signaling as the unique adaptive strategy in Tibetans. Instead, Tibetans have a relatively lower circulating NOx level at high altitude. This observation is further supported by data from the hypoxic experiments using human umbilical vein endothelial cells and gene knockout mice. No difference is detected between Tibetans and Han Chinese for eNOS, the key enzyme for circulating NO synthesis, suggesting that eNOS itself is unlikely the cause. We show that other NO-synthesis-related genes (e.g. GCH1) carry Tibetan-enriched mutations significantly associated with the level of circulating NOx in Tibetans. Furthermore, gene network analysis reveal that the downregulation and the upregulation of NOx are possibly through distinct pathways. Collectively, our findings provide novel insights into the physiological and genetic mechanisms of the evolutionary adaptation of Tibetans to high altitude hypoxia. **He et al.** ***National Science Review*** 5, 516-529 (2018)

2. Darwinian Positive Selection on the Pleiotropic Effects of KITLG Explain Skin Pigmentation and Winter Temperature Adaptation in Eurasians

Human skin color diversity is considered an adaptation to environmental conditions such as UV radiation. Investigations into the genetic bases of such adaptation have identified a group of pigmentation genes contributing to skin color diversity in African and non-African populations. Here, we present a population analysis of the pigmentation gene KITLG with previously reported signal of Darwinian positive selection in both European and East Asian populations. We demonstrated that there had been recurrent selective events in the upstream and the downstream regions of KITLG in Eurasian populations. More importantly, besides the expected selection on the KITLG variants favoring light skin in coping with the weak UV radiation at high latitude, we observed a KITLG variant showing adaptation to winter temperature. In particular, compared with UV radiation, winter temperature showed a much stronger correlation with the prevalence of the presumably adaptive KITLG allele in Asian populations. This observation was further supported by the in vitro functional test at low temperature. Consequently, the pleiotropic effects of KITLG, that is, pigmentation and thermogenesis were both targeted by natural selection that acted on different KITLG sequence variants, contributing to the adaptation of Eurasians to both UV radiation and winter temperature at high latitude areas. **Yang et al.** ***Molecular Biology and Evolution,*** **35, 2272-2283 (2018).**

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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科组负责人。2008 年入选中科院“百人计划”，2013 年获国家杰出青年基金，2014 年获科技部中青年科技创新领军人才，2016 年入选中组部万人计划，2017 年入选人社部“国家百千万人才”。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。 Email: ship@mail.kiz.ac.cn Tel: 0871-68125411

重要成果及产出：

1. **Zhen Liu**[1,2] and Jianzhi Zhang[*]. Human C-to-U Coding RNA Editing Is Largely Nonadaptive. ***Molecular Biology and Evolution.*** 2018, 35(4), 963-969.
2. **Zhen Liu**[1*], **Fei-Yan Qi**[1,2*], **Dong-Ming Xu**[1*], **Xin Zhou**[1], **Peng Shi**[1,3,4†]. Genomic and functional evidence reveals molecular insights into the origin of echolocation in whales. ***Science Advances.*** 2018, 4(10):eaat8821.

1. C-to-U RNA 编辑在进化上是非适应的

在人类中发现了上千个 C−to−U RNA 编辑的编码位点，但是该现象的生物学意义还不清楚。非同义编辑适应性演化的假说预测，与同义编辑相比，非同义编辑的编辑位点的比例和编辑水平应该更高。然而，我们的分析结果与这些预测相反。而且，相对于同义编辑，非同义编辑的频率随着基因的重要性和进化保守性的升高而降低。总之，这些发现驳斥了适应性的假说，相反它们表明了 C−to−U RNA 编辑整体上是轻微有害或中性的，可能产生自 RNA 编辑酶的脱靶活性。综合 RNA 分子上的更为普遍的 A−to−I RNA 编辑和 m6A 修饰的相似结论，我们的研究提示着，至少在人类中，每一种类型的转录后编码 RNA 修饰的大部分事件可能来自于细胞错误而不是适应性演化，因此在转录后修饰的研究中需要一种思维范式的转换。

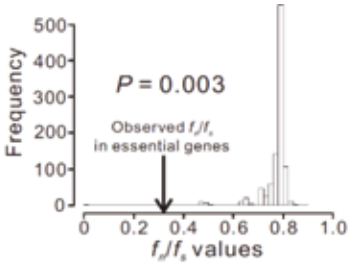

图 1. 必需基因的非同义编辑显著低于非必需基因的非同义编辑

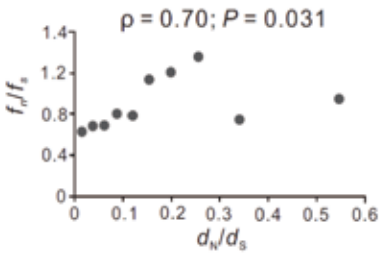

图 2. 非同义编辑频率随着进化保守性的升高而降低

2. 利用比较基因组学和功能实验的方法追溯和验证适应性复杂性状起源和演化的分子遗传机制

从系统发育关系上看，齿鲸和须鲸分别聚类成了两个独立的并系群，提示着，回声定位或者起源于齿鲸的共同祖先，或者起源于鲸的共同祖先然后在须鲸中丢掉了。不同演化阶段的鲸类化石对这两种假说都有不同程度上的支持，因此，回声定位（或高频听力）在鲸类中的起源问题一直存在的很大争议。通过对齿鲸和回声定位蝙蝠基因组范围的趋同进化分析，与处于相同进化尺度的非回声定位类群相比，齿鲸与回声定位蝙蝠在听力相关基因上发生了更强的趋同演化。功能实验进一步表明，鲸类共同祖先和须鲸共同祖先的 prestin 的功能与现生非回声定位鲸的 prestin 相同，而齿鲸共同祖先的 prestin 的功能则与现生回声定位鲸的 prestin 相同。该研究打破了传统上仅通过化石追溯适应性复杂性状起源和演化的局限性，从基因组范围的分析和分子功能水平上支持了适应性复杂性状回声定位（或高频听力）起源于齿鲸共同祖先的假说。

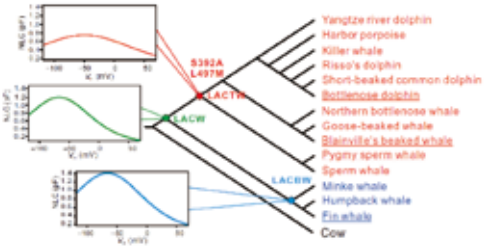

图 3. 不同演化阶段的鲸的 prestin 的功能检测

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.
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1. Human C-to-U Coding RNA Editing Is Largely Nonadaptive

Hundreds to thousands of coding sites were recently found to be C-to-U edited or editable in humans, but the biological significance of this phenomenon is elusive. Adaptive hypothesis that nonsynonymous editing is beneficial predicts that the fraction of sites edited and the median proportion of RNA molecules edited are both higher for nonsynonymous than synonymous editing. However, our empirical observations are opposite to these predictions. Furthermore, the frequency of nonsynonymous editing, relative to that of synonymous editing, declines as genes become functionally more important or evolutionarily more constrained. Together, these findings refute the adaptive hypothesis; they instead indicate that the reported C-to-U coding RNA editing is mostly slightly deleterious or neutral, probably resulting from off-target activities of editing enzymes. Along with similar conclusions on the more prevalent A-to-I editing and m6A modification of coding RNAs, our study suggests that, at least in humans, most events of each type of posttranscriptional coding RNA modification likely manifest cellular errors rather than adaptations, demanding a paradigm shift in the research of posttranscriptional modification.

2. Genomic and functional evidence reveals molecular insights into the origin of echolocation in whales

Echolocation allows toothed whales to adapt to underwater habitats where vision is ineffective. Because echolocation requires the ability to detect exceptional high-frequency sounds, fossils related to the auditory system can help to pinpoint the origin of echolocation in whales. However, because of conflicting interpretations of archaeocete fossils, when and how whales evolved the high-frequency hearing correlated with echolocation remain unclear. We address these questions at the molecular level by systematically investigating the convergent evolution of 7206 orthologs across 16 mammals and find that convergent genes between the last common ancestor of all whales (LCAW) and echolocating bats are not significantly enriched in functional categories related to hearing, and that convergence in hearing-related proteins between them is not stronger than that between nonecholocating mammalian lineages and echolocating bats. However, these results contrast with those of parallel analyses between the LCA of toothed whales (LCATW) and echolocating bats. Furthermore, we reconstruct the ancestral genes for the hearing protein prestin for the LCAW and LCATW; we show that the LCAW prestin exhibits the same function as that of nonecholocating mammals, but the LCATW prestin shows functional convergence with that of extant echolocating mammals. Mutagenesis shows that functional convergence of prestin is driven by convergent changes in the prestins S392A and L497M in the LCATW and echolocating bats. Our results provide genomic and functional evidence supporting the origin of high-frequency hearing in the LCATW, not the LCAW, and reveal molecular insights into the origin and evolutionary trajectories of echolocation in whales.

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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. **Xue, M**, **Chen, B**, **Ye, QQ**, **Shao, JR**, **Lyu, ZX**, and **Wen, JF***.Sense-antisense gene overlap is probably a cause for retaining the few introns in *Giardia* genome and the implications. ***Biology Direct.*** 2018,13: 23.
2. **Lyu, ZX**, **Shao, JR**, **Xue, M**, **Ye, QQ**, **Chen, B**, **Qin, Y.**, and **Wen, JF***. A new species of *Giardia* Kunstler, 1882 (Sarcomastigophora: Hexamitidae) in hamsters. ***Parasites & Vectors.*** 2018, 11(1): 202.
3. **Zhang YJ**, Zhu CX, Ding YR, Yan ZW, **Li GH**, Lan Y, **Wen JF***, Chen B*. Subcellular stoichiogenomics reveal cell evolution and electrostatic interaction mechanisms in cytoskeleton. ***BMC Genomics.*** 2018, 19(1):469.

1. 四种腔道寄生原虫能量代谢途径对微氧环境适应的趋同进化

蓝氏贾第虫，阴道毛滴虫，痢疾阿米巴和微小隐孢子虫是常见的寄生于脊椎动物包括人在内的寄生原虫，危害人类健康和畜牧业的发展。这四种原虫属于不同的进化类群，彼此亲缘关系较远，但都寄生在相似的氧气含量少的腔道（肠道和生殖道）中。为了适应腔道环境中这一相似的微氧环境，这四种寄生原虫的能量代谢途径发生了怎样的适应性进化以及它们的适应性策略有着怎样的异同是有趣的生物学问题，对该问题的研究也能为这些寄生虫更有效的防治提供重要基础。基于基因组数据和生物信息学分析（本地化同源搜索，功能结构域分析，定位分析等），我们重构了该四种腔道寄生原虫的能量代谢途径（糖酵解，三羧酸循环，氧化呼吸链等）并进行了系统的比较分析。结果显示它们在能量代谢网络方面发生了惊人相似的适应性改变：1）都丢失了高效产生 ATP 的三羧酸循环和氧化呼吸链，同时都发展出一些利用焦磷酸而不是 ATP 的代谢酶来尽量减少有限的 ATP 的消耗，相应地，它们负责产生焦磷酸的酶均发生了扩增；2）都发展出了一种特别的具有可塑性的丙酮酸代谢途径来适应环境中氧气浓度的动态变化而生成不同的终产物，不仅可用于消除氧（尽管是微量）的毒害作用也可解决细胞内的氧化还原势的平衡问题；3）虽物种不同，但它们相当一部分的代谢酶都是通过水平基因转移方式从细菌获得的。这些研究结果揭示了这四种寄生原虫因处在相似的低氧寄生环境，尽管它们彼此近缘关系较远，却在能量代谢方面发生了十分趋同的适应性进化的现象。

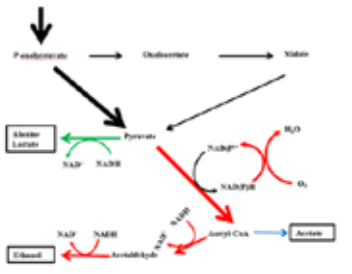

图 1. 四种腔道寄生原虫均发展出一样的丙酮酸代谢途径应对腔道内氧气浓度的动态变化

2. 蓝藻重要光合作用酶 F/SBPase II 的光激活特性的进化

在光合生物中，光不仅为二氧化碳的固定提供能量来源，而且还参与了其中多种酶活性的激活，从而避免了黑暗条件下两个方向相反的代谢途径同时进行时所导致的无效循环的发生。果糖 −1,6− 二磷酸酶（FBPase）和景天庚酮糖 −1,7− 二磷酸酶（SBPase）是真核光合生物卡尔文循环中受光激活的两个关键酶。FBPase 虽然普遍存在于光合原核和真核生物中，但一般认为只有光合真核生物的叶绿体型 FBPase 才是受到光激活的。由于光合真核生物的叶绿体是由蓝藻内共生而来的，那么，作为叶绿体前身的蓝藻，其参与卡尔文循环的 FBPase（实为 F/SBPase II 双功酶）是否也受到光激活呢？我们通过对已测序的蓝藻进行系统的分析和比较，发现一些蓝藻中参与卡尔文循环的 F/SBPase II 具有与光合真核生物叶绿体型 FBPase 类似的包含三个半胱氨酸残基的保守序列，这些保守序列正是叶绿体型 FBPase 受到光激活调节的结构基础。进一步的实验表明，蓝藻中具有这种保守序列的 F/SBPase II，其活性确实是受到光激活的；而不具有这种保守序列的蓝藻 F/SBPase II，光照对其活性没有影响。进一步的调查发现，存在上述保守序列的 F/SBPase II 在目前认为最早分支的蓝藻以及与叶绿体关系最近的蓝藻中均存在，因此，我们的研究表明，光合生物中参与卡尔文循环的 FBPase 受到光激活的机制在蓝藻中就已存在，而不是叶绿体内共生之后才发展出来的。由于蓝藻中受到光激活的是 F/SBPase II，而光合真核生物中是 FBPase I，因此，虽然光合真核生物的叶绿体来源于蓝藻的内共生，但其叶绿体型 FBPase 受到光激活的特性却是内共生之后另外重新发展出来的。

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 applicationsof the effective and specifc metabolic pathways

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1. The convergent adaptation of energy metabolism to microaerobic environments in four lumen-dwelling protozoan parasites

Giardia lamblia, *Entamoeba histolytica*, *Trichomonas vaginalis* and *Cryptosporidium parvum* are several parasitic protozoa of vertebrates including human, bringing about serious public health and economic burden. Despite being evolutionarily distantly related (belonging to different eukaryotic supergroups), they all live successfully in a similar oxygen-poor lumen environment (intestinal tract and urogenital tract). To adapt to the similar microaerobic conditions in lumina, what adaptive evolution has occurred in their energy metabolic pathways and what are the similarities and differences among their adaptive strategies are interesting biological questions and are worth studying for more efficient treatment of these parasites. Here, based on the genome data and using bioinformatics methods (such as homology search, domain analysis, localization prediction and so on), we reconstructed the energy metabolic pathways of the four protozoa (including glycolysis, TCA, ETC and so on) and a comparative genome analysis was carried out. The results showed that these four parasites have undergone surprisingly similar adaptive changes in energy metabolic networks: 1) they all lost TCA cycle and ETC which can produce ATP efficiently in aerobic eukaryotes. Meanwhile, they all have developed enzymes that can utilize pyrophosphate rather than ATP as substrates to minimise the consumption of the limited ATP, accordingly, the enzymes which are responsible for the generation of pyrophosphate were amplified in all the four protozoa; 2) they all developed flexible pathway of pyruvate metabolism to response to the dynamitic oxygen concentrations in the lumen, and to achieve the oxygen detoxification and redox balance; 3) quite a number of metabolic enzymes in these protozoa were all secondarily obtained from bacteria through lateral gene transfer. Thus, our study revealed an interesting phenomenon of remarkable convergent evolution of energy metabolism in four evolutionarily distantly-related lumen protozoa due to the similar oxygen-poor parasitic environment

2. Evolution of the light-activated property of F/SBPase II in cyanobacteria

In photosynthetic organisms, sunlight provides the energy source for the assimilation of carbon dioxide by photosynthesis, but it also involved in the activation of multiple enzyme, thereby avoiding the occurrence of a futile cycle caused by two metabolic pathways run simultaneously in opposite directions under dark conditions. In eukaryotic photosynthetic organisms, there are two key Calvin cycle enzymes that are activated by light, the fructose-1,6-bisphosphatase (FBPase) and sedoheptulose-1,7-bisphosphatase (SBPase). Although FBPase is ubiquitous in prokaryotic and eukaryotic photosynthetic organisms, it is generally supposed that only the chloroplastic FBPase of photosynthetic eukaryotes is light-activated. In the light of the fact that chloroplasts are considered to have originated from cyanobacteria through endosymbiosis, wthether the FBPase (to be exactly, biofunctional F/SBPase II) in cyanobacteria, the precursor of the chloroplast, is light-activated is an interesting question. By systematically analyzing and comparing the sequenced cyanobacteria, we found that F/SBPase II in some cyanobacteria has a conserved sequence containing three cysteine residues, which similar to photosynthetic eukaryotic chloroplastic FBPase. In eukaryotic chloroplastic FBPase, these conserved cysteine residues-contained sequences are the structural basis for the light-activation of chloroplastic FBPase, implying that the F/SBPase II in cyanobacteria is also light-activated. Further experiments showed that F/SBPase II with this conserved sequence in cyanobacteria is indeed activated by light, but the enzyme without this conserved sequence not. Further investigations have found that the F/SBPase II with the conserved sequence exists in lineages that is currently considered to be the earliest branching and most closely related to the chloroplast. Therefore, our research indicates that the mechanism of FBPase's light activation is already present in cyanobacteria, but not developed after the endosymbiosis of chloroplast. Since F/SBPase II is light-activated in cyanobacteria and FBPase I in photosynthetic eukaryotes, it is obvious that the mechanism of light-activation of chloroplatic FBPase in photosynthetic eukaryotes is redeveloped independently after the origin of chloroplast, but not derived from cyanobacteria.

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计算生物与医学生态学

马占山，研究员，博导，计算生物与医学生态学学科负责人。 2010 年 11 月中科院“百人计划 (引进杰出技术人才)”引进。2011 年入选“云南省高端科技人才”和“百名海外高层次人才”计划；2015 年入选“云岭产业技术领军人才”。美国 Idaho 大学计算机科学 (2008 年) 和昆虫学 (1997 年) 双博士、计算机科学和计算生物学研究科学家。并具有在硅谷等地长达八年多的涵盖电子、网络、软件、信息安全领域的计算机高级工程师经历。曾是美国“人类微生物菌群宏基因组研究计划 (HMP) 主要研发科学家之一 (2008-2010)，总部设在英国伦敦的 “Faculty 1000 of Biology & Medicine” 成员 (2008-2016)，并担任 I. J. Network Science 主编 (2015-2017)。以第一或责任作者在计算机科学、工程数学、计算智能、昆虫学、生态学、医学微生物学等领域发表八十余篇论文。

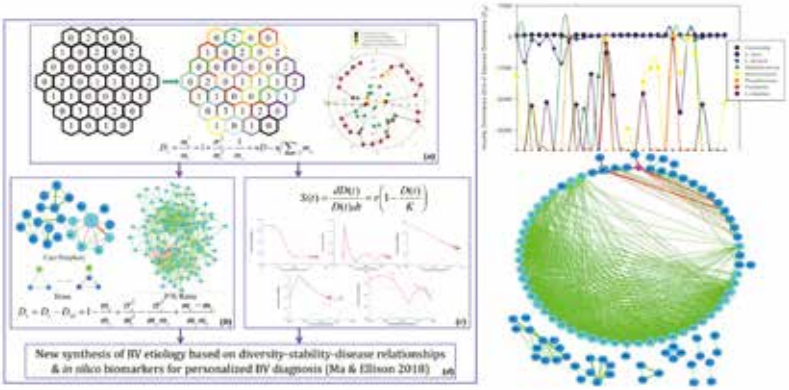
重要成果及产出：

1. Ma ZS* & Ellison AM (2018) Dominance network analysis provides a new framework for studying the diversity-stability relationship. *Ecological Monographs*. (Accepted)
2. Ma ZS* & Ellison AM (2018) A unified concept of dominance applicable at both community and species scale. *Ecosphere*, https://doi.org/10.1002/ecs2.2477.
3. Ma ZS (2018) Extending species-area relationships (SAR) to diversity-area relationships (DAR), *Ecology and Evolution*. DOI: 10.1002/ece3.4425
4. Ma ZS (2018) Sketching the Human Microbiome Biogeography with DAR (Diversity-Area Relationship) Profiles. *Microbial Ecology*. https://doi.org/10.1007/s00248-018-1245-6
5. Ma ZS (2018) Diversity time-period and diversity-time-area relationships exemplified by the human microbiome. *Scientific Reports*, 8(1):7214.
6. Ma ZS*, Li Lianwei, Li Wendy (2018). Assessing and interpreting the within-body biogeography of human microbiome diversity. *Frontiers in Microbiology*, vol.9:1619.
7. Ma ZS*, Li Lianwei (2018) Measuring metagenome diversity and similarity with Hill Numbers. *Molecular Ecology Resources*, vol. 18(6):1339-1355.
8. Li Wendy *et al*. (2018) A cross-scale neutral theory approach to the influence of obesity on community assembly of human gut microbiome. *Frontiers in Microbiology*.
9. Sun Y. *et al*. (2018) The gut microbiota heterogeneity and assembly changes associated with the IBD. *Scientific Reports*, DOI:10.1038/s41598-018-37143-z
10. Li LW & Ma ZS* (2018) Global microbiome diversity scaling in hot springs with DAR (diversity-area relationship) profiles. *Frontiers in Microbiology* (accepted).

11-12. 三项关于“三代基因测序软件技术、菌群相关疾病风险估计”发明专利受理：
201810159081.8
201810159082.2
201810927933.3

Dominance network analysis provides a new framework for studying the diversity-stability relationship

The diversity-stability relationship is a long-standing, central focus of community ecology. Two major challenges have impeded studies of the diversity-stability relationship (DSR): the difficulty in obtaining high-quality longitudinal datasets; and the lack of a general theoretical framework that can encompass the enormous complexity inherent in “diversity,” “stability,” and their many interactions. Metagenomic “Big Data” now provide high quality longitudinal datasets, and the human microbiome project (HMP) offers an unprecedented opportunity to reinvigorate investigations of DSRs. We introduce a new framework for exploring DSRs that has three parts: (i) a cross-scale measure of dominance with a simple mathematical form that can be applied simultaneously to individual species and entire communities, and can be used to construct species dominance networks (SDNs); (ii) analysis of SDNs based on special trio motifs, core-periphery, rich-club, and nested structures, and high salience skeletons; and (iii) a synthesis of coarse-scale core/periphery/community-level stability modeling with fine-scale analysis of SDNs that further reveals the stability properties of the community structures. We apply this new approach to data from the human vaginal microbiome of the HMP, simultaneously illustrating its utility in developing and testing theories of diversity and stability while providing new insights into the underlying ecology and etiology of a human microbiome-associated disease.

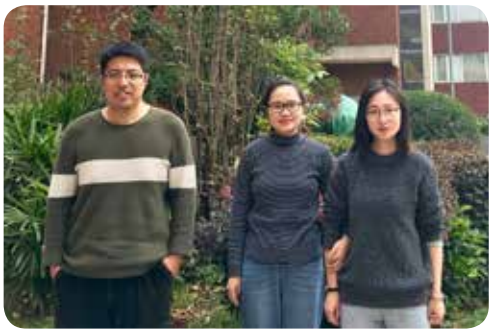


多样性 — 稳定性 (Diversity-Stability Relationship) 关系被认为是生态学中最重要的核心理论之一，并具有极其重要的实际意义。例如：生物多样性保护的最大收益可能是维持生态系统稳定性，从而有利于人类生存、健康和社会经济的可持续发展。类似地，人体微生物群系（菌群）生态系统的稳定性与人体健康和疾病状态密切相关。该系列研究所提出优势度概念其实是换一个角度刻画多样性的方法，但优势度网络 (SDN) 技术使得对稳定性研究较其经典方法更加直接有效：因为系统稳定性的维持很可能是由于优势物种控制着系统的动态平衡！

Ma ZS* & AM Ellison (2018a) ***Ecosphere***
Ma ZS* & AM Ellison (2018b) ***Ecological Monographs***

Computational Biology and Medical Ecology Lab

Bio-sketch of the lab Principal Investigator: **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 Principal Investigator by Kunming Institute of Zoology (KIZ), the Chinese Academy of Sciences (CAS) through "The Elite 100 Scientists Program" of the CAS. Prior to joining in KIZ, he was a Research Scientist (in Computational Biology & Computer Science) at UI. He was a senior network and 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 80 peer-refereed papers in premier platforms such as *IEEE Transactions on Reliability*, *Science Translational Medicine*, *The ISME Journal, Ecological Monographs*. He was a member of London-based "*Faculty 1000 of Biology and Medicine*".



扩展“生物多样性随时空尺度变化”的经典系列理论
DAR/DTR/DTAR: Extending Classic SAR/STR/STAR

英国植物学家 HC Watson 在 1835 年研究植物地理分布时发现，植物种类与生境面积大小往往成正比。随后数十年，自然学家和数学家们经过进一步研究发现，物种数量与生境面积的关系遵从幂法则（S=cAz，其中 S 是某生境内物种数量，A 是该生境面积，c 和 z 是待估计参数）。在经历了数代自然学家的努力后，作为生态学和生物地理学中少有的经典法则之一，物种数量随生境面积空间尺度变化的幂法则关系， 也就是“物种 — 面积关系”（SAR：Species Area Relationship) 也载入了教科书中。与此同时，这一关系为研究物种灭绝以及珍惜物种保护提供了重要理论基础。显然，根据 SAR 理论的预测，如果自然生境面积不断减少，其中某些物种必然要灭绝。如果能够估计出某一类群 (例如高等植物或哺乳动物)SAR 模型的参数 c 和 z, 则有可能预测某一地区中所能容纳的高等植物或哺乳动物数量。基于物理学中时空遍历理论 (Ergodic Theory)，1960 年代科学家提出了“物种 — 时间关系”(Species-Time Relationship or STR)，并在古生物进化领域研究获得了一系列验证。1990 年代科学家进一步扩展提出了“物种 — 时间空间关系” (Species-time-area relationship or STAR)。一直以来，SAR/STR/STAR 是生态学、生物地理学、保护生物学研究的热点课题之一，也是评估设置自然保护区不可或缺的最重要理论基础之一。SAR/STR/STAR 理论有一明显局限性：忽略了物种的“丰度”(丰富程度：Abundance)。也就是说，一只大熊猫和 1000 只大熊猫在该理论体系中所占份量没有区别；因为该理论只考虑物种的数量（熊猫是一种动物），而不考虑具体某个物种（熊猫）的数量多少。同样，10 亿只小龙虾也代表一个物种，与一只大熊猫代表的多样性没有任何区别。这一不合理的度量体系显然与人类对生物多样性重要性认识的历史局限性有关。 当然，人类对生物多样性的认知一直在不断深入。科学家自然注意到了仅仅将物种数量作为生物多样性度量的严重缺陷。1948 年，现代信息论创始人香农 (CE Shannon) 著作《通讯的数学理论》一经出版，生态学家就立即将 Shannon 用于度量信息的熵指标 (Shannon's Entropy) 引入生物多样性度量，而成为迄今为止最为常用的度量生物多样性的方法。Shannon 于 70 年前创立的信息论为今天信息时代奠定了最早的理论基础，但据考证，Shannon 本人并没有做过生物多样性研究，生态学家敏锐的将其成果应用于生物多样性度量。几乎是同一时间，EH Simpson 于 1949 年在 Nature 发表了度量多样性的 Simpson 指数。1950-1990 年代生态学家、数学家陆续提出了诸多多样性度量指数，但这也使得应用生态学家有些无所适从。而且就 SAR/STR/STAR 理论和实践而言，多样性概念和度量方法领域的进展并没有被纳入 SAR/STR/STAR 领域的理论研究或实际应用。

学科组通过系列研究对于“生物多样性随时空尺度变化”的经典理论做出的扩展，从根本上解决了以上提到的、经典 SAR/STR/STAR 理论所存在的缺陷；而经典理论则成为了新理论 (模型) 的特例。从基础概念角度看，是将“物种数 — 面积关系”(SAR) 扩展到一般化的“多样性 — 面积关系” (DAR, Diversity-Area Relationship)；采用以 Renyi 熵为基础推导出来的“希尔数”(Hill Numbers) 作为通用的“多样性指数”取代 SAR 模型中的“物种数”。这一推广从根本上解决了传统 SAR 存在的缺陷。Renyi 熵由数学家 Renyi (1961) 年提出，其应用范围非常广泛 (例如量子纠缠的信息度量、经济学中财富分布等)。 香农熵其实是 Renyi 熵的特例。此外，该系列研究还提出了：DAR Profile, PDO (pair-wise diversity overlap) profile, MAD (maximal accrual diversity) profile, LRD profile (local to regional diversity ratio), LRG profile (local to global diversity ratio) 的全新概念，并推导出了估计它们的数学模型和计算方法。(相关论文见 [3-7], [10])

三代基因测序组装技术领域再次取得重要进展
Hybrid Assembly of Ultra-long Nanopore Reads Augmented with 10x-Genomics Contigs: Demonstrated with a Human Genome

Zhanshan (Sam) Ma* Lianwei Li Chengxi Ye Minsheng Peng Ya-Ping Zhang*

The 3rd generation of sequencing (3GS) technologies generate ultra-long reads (up to 1Mb), which makes it possible to eliminate gaps and effectively resolve repeats in genome assembly. However, the 3GS technologies suffer from the high base-level error rates (15%-40%) and high sequencing costs. To address these issues, the hybrid assembly strategy, which utilizes both 3GS reads and inexpensive NGS (next generation sequencing) short reads, was invented. Here, we use 10x-Genomics® technology, which integrates a novel bar-coding strategy with Illumina® NGS with an advantage of revealing long-range sequence information, to replace common NGS short reads for hybrid assembly of long erroneous 3GS reads. We demonstrate the feasibility of integrating the 3GS with 10x-Genomics technologies for a new strategy of hybrid de novo genome assembly by utilizing DBG2OLC and Sparc software packages, previously developed by the authors for regular hybrid assembly. Using a human genome as an example, we show that with only 7′ coverage of ultra-long Nanopore® reads, augmented with 10x reads, our approach achieved nearly the same level of quality, compared with non-hybrid assembly with 35′ coverage of Nanopore reads. Compared with the assembly with 10x-Genomics reads alone, our assembly is gapless with slightly high cost. These results suggest that our new hybrid assembly with ultra-long 3GS reads augmented with 10x-Genomics reads offers a low-cost (less than ¼ the cost of the non-hybrid assembly) and computationally light-weighted (only took 109 calendar hours with peak memory-usage=61GB on a dual-CPU office workstation) solution for extending the wide applications of the 3GS technologies. (Patent Receipt No: 201810927933.3)

人类进化与疾病基因组学

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重要成果及产出：

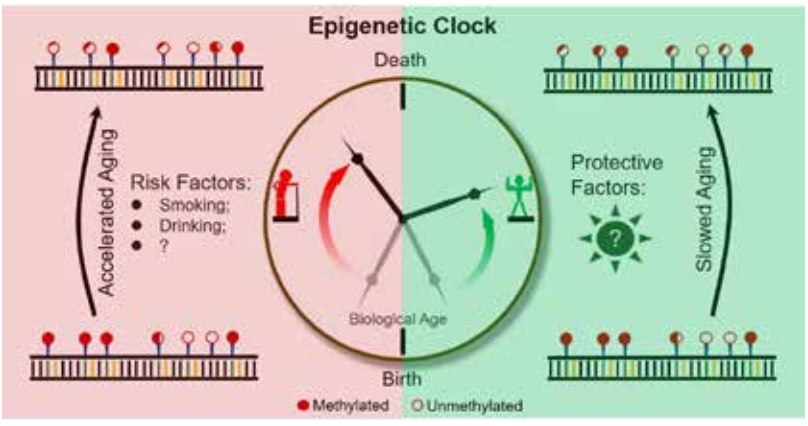
1. **Xiao FH**[1], **Chen XQ**[1], **Yu Q**[1], Ye Y[1], **Liu YW**, Yan D, **Yang LQ**, Chen G, Lin R, Yang L, Liao X, Zhang W, Zhang W, Tang N, Wang XF, Zhou J*, Cai WW*, **He YH***, **Kong QP***. Transcriptome evidence reveals enhanced autophagy-lysosomal function in centenarians. ***Genome Research***, 2018, **28**:1601-1610 (**Cover Story**). (IF5-Y : 13.796)
2. **Xiao FH**, **Chen XQ**, **He YH**, **Kong QP***. Accelerated DNA methylation changes in middle-aged men define sexual dimorphism in human lifespans. ***Clinical Epigenetics***, 2018, **10**:133. (IF5-Y: 5.799)
3. **Tian JY**, **Li YC**, **Kong QP***, Zhang YP. The origin and evolution history of East Asian populations from genetic perspectives**.** ***Hereditas***, 2018, **40**:814-824.

1. 转录组证据揭示自噬－溶酶体信号通路功能增强是百岁老人长寿重要的健康保护机制

作为人类健康老龄典范的长寿老人（尤其是百岁老人），往往能延缓甚至规避一些重大老年性疾病的困扰。揭示其健康衰老保护机制，将为延缓衰老、改善老年人健康提供新视角和新策略。我们基于长寿家系成员 171 例样本（百岁老人，百岁 F1 后代及 F1 后代配偶）的外周血转录组数据，发现自噬 - 溶酶体信号通路基因表达上调为百岁老人最为显著的信号，且该信号同样存在于百岁老人 F1 后代。同时，对 4 个自噬 - 溶酶体信号通路基因（CTSB、ATP6V0C、WIPI1 和 ATG4D）在人胚肺成纤维细胞 IMR-90 中分别进行过表达实验，发现这 4 个基因高表达均可增强细胞自噬功能并显著延缓细胞衰老；在果蝇中进行 Atg18a（WIPI1 在果蝇中的同源基因）的过表达研究，也发现其确实可显著延长果蝇寿命。因此，我们基于组学分析及细胞、果蝇等功能实验，提示自噬 - 溶酶体信号通路功能增强可能有助于人类健康寿命延长（**Xiao, Chen, Yu, and Ye et al. 2018 *Genome Research***）。

2. 男性中年时期年龄相关 DNA 甲基化加速变化是男女寿命差异的重要原因

长寿人群中男性数量明显少于女性。与此同时，一般人群中男性平均寿命也往往短于女性，而心血管疾病早发被认为是男性寿命较短的重要原因之一。鉴于年龄相关的 DNA 甲基化变化与衰老、老年病发生的紧密联系，我们比较分析了男女两性间 DNA 甲基化的年龄相关变化模式。结果发现男性中年时期 DNA 甲基化伴随年龄增长呈现加速趋势，这可能是男性心血管疾病早发而导致平均寿命缩短的重要原因。进一步分析表明，男性群体中更为普遍存在的吸烟及酗酒等因素对其年龄相关甲基化变化加速具有促进作用。基于年龄相关甲基化位点的表观遗传学时钟与个体的生物学年龄密切相关，可用于年龄相关结果的预测（**Xiao et al. 2018 *Clinical Epigenetics*；Unpublished data**）。



Human Evolution and Disease Genomics

Prof.Qing-Peng Kong, Principle 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 80 papers on the international peer-reviewed journals such as *Am J Hum Genet, PNAS, Genome Res, Mol Biol Evol*, *Theranostics* with total citations over 2,900 times.

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1. Transcriptome evidence reveals enhanced autophagy-lysosomal function in centenarians

Centenarians (CENs) exhibit unique characteristics of delaying or even escaping many serious age-related diseases afflicting the normal population (e.g., cardiovascular disease, Alzheimer's disease, type-2 diabetes, and cancer). Therefore, CENs serve to as excellent subjects to study the mechanisms of human longevity and healthy aging. In the present study, we obtained and analyzed the transcriptomes of a cohort of 171 subjects from centenarian families, consisting of 76 CENs, 54 F1, and 41 F1SP. We identified a large number of differentially expressed genes (DEGs) in CENs, among which the autophagy-lysosomal pathway is significantly up-regulated. Overexpression of several genes from this pathway, *CTSB*, *ATP6V0C*, *ATG4D*, and *WIPI1*, could promote autophagy and delay senescence in cultured IMR-90 cells, while overexpression of the *Drosophila*homolog of *WIPI1*, *Atg18a*, extended the life span in transgenic flies. Interestingly, the enhanced autophagy-lysosomal activity could be partially passed on to their offspring, as manifested by their higher levels of both autophagy-encoding genes and serum beclin 1 (BECN1). In light of the normal age-related decline of autophagy-lysosomal functions, these findings provide a compelling explanation for achieving longevity in CENs, and suggest that the enhanced waste-cleaning activity via autophagy may serve as a conserved mechanism to prolong the life span from *Drosophila* to humans. (**Xiao, Chen, Yu, and Ye et al. 2018 *Genome Research***).

2. Accelerated DNA methylation changes in middle-aged men define sexual dimorphism in human lifespans

In longevity population, the number of male centenarians is about 1/2-1/7 lesser than that of males. In addition, for general population, men often live shorter than women, which is partly explained by their higher mortality and earlier onset of some age-related diseases, especially cardiovascular disease (CVD). Since the close associations between dynamic DNA methylation and lifespan and age-related diseases including CVD, we analyzed the sexual differences of methylation profiles (Illumina HumanMethylation450 BeadChip) during aging in two independent cohorts containing 708 and 2711 samples. Our results revealed that the sex-biased methylation changes occurred in middle-aged men in an acceleration manner, which likely contribute to the sexual dimorphism observed in human lifespan by promoting the occurrence of CVD. As drinking and smoking were also found to be associated with this accelerated methylation change in men, it is possible that male lifespan may be prolonged by improving unhealthy lifestyles at or before middle age. Currently, the DNA methylation age has been considered a “prophet” of age-related outcomes (**Xiao et al. 2018, *Clinical Epigenetics*; Xiao et al. 2018; Unpublished data**).

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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. **Sun J[1], Wang X[1], Shi Y, Li J, Li C,** Shi Z, Chen Y, **Mao B*.** EphA7 regulates claudin6 and pronephros development in Xenopus. ***Biochem Biophys Res Commun.*** 2018, 495:1580–1587.
2. Xu HB[1], **Li YX[1]**, Li Y, Otecko NO, Zhang YP, **Mao BY***, Wu DD*. Origin of new genes after zygotic genome activation in vertebrate. ***J Mol Cell Biol.*** 2018，10:139-146.
3. Yang ZH[1], Shi H[1], **Ma PC[1]**, Zhao SL, Kong QH,Bian TH, Gong C, Zhao Q, Liu Y, Qi XB, Zhang XM,Han YL, Liu JW, Li QW, Chen H*, Su B*, Darwinian positive selection on the pleiotropic effects of KITLG explain skin pigmentation and winter temperature adaptation in Eurasians. ***Molecular Biology and Evolution.*** 2018，35:2272–2283

EphA7 在非洲爪蛙原肾发育中的功能与作用机制

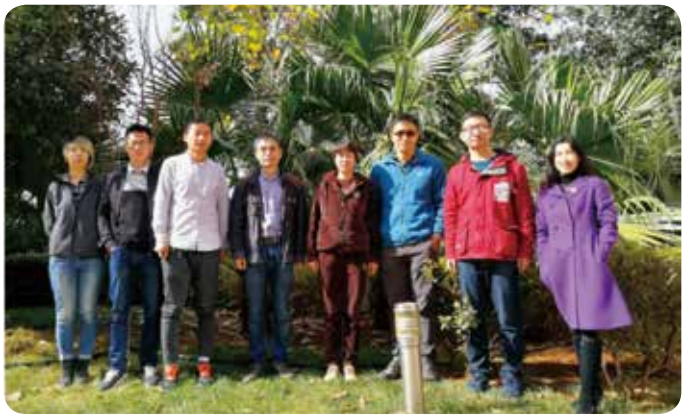
Ephrin-Eph 信号通路在多种组织器官发育中都具有重要作用。我们发现 EphA7 在非洲爪蛙胚胎原肾小管中有特异的表达，并发现了 EphA7 存在另一个 RNA 可变剪切，编码一种分泌型的 EphA7（EphA7-S）。在胚胎中通过反义 morpholino 抑制 EphA7 的表达会导致原肾小管细胞分化与结构异常。我们设计了一种剪切型 morpholino（EphA7-sp-MO），特异性阻断全长形式 EphA7 的表达，而不影响 EphA7-S 的表达。注射 EphA7-sp-MO 同样会抑制原肾细胞的分化，并可被 EphA7-FL mRNA 挽救，但原肾小管的管腔仍无法形成，表明 EphA7-S 可能在原肾小管的形态发生中具有一定作用。

我们发现，抑制 Eph7 的表达会抑制细胞连接相关蛋白 Claudin6 在细胞膜表面的分布，而不影响其 mRNA 的表达。有意思的是，在 EphA7-sp-MO 注射胚胎中，原肾细胞中的 Claudin6 蛋白分布正常，表明分泌型 EphA7-S 可能在调节 Claudin6 的稳定性中具有主导作用。在培养细胞中，EphA7 和 EphA7-S 均可与 Claudin6 结合，EphA7 共表达会促进 Claudin6 的磷酸化，并降低 Claudin6 在膜上的分布，而 EphA7-S 可抑制 EphA7 对 Claudin6 的磷酸化与稳定性调节。EphA7 过表达可促进 JNK 的磷酸化，而 EphA7-S 可以抑制 EphA7 对 JNK 的激活。上述结果揭示了 EphA7 在肾脏发育中新的作用与机制。

图 1. **EphA7 调控爪蛙原肾小管发育。**（A）EphA7-ATG-MO 可显著抑制外源 EphA7 的表达。（B）注射 EphA7-ATG-MO 造成胚胎心包区水肿，提示肾脏发育缺陷。（C）通过注射荧光素葡聚糖示踪，显示 EphA7-ATG-MO 注射胚胎原肾小管结构异常。

Fig. 1. **EphA7 is required for pronephros development in Xenopus.** (A) Injection of the EphA7-ATG-MO reduced exogenous EphA7 level from stage11 embryos as revealed by Western blot. (B) Embryos injected bilaterally with the EphA7-ATG-MO developed pericardial edema (arrowhead) at stage 43. (C) Fluorescent dextran excretion assay showing the tubule defects in EphA7-ATG-MO injected embryos.

Mechanisms of Neural Patterning and Evolution



Prof. 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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EphA7 regulates claudin6 and pronephros development in Xenopus

Eph/ephrin molecules are widely expressed during embryonic development, and function in a variety of developmental processes. Here we studied the roles of the Eph receptor EphA7 and its soluble form in Xenopus pronephros development. EphA7 is specifically expressed in pronephric tubules at tadpole stages and knockdown of EphA7 by a translation blocking morpholino led to defects in tubule cell differentiation and morphogenesis. A soluble form of EphA7 (sEphA7) was also identified. Interestingly, the protein level of claudin6 (CLDN6), a tetraspan transmembrane tight junction protein, was dramatically reduced in the translation blocking morpholino injected embryos, but not when a splicing morpholino was used, which blocks only the full length EphA7. In cultured cells, EphA7 binds and phosphorylates CLDN6, and reduces its distribution at the cell surface. sEphA7 also binds CLDN6 and coexpression of sEphA7 reversed the effect of EphA7 on CLDN6. We showed evidence that the role of EphA7 in tubule cell differentiation is mediated by Eph/JNK1 signaling. sEphA7 overexpression also blocks Eph/JNK1 signaling and tubule cell differentiation, likely through dimerization with EphA7. We propose that sEphA7 works as a buffering system to balance endogenous EphA7/JNK1 signaling and block its effect to destabilize CLDN6, allowing proper pronephros differentiation and morphogenesis.

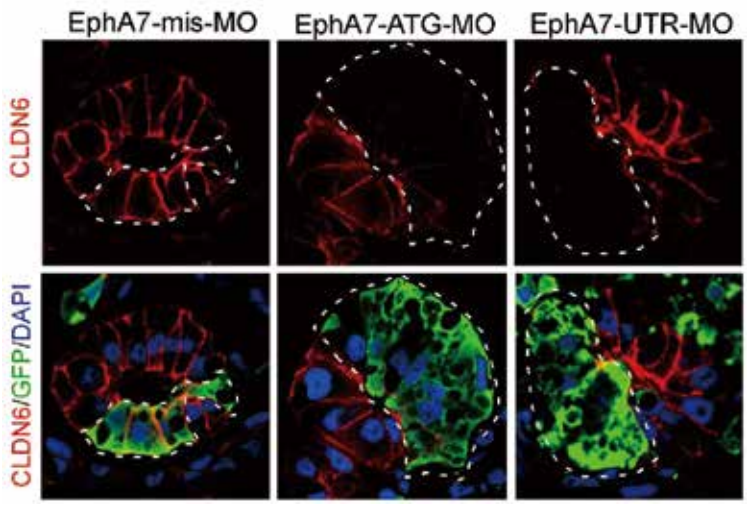

图 2. **EphA7 调控紧密连接蛋白 claudin6 在原肾小管细胞膜上的稳定性。**在 EphA7-ATG-MO 或 EphA7-UTR-MO 注射区域，原肾小管细胞膜上的 claudin6 水平显著降低，而注射携带突变位点的 EphA7-mis-MO 则不会。

Fig.2. **EphA7 regulates membrane claudin6 level.** The membrane level of CLDN6 was strongly reduced in EphA7-ATG-MO or a non-overlapping EphA7-UTR-MO injected tubular cells (outlined) in stage 35 embryos, but not the control EphA7-mis-MO.

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哺乳动物胚胎发育

郑　萍，博士，研究员，2009 年入选中国科学院“百人计划”。云南省高端科技人才，中国科学院王宽诚人才奖“西部学者突出贡献奖”获得者。实验室主要研究方向包括：1）干细胞维持遗传物质稳定性的调控机制；2）生殖干细胞的基础生物学及其在动物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. Liu D#, Wang X#, He D#, Sun C#, He X, Yan L, Li Y, Han JJ*, **Zheng P***. Single-cell RNA-sequencing reveals the existence of naive and primed pluripotency in pre-implantation rhesus monkey embryos. ***Genome Research***, 2018, 28:1481–1493. (封面论文，期刊 5 年影响因子 13.796).
2. Zhao B#, Zhang WD#, Cun YX, Li JZ, Liu Y, Gao J, Zhu HW, Zhou H, Zhang RG, **Zheng P***. Mouse embryonic stem cells have increased capacity for replication fork restart driven by the specific Filia-Floped protein complex. ***Cell Research***, 2018, 28(1):69-89. (期刊 5 年影响因子 15.973).
3. Fan Y#, Luo R#, Su L-Y, Xiang Q, Yu D, Xu L, Chen J-Q, Bi R, Wu D-D, **Zheng P***, Yao Y-G*. Does the genetic feature of the Chinese tree shrew (Tupaia belangeri chinensis) support its potential as a viable model for Alzheimer’s disease research? ***Journal of Alzheimers Disease***, 2018; 61(3):1015-1028.
4. He DJ#, Wang L#, Zhang ZB#, Guo K, Li JZ, He XC, Cui QH*, **Zheng P***. Maternal gene Ooep may participate in homologous recombination-mediated DNA double-strand break repair in mouse oocytes. ***Zool Res***, 2018, 39(6):387-395.

1. 发现人 *KHDC3L* 基因在多能干细胞及人类胚胎发育中的重要作用

早期胚胎细胞遗传物质的稳定性决定了胚胎能否顺利发育。我们以往的系列研究表明，小鼠 Filia 对维持早期胚胎多能细胞的遗传稳定性至关重要，Filia 缺失可导致早期胚胎发育停滞。但其人类同源基因 *KHDC3L* 的功能及其与疾病的关系尚不清楚。我们发现：*KHDC3L* 基因在人胚胎干细胞的遗传稳定性维持中起重要作用，可调控同源重组介导的损伤修复，并激活 PARP1 酶活性，上述功能受两个重要的苏氨酸磷酸化调控。在女性复发性流产病人中，我们筛选到该基因存在两类片段缺失突变（分别缺失 11 个和 23 个氨基酸）。利用人胚胎干细胞体系，我们确定了这些缺失突变由于丢失了其中一个重要的苏氨酸磷酸化位点（T156），从而严重破坏了 KHDC3L 蛋白功能，导致早期胚胎细胞 DNA 损伤严重，并诱导细胞凋亡，从而发生胚胎致死和复发性流产（论文待投稿）。

2. 揭示灵长类胚胎发育多能性的变化模式

小鼠早期胚胎多能细胞在着床前呈 naïve pluripotency 状态（原始多能态，具发育全能性），在着床后过渡到 primed pluripotency 状态（始发多能态，具局限的发育能力）。但是，灵长类早期胚胎的发育多能性变化特征并不清楚。通过单细胞 RNA-seq，我们分析了猕猴着床前 7 个发育阶段胚胎细胞的转录组 [包括 16 细胞期、早桑椹胚期、晚桑椹胚期、早期囊胚 (EB)、中期囊胚 (MB)、晚期囊胚 (LB) 和孵化囊胚 (HB)]，发现猕猴早期胚胎发育的多能性变化特征与小鼠显著不同：naïve pluripotency 状态仅短暂存在于着床前

囊胚期的早期 (EB) 和中期 (MB)，在囊胚后期 (LB) 即转变为 primed pluripotency 状态（图 1）。这一发现提示，选择早期和中期囊胚，将可能成功分离和建立具 naïve pluripotency 特征的灵长类胚胎干细胞系（*Genome Research*, 2018, 28:1481–1493，封面文章）。

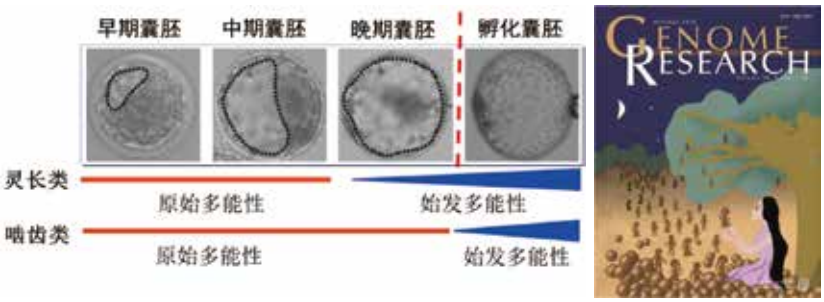
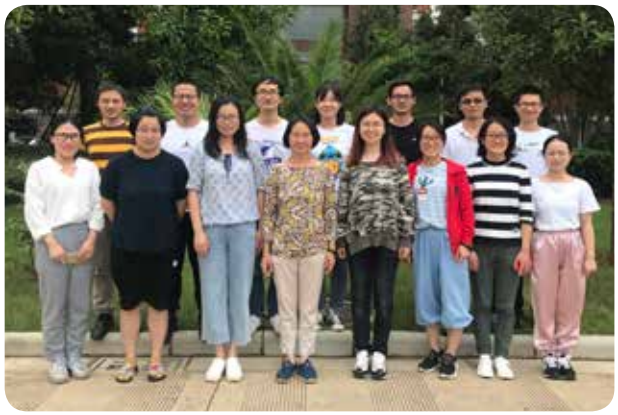


图 1. 灵长类和啮齿类早期胚胎多能性的变化模式。

Mammalian Embryonic Development



Prof. Ping Zheng, Principal Investigator, joined in Kunming Institute of Zoology, Chinese Academy of Sciences in 2009. The laboratory studies how stem cells safeguard their genomic stability, and the biology of germ-line stem cells in male and female. We use mouse, monkey and tree shrew as animal models.
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1. KHDC3L ensures genome stability of human early embryonic cells and its dysfunction is associated with recurrent pregnancy loss (RPL)

Mouse Filia plays critial roles in maintaining genomic stability of early embryonic cells and ensuring embryo development. However, the roles of its human ortholog KHDC3L remain unknown. By utilizing human embryonic stem cells (ESCs) combined with screening the genomic DNA samples from female patients with recurrent pregnancy loss (RPL), we show that human KHDC3L is critical for genomic integrity of early embryonic cells and its dysfunction is associated with RPL. KHDC3L functions through two independent pathways: ensuring the homologous recombination (HR)-mediated DNA repair and stimulating PARP1 activation. Of note, regulations on both pathways require the ATM-dependent phosphorylation of T145 and T156, which synergistically control KHDC3L's functions. By screening the *KHDC3L* gene in genomic DNA samples of female patients with primary infertility, we found two deletion mutations of KHDC3L (Δ11 and Δ23) in two patients with RPL. Importantly, these two deletion mutations bear a common loss of the critical phosphorylation site T156. Taken together, our study identified KHDC3L as a novel potential factor associated with RPL and discovered two phosphorylation sites which are critical for KHDC3L's functions and therefore implicated in the etiology of RPL (manuscript in preparation).

2. Pluripotency dynamics in rhesus monkey early embryos

Naïve pluripotency exists in epiblast cells of the mouse pre-implantation embryos. However, whether the naïve pluripotency is transient or non-existent in primate embryos remains unclear. Using RNA-seq in single blastomeres from 16-cell embryos through to hatched blastocysts of rhesus monkey, we constructed the lineage segregation roadmap in which the specification of trophectoderm, epiblast and primitive endoderm is initiated simultaneously at the early blastocyst stage. Importantly, we uncovered the existence of distinct pluripotent states in monkey pre-implantation embryos. At the early- and middle-blastocyst stages, the epiblast cells have the transcriptome features of naïve pluripotency, whereas they display a continuum of primed pluripotency characteristics at the late- and hatched-blastocyst stages. Moreover, we identified some potential regulators that might play roles in the transition from naïve to primed pluripotency. Thus, our study suggests the transient existence of naïve pluripotency in primates and proposes an ideal time-window for derivation of primate embryonic stem cells with naive pluripotency.
(*Genome Research*, 2018, 28:1481–1493, cover story).

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龚道华	Gong, Daohua	2018
唐 敏	Tang, Min	2018
谢 恒	Xie, Heng	2018

表观遗传与发育调控

焦保卫，博士，研究员，博士生导师。“青年千人计划”引进人才。云南省细胞生物学学会第五届理事会秘书长。长期从事乳腺发育、乳腺癌及乳腺干细胞的研究。 鉴定了 RLIM 基因在乳腺发育中的关键作用，发现 X 染色体失活（XCI）在成体细胞中的新模式，阐明了 RLIM 基因在乳腺发育和胚胎发育早期的调控机制及其进化意义。在乳腺癌研究中首次发现三阴性乳腺癌（TNBC）存在独特剪接模式，并详实地阐明其主要调控因子 TDP-43 的分子作用机制。同时鉴定了 TNBC 特异性高表达的长链非编码 RNA（lncRNA）MIR100HG，通过形成 lncRNA-DNA 三螺旋结构调控肿瘤进程。目前已经在 *Cell*、*PNAS*、*Cell Death & Disease* 等国际期刊杂志发表论文 20 余篇。

重要成果及产出：

1. **Wang S[1], Ke H[1], Zhang H, Ma Y**, Ao L, **Zou L, Yang Q**, Zhu H, Nie J, Wu C, **Jiao B***.LncRNA MIR100HG promotes cell proliferation in triple-negative breast cancer through triplex formation with p27 loci. ***Cell Death Dis***. 2018 Jul 24;9(8):805.
2. **Chen W[1] , Wang H[1] , Cheng M**, Ni L, **Zou L, Yang Q**, Cai X, **Jiao B***. Isoharringtonine inhibits breast cancer stem-like properties and STAT3 Signaling. ***Biomed Pharmacother***. 2018 Apr 18;103:435-442.
3. **Ke H[1], Zhao L[1], Zhang H[1], Feng X, Xu H**, Hao J, **Wang S, Yang Q, Zou L**, Su X, Wang L, Wu C, Wang Y, Nie J, **Jiao B***, Loss of TDP43 inhibits progression of triple-negative breast cancer in coordination with SRSF3. ***Proc Natl Acad Sci U S A***. 2018 Apr 10;115(15):E3426-E3435.
4. **Zhang H[1], Yang X[1], Feng X, Xu H, Yang Q, Zou L**, Yan M, Liu D, Su X, **Jiao B***. Chromosome-wide gene dosage rebalance may benefit tumor progression. ***Mol Genet Genomics.*** 2018 Aug;293(4):895-906.

1. 可变剪接因子 TDP43 结合 SRSF3 共同调控 TNBC 进程

可变剪切的异常已被认为肿瘤的另一个潜在的标志物。我们发现三阴性乳腺癌（TNBC）在剪切水平呈现一个特殊的模式，而 TDP43 是一个重要的剪切调控因子。临床数据显示 TDP43 的高表达正相关病人预后差。敲低 TDP43 抑制肿瘤的进程，包括细胞增殖、迁移，过表达 TDP43 促进细胞恶性生长。深度测序与后续功能实验表明 TDP43 结合 SRSF3 共同调控 TNBC 进程。TDP43/SRSF3 复合物调控特异性剪切模式，其中包括下游 PAR3 和 NUMB。PAR3 和 NUMB 分别介导 TDP43 与 SRSF3 对细胞迁移与增殖的调控。TDP43/SRSF3 复合物与下游 PAR3 是潜在的 TNBC 的治疗靶点。【Ke H et al. 2018 *Proc Natl Acad Sci U S A*, IF=10.359】

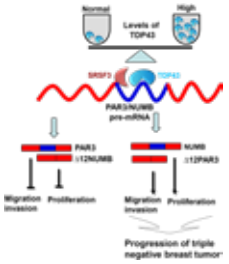

图 1. TDP43 在剪接事件中的调控作用

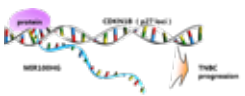

图 2.16 种肿瘤原发实体瘤标本与正常组织标本 X:AA 比值

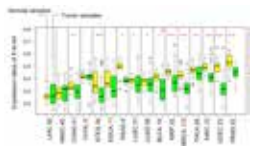

图 3. MIR100HG 与 CDKN1B 形成三螺旋结构调控 TNBC 进程

2. 染色体水平基因剂量重平衡有利于肿瘤进程

研究组利用 TCGA 数据库系统分析了 16 种实体瘤的转录组数据，我们发现多种类型肿瘤在染色体水平存在保守的变化规律，即 X 染色体在绝大多数肿瘤类型中都被下调，通过基因功能富集分析和细胞系实验发现该过程有利于肿瘤进程，而当扰乱该过程能够显著抑制肿瘤发展。该研究为揭示肿瘤的发生发展和开发新的肿瘤治疗药物提供了新的视角。 【Zhang H et al. 2018 *Mol Genet Genomics*. IF=2.716】

3.MIR100HG 与 p27 形成 RNA-DNA triplex 结构调控细胞增殖

三阴性乳腺癌由于其高转移，低生存率等特点受到高度关注。据报道，长链非编码 RNA 在肿瘤发生发展过程中起着重要的作用。研究组发现敲降 MIR100HG 抑制细胞增殖，细胞周期停滞在 G1 期；过表达 MIR100HG 明显促进细胞增殖。进一步的研究发现 MIR100HG 通过与 p27 形成 RNA-DNA triplex 结构调控细胞周期进而影响三阴性乳腺癌的进程。该研究可能为三阴性乳腺癌的治疗提供新的靶点。【Wang S et al. 2018 *Cell Death Dis*. IF=6.187】

4. IHT 抑制乳腺癌干细胞样特征及 STAT3 信号途径

乳腺癌干细胞（Breast cancer stem cells，BCSCs) 会影响乳腺癌的肿瘤发病进程、肿瘤的复发以及治疗过程中的药物抗性。而三阴性乳腺癌是乳腺癌治疗中面对的具有挑战性的一种亚型。确定对乳腺肿瘤干细胞对三阴性乳腺癌的临床治疗有举足轻重的意义。研究组探究了 iso-harringtonine(IHT) 对三阴性乳腺癌干细胞的抑制作用。【Chen W et al. 2018 *Biomed Pharmacother*. IF=3.224】

Epigenetic and Developmental Regulation

Dr. Baowei Jiao, Principal Investigator, doctoral supervisor. The research team is mainly interested in regulation of mammary gland stem cells, mechanism and evolutionary significance of X chromosome inactivation, imprinted genes and long non-coding RNA in development and evolution. The unique splicing pattern of tri-negative breast cancer (TNBC) was found for the first time in breast cancer research, and the molecular mechanism of its main regulatory factor TDP43 was elucidated in detail. Meanwhile, lncRNA MIR100HG which specifically expressed in TNBC was identified to regulate tumor progression by forming LncRNA-DNA triple helix structure.Currently, over 20 papers have been published in international journals,such as *Cell*、*PNAS*、*Cell Death & Disease*.
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1. Loss of TDP43 inhibits progression of triple-negative breast cancer in coordination with SRSF3

Aberrant alternative splicing has been highlighted as a potential hallmark of cancer. Here, we identify TDP43 as an important splicing regulator responsible for the unique splicing profile in TNBC. Mechanistically, TDP43 regulates extensive alternative splicing events, including downstream gene PAR3, by forming a complex with SRSF3 to regulate alternative splicing events coordinately.

2. Chromosome-wide gene dosage rebalance may benefit tumor progression

We assess the relative expression ratios of X chromosome and autosomes (expression ratios of X:AA) between tumor samples and adjacent normal samples across 16 tumor types using expression datasets from The Cancer Genome Atlas (TCGA) project. Our results demonstrate that the prevalent chromosome-wide gene dosage rebalance (CDR) across tumor types serve as an important mechanism in promoting tumor progression, which partially explains the high risk of tumor in patients with Turner syndrome (TS) and also provides a new cancer therapy from the CDR perspective.

3. LncRNA MIR100HG promotes cell proliferation in triple-negative breast cancer through triplex formation with p27 loci

We identified MIR100HG as pro-oncogene on TNBC progression.Knockdown of MIR100HG decreased cell proliferation and induced cell arrest in G1 phase. Moreover, overexpression of MIR100HG significantly increased cell proliferation. Further results suggested MIR100HG participated in the formation of RNA–DNA triplex structures to control the cell cycle and subsequently impacted the progression of TNBC, which may be a potential therapeutic target in such cancers.

4. Isoharringtonine inhibits breast cancer stem-like properties and STAT3 Signaling

Breast cancer stem cells (BCSCs) contribute to breast cancer progression,relapse and treatment resistance. Triple negative breast cancer (TNBC) is a kind of challenging subtype of breast cancer. Identification of inhibitory natural compents of BCSCs is therefore critical for the clinical treatment development. Here, we investigated whether Iso-harringtonine (IHT) had inhibitory effects on BCSCs in TNBC cell lines.

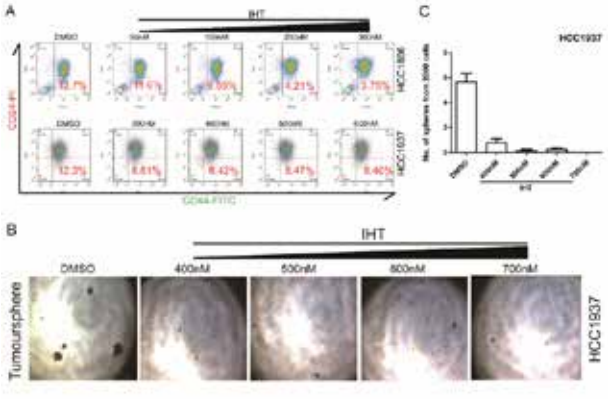

Fig.4 IHT impairs the proportion of the BCSC population.

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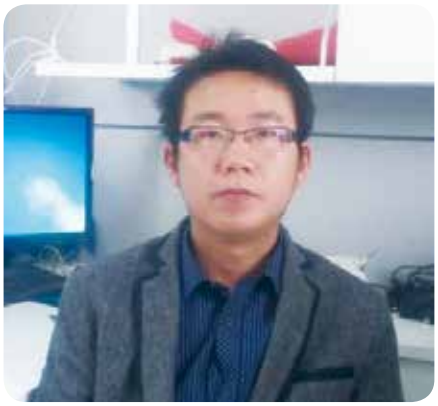

进化与发育转录组学

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。以第一作者或共同通讯作者在 *Nat Genet*, *Nat Ecol Evol*, *Cell Res*, *Mol Biol Evol*, *PloS Genet*, *J Mol Cell Biol*, *Hum Mol Genet* 等杂志发表论文30余篇。

重要成果及产出：

1. **Dong-Dong Wu** *,Xiang-Dong Ding, **Sheng Wang,** Jan M. Wójcik,Yi Zhang, Małgorzata Tokarska,Yan Li, **Ming-Shan Wang**,Omar Faruque, Rasmus Nielsen *,Qin Zhang * and Ya-Ping Zhang*.Pervasive introgression facilitated domestication and adaptation in the Bos species complex. ***Nature Ecology & Evolution***. 2018,2(7):1139-1145
2. Hai-Bo Xu#, Yong-Xin Li# ,Yan Li , Newton O Otecko , Ya-Ping Zhang, Bingyu Mao*, **Dong-Dong Wu*.**Origin of new genes after zygotic genome activation in vertebrate. ***Journal of Molecular Cell Biology***. 2018, 10(2), 139-146.
3. **Zeng L**,Ming C, Li Y, Su LY,Su YH, N O. Otecko, Liu HQ,Wang MS, Yao YG,-Li HP, **Wu DD**,*and Zhang YP*.Rapid Evolution of Genes Involved in Learning and Energy Metabolism for Domestication of the Laboratory Rat. ***Molecular Biology and Evolution.*** 2018, 35(1):149-158.
4. **Guo X**, Li YQ, Wang MS, Wang ZB, Zhang Q, Shao Y, Jiang RS, Wang S, Ma CD, Murphy RW, Wang GQ, Dong J, Zhang L, **Wu DD***, Du BW*, Peng MS*, Zhang YP*. A parallel mechanism underlying frizzle in domestic chickens . ***Journal of Molecular Cell Biology***. 2018 doi: 10.1093/jmcb/mjy037.
5. **Wu DD**, Irwin DM. Evolution of Trichocyte Keratin Associated Proteins. ***Adv Exp Med Biol***. 2018, 1054:47-56.

1. 基因交流在牛属动物的驯化及环境适应中的作用

对多种牛属动物进行了全基因组高覆盖测序以及群体基因组测序，分析确定了牛属之间的系统发育关系，得出大额牛是一个独立的物种或亚种的结论。分析发现牛属之间存在广泛的基因交流，并挖掘出瘤牛与巴厘牛（爪哇野牛驯化种），瘤牛与大额牛发生基因交流的区域，发现许多神经系统基因、免疫系统基因从瘤牛扩散至巴厘牛以及大额牛中。推测基因交流在促进动物被成功驯化的过程中起到重要的作用发现分布在青藏高原上的牦牛与藏黄牛之间存在显著的基因交流。在家牛中受到选择作用的与毛色相关的MITF基因通过基因交流被导入到了牦牛基因组中，部分藏黄牛基因组中的低氧诱导通路基因EGLN1、EGLN2、HIF3a从牦牛中获得，这也提示，藏黄牛通过“拿来主义”从牦牛中快速获得适应高原低氧环境的遗传变异。

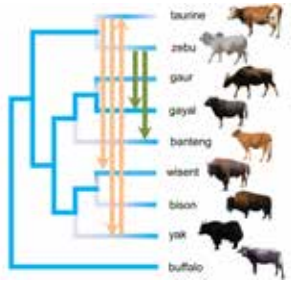

图1. 牛属动物之间的系统发育关系

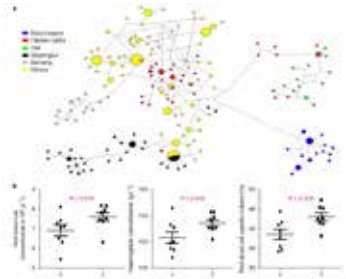

图2. EGLN1基因从牦牛向西藏牛的遗传渗入

2. 脊椎动物合子基因组活化后新基因的起源

新基因是进化革新和表型进化的驱动力。在早期发展中，新基因的表达增加了新的基因可能产生并有参与到胚胎发育中的可能性，但这可能只是一个假说。在此基础上，基于在不同发育时间阶段中的基因表达，我们发现，在中期胚芽过渡（MBT）之后，年轻的蛋白编码基因显著地表达，并在MBT之后的后续阶段显示出了一个不断下降的趋势。为了补充这一发现，我们找到了一种名为“Fog2”的年轻孤立基因，数据表明，新的基因可以在MBT之后产生，并参与胚胎发育，从而为更好地理解新基因的起源、进化和功能提供依据。

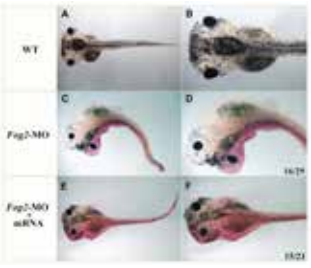

图3. 在发育后期，注射Fog2–MO基因会导致胚胎畸变

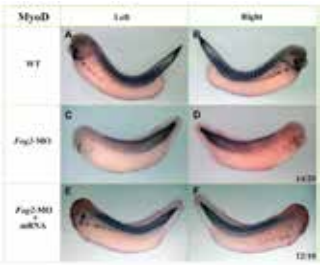

图4. Fog2会引起肌分化因子下调

Evolutionary and Developmental Transcriptomics

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 30 research papers in *Nat Genet, Cell Res, Mol Biol Evol, PloS Genet, J Mol Cell Biol, Hum Mol Genet,* etc, as first author or co-corresponding author.
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1. Pervasive introgression facilitated domestication and adaptation in the Bos species complex

Species of the Bos genus, including taurine cattle, zebu, gayal, gaur, banteng, yak, wisent and bison, have been domesticated at least four times and have been an important source of meat, milk and power for many human cultures. We sequence the genomes of gayal, gaur, banteng, wisent and bison, and provide population genomic sequencing of an additional 98 individuals. We use these data to determine the phylogeny and evolutionary history of these species and show that the threatened gayal is an inde-pendent species or subspecies. We show that there has been pronounced introgression among different members of this genus,and that it in many cases has involved genes of considerable adaptive importance. For example, genes under domestication selection in cattle (for example, MITF) were introgressed from domestic cattle to yak. Also, genes in the response-to-hypoxia pathway (for example, EGLN1, EGLN2 and HIF3a) have been introgressed from yak to Tibetan cattle, probably facilitating their adaptation to high altitude. We also validate that there is an association between the introgressed EGLN1 allele and haemoglo-bin and red blood cell concentration. Our results illustrate the importance of introgression as a source of adaptive variation and during domestication, and suggest that the Bos genus evolves as a complex of genetically interconnected species with shared evolutionary trajectories.

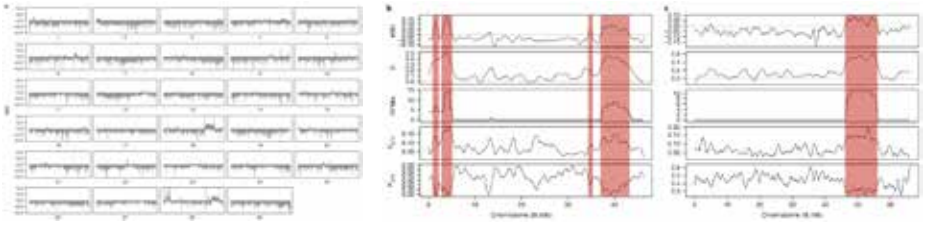

Fig 5. Distribution of regions in the genome where introgression occurred between Tibetan cattle and yak

2. Origin of new genes after zygotic genome activation in vertebrate

New genes are drivers of evolutionary innovation and phenotypic evolution. Expression of new genes in early development raises the possibility that new genes could originate and be recruited for functions in embryonic development, but this remains undocu-mented. Here, based on temporal gene expression at different developmental stages in , we found that young protein-coding genes were significantly enriched for expression in developmental stages occurring after the midblastula trans-ition (MBT), and displayed a decreasing trend in abundance in the subsequent stages after MBT. To complement the finding, we demonstrate essential functional attributes of a young orphan gene, named as Fog.2, in morphological development. Our data indicate that new genes could originate after MBT and be recruited for functions in embryonic development, and thus provide insights for better understanding of the origin, evolution, and function of new genes.

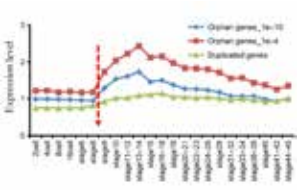

Fig 6. Expression level of young protein–coding genes at different developmental stages in X. tropicalis.

Fig 7. Expression patterns of Fog1 and Fog2 in X. laevis embryos.

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神经突触机制与功能

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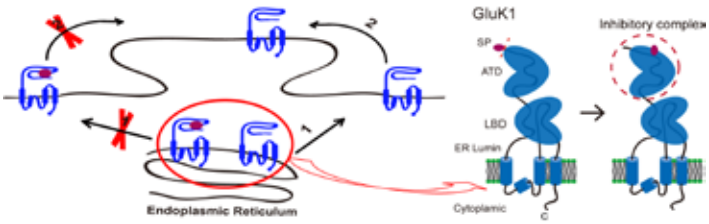
重要成果及产出：

1. Duan GF, Ye Y, Xu S, Tao W, Zhao S, Jin T, Nicoll RA, Shi YS*, **Sheng N***. (2018) Signal peptide represses GluK1 surface and synaptic trafficking through binding to amino-terminal domain. ***Nature Communications*** doi: 10.1038/s41467-018-07403-7.
2. **Sheng N***, Bemben MA, Díaz-Alonso J, Tao W, Shi YS, Nicoll RA*. (2018) LTP requires postsynaptic PDZ-domain interactions with glutamate receptor/auxiliary protein complexes. ***Proc. Natl. Acad. Sci. U. S. A.*** 115: 3948-3953.
3. Tao W, Díaz-Alonso J, **Sheng N**, Roger A. Nicoll. (2018) Postsynaptic δ1 glutamate receptor assembles and maintains hippocampal synapses via Cbln2 and neurexin. ***Proc. Natl. Acad. Sci. U. S. A.*** 115: E5373-E5381.

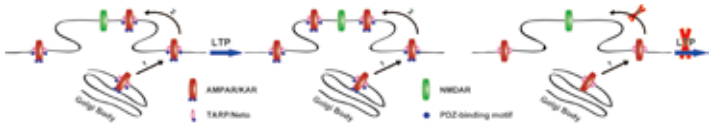
1. 谷氨酸受体信号肽在神经突触信息传递中的新功能

在大脑内，谷氨酸是主要的兴奋性神经递质传递，而其所作用的谷氨酸受体在神经元突触部位的表达水平，则是大脑实现正常功能的生理基础。我们以小鼠和大鼠脑片为研究系统，结合神经电生理、神经药理学、分子细胞生物学等研究手段，系统性研究了其家族成员红藻氨酸受体的突触转运和生理活性的调控机制。我们前期工作发现其成员 GluK1 和 GluK2 的突触转运依赖于不同的分子机理：GluK1 依赖于其辅基 Neto 蛋白（ Sheng N et al. 2015 Elife）；而 GluK2 自身具有突触转运能力且不受 Neto 蛋白调控，它们转运能力的差异性是由 GluK1 和 GluK2 的胞外氨基端功能区域所决定的（Sheng N et al. 2017 PNAS）。在此基础之上，我们进一步深入研究其中具体的调控元件和作用机制。发现在成熟的 GluK1 和 GluK2 受体中，其信号肽均被有效切割，但 GluK1 的信号肽释放后可以和其氨基端结构域（ATD）发生直接相互作用，形成抑制性复合物以协同调控 GluK1 的细胞膜转运和突触定位。若破坏此抑制性复合物，如将 GluK1 的信号肽或 ATD 分别替换为 GluK2 的对应序列，则可解除 GluK1 信号肽的转运抑制作用。该研究揭示了谷氨酸受体信号肽的一种非经典功能和作用机制，发现信号肽能够作为非常规配体，通过反式抑制作用调控谷氨酸受体的细胞转运和突触传递活性。相关工作发表于 Duan GF *et al.* 2018 *Nature Communications*。



2. LTP 神经突触后分子机制

大脑最重要的特征之一就是能够存储大量的信息，即学习和记忆能力，其物质基础是神经突触联系强度的变化，即突触可塑性。长时程增强（LTP）是突触可塑性重要的表现形式之一，是目前研究学习记忆最重要的分子细胞模型。目前关于 LTP 研究主要集中于突触外兴奋性 AMPA 受体的转运机制，而突触后分子调控机制不甚清楚。为解决这一科学问题，我们以 AMPA 受体基因条件性敲除小鼠为研究系统，利用单细胞基因操作技术将海马锥体神经元中的 AMPA 受体替换为 GluA1- γ -8 融合性受体或相关突变体。通过神经电生理分析发现，谷氨酸受体和其辅基 γ -8 所形成的复合物，与突触后支架蛋白中 PDZ 结构域之间的相互作用是 LTP 所必须的。该研究表明，无论是由何种谷氨酸受体所介导，LTP 表达的突触后机制很保守且由共同的机制所调控；在 LTP 过程中，突触后 PDZ 支架蛋白是主要功能靶点，而谷氨酸受体的突触转运则可能为被动协同过程。相关工作发表于 Sheng N *et al.* 2018 *PNAS*。



3. 大脑进化发育与神经精神疾病

与目前广泛采用的研究模型如啮齿类动物相比，人类大脑中的细胞类型、神经元结构和相关间连接等都更为复杂，且进化出与高级认知功能相关的关键脑区及神经环路。为此，我们拟以小鼠、树鼩和猕猴为模型，通过进化基因表型系统生物学分析，结合发育生物学、神经电生理、显微成像、光遗传学等技术手段，研究特定关键脑区的神经元突触连接的发育进化的遗传机制，以及相关神经环路进化与高级认知功能、神经精神疾病的内在联系关系和分子机制。

Synaptic Function and Mechanism

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, shrew and rhesus monkey as model systems: (1) The regulatory mechanisms underlying synaptic physiological conditions; (2) The genetic bases underlying evolution and development of primate synapse; (3) The internal relationship between the evolution of human neural circuit and neuropsychiatric disorders.
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1. A novel function of glutamate receptor signal peptide for synaptic transmission

Glutamate is the major excitatory neurotransmitter in the brain, and the postsynaptic expression level of glutamate receptors is a critical basis for the physiological functions of our brain circuit. Using mice and rat brain slices as model systems and combining the techniques including electrophysiology, neuropharmacology, molecular and cellular biology, we systematically studied the regulatory mechanisms for KARs, a subfamily of glutamate receptors, synaptic trafficking and physiological properties modulation. Our previous studies have found that synaptic targeting of the two subunits GluK1 and GluK2 is relied on distinct molecular machinery. Synaptic expression of GluK1 receptor is depended on its auxiliary subunits Neto proteins (***Sheng N et al. 2015 Elife***). In contrast, GluK2 itself harbors synaptic trafficking ability, which is independent on Neto proteins, and it is the excellular amino-terminal regions of GluK1 and GluK2 determining their distinct trafficking performance (***Sheng N et al. 2017 PNAS***). On the basis of these work, we continued to study the underlying regulatory element(s) and functional mechanism(s). We found that in the matured GluK1 and GluK2 receptors, both signal peptides are efficiently cleaved. However, the released GluK1 signal peptide could interact with the receptor's amino-terminal domain (ATD) directly, and then forming an inhibitory complex to synergistically regulate GluK1 surface trafficking and synaptic targeting. The repressive function of GluK1 signal peptide will be reversed by disrupting the inhibitory complex, through replacing the GluK1 signal peptide or ATD with the corresponding sequences of GluK2 respectively. Taken together, this study has uncovered a non-canonical function of glutamate receptor's signal peptide. A working model is proposed that in a *trans* manner and behaving as ligand of GluK1, the cleaved signal peptide binds to the ATD of glutamate receptor and forms an inhibitory complex to regulate its forward trafficking and then the synaptic activity. The results of this study has been published as ***Duan GF et al. 2018 Nature Communications***.

2. The postsynaptic mechanism for LTP

One of the most important traits of brain is the storage of massive information, the ability and process of learning and memory. And the underlying material basis is the change of the transmission strength of synapses, named synaptic plasticity. Long-term potentiation (LTP) is a critical form of synaptic plasticity and is also regarded as an important cellular and molecular model to study learning and memory. Currently, most of the studies on LTP are focused on the trafficking mechanisms of extrasynaptic excitatory AMPARs, while the postsynaptic molecular basis is still unclear. To study this question, we applied conditional knock-out mice of AMPA receptors as the model system and used the technique of single-cell genetic manipulation to replace the endogenous AMPA receptors of hippocampal pyramidal neuron with the tethered GluA1-γ-8 receptor or related mutants. With the analysis of electrophysiological recording, we found that the PDZ-binding motif-mediated interaction, between AMPAR receptor/auxiliary subunit complex and postsynaptic scaffolding proteins, is necessary for the synaptic basal transmission and LTP expression of this receptor complex. This study suggested that the postysynaptic mechanism underlying LTP is conserved and regulated by a general mechanism, regardless of the subtype of glutamate receptors. And a working model is proposed that the PDZ domain-contained scaffolding proteins are the targets for modification during LTP, whereas the glutamate receptor/auxiliary subunit complexes play passive roles. The results of this study has been published as ***Sheng N* et al. 2018 PNAS***.

3. The brain evolution and neuropsychiatric disorders

Compared to the widely-used animal models such as rodent, the human brain is more complex of cellular types, neuronal morphology and inter-connections, and has been evolved critical brain regions and neural circuitry for higher cognitive functions. We are trying to use mice, shrew and rhesus monkey as model systems and combine techniques, including evolutionary genotype-phenotype system biology (eGPS), developmental biology, electrophysiology, high-resolution microimaging, optogenetics, to uncover the secrets of brain evolution and function. Our long-term goals are to study the genetic bases for the evolution and development of the neural cells in specific and critical brain regions, and reveal the internal relationship and mechanism between the evolution of neural circuits and higher cognitive function, as well as related neuropsychiatric disorders.

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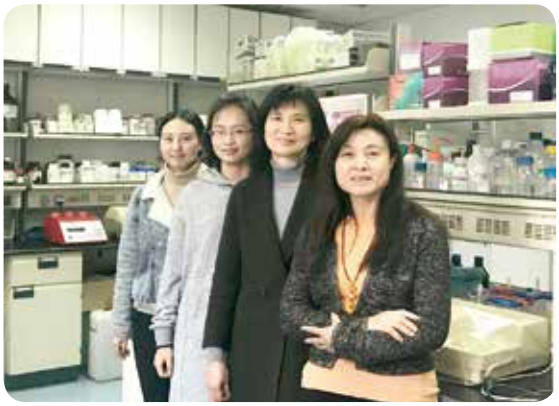


昆明野生动物细胞库

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 343 种动物的细胞系 2186 株 10000 余份。大多数为哺乳动物的细胞系，其中包括 60 种国家级重点保护动物的细胞系。目前，昆明细胞库是国家实验细胞资源共享服务平台、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：

1. **Nie W**, **Wang J**, **Su W**, **Hu Y**, He S, Jiang X, He K. 2018. Species identification of crested gibbons (Nomascus) in captivity in China using karyotyping- and PCR-based approaches. Zoological Research, 39 (5): 356-363.
2. Ai H, He K, Chen Z, Li J, Wan T, Li Q, **Nie W**, **Wang J**, **Su W**, Jiang X. 2018. Taxonomic revision of the genus Mesechinus (Mammalia: Erinaceidae) with description of a new species. Zoological Research , 39 (5): 335-347.

1. 细胞资源的收集和保藏

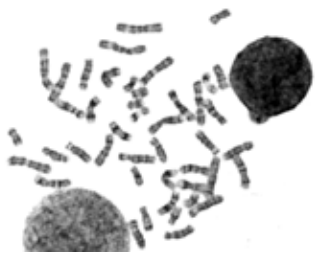
2018 年度，昆明细胞库利用从野外采集以及从其他途径获得的动物材料，共新建各类动物细胞系 78 株，其中包括怒江金丝猴、鬣猬、林猬、复齿鼯鼠等 8 种野生动物的细胞系 33 株，建立家猪、狗、绵羊、和大足黑山羊等家养动物的正常细胞系 16 株，EBV 转化的人淋巴细胞系 11 株以及人和实验动物的正常细胞系和肿瘤细胞系 18 株。复苏和扩增各类动物细胞系 692 株次。

2. 对外服务

在 2018 年度，昆明细胞库为全国各地的 501 家单位，其中高等院校 240 家，科研院所 123 家，企业 138 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及肿瘤细胞系共计 692 株次。除提供细胞服务外，我们还提供了核型分析和 STR 检测等技术服务 71 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. 怒江金丝猴不同组织来源细胞系的建立

怒江金丝猴是 2010 年新发现的灵长类新物种，是世界的第五种金丝猴。利用保护区提供的病死怒江金丝猴个体的组织材料，我们成功建立并冻存了包括怒江金丝猴的心、肺、肾、肝、脾、肌肉、骨髓和血液等不同组织来源的体细胞系 10 株，为后续开展相关研究储备了细胞材料。



4. 独龙牛的核型分析

通过外周血培养、染色体制备和 G 带显示等方法， 我们为云南省草地动物科学研究院开展独龙牛的核型分析工作。我们一共完成了 35 头独龙牛个体的核型分析工作，确定了这些独龙牛个体的染色体数目、G 带核型，发现其中有独龙牛和黄牛的杂种以及黄牛的个体存在，为云南省草地动物科学研究院开展独龙牛的人工繁殖，提供清晰的遗传信息。

Kunming Wild Animal Cell Bank

In order to conserve genetic resource and genetic diversity of animals, Kunming wild animal cell bank was established in Kunming Institute of Zoology, Chinese Academy of Science in 1986. Up to now 2186 cell lines from 343 species have been preserved in our cell bank. Most cell lines are derived from mammals. Among the species, 60 are national protected wildlife in China. Now it is one branch of National Platform of Experimental Cell Resources for Sci-Tech, Biological Genetic Resource Bank of CAS, China Germplasm Bank of Wild Species, and State Key Laboratory of Genetic Resources and Evolution.

1. The collection and preservation of cell lines

In 2018, 78 cell lines from various wild and domestic animals had been established and frozen. Among these cell lines, 33 cell lines were derived from 8 species of wild animals such as Stryker's Snub-nosed Monkey, Shrew-hedgehog, Shanxi hedgehog, Complex-toothed flying squirrel etc; 16 cell lines were established from domestic animals such as domestic pigs, dogs, sheeps and goats; 11 cell lines were obtained by EBV-transferred human lymphocytes; and 18 cell lines were normal cell lines and tumor cell lines from human and experimental animals. Six hundred and ninety-two of frozen-stored cell lines were also resuscitated and subcultured.

2. Cell lines service and technical service

In this year, 692 cell lines, 71 times of karyotype analysis and 35 STR test had been provided for the researchers not only at State key laboratory of genetic resources and evolution, but also at other 72 scientific research institutions, 98 enterprises, and 228 Chinese universities. In addition, we also had provided a lot of cell culture technical advisory services by using the telephone and the email.

3. The establishment of cell lines from Stryker's Snub-nosed Monkey

Stryker's Snub-nosed Monkey, a new primate species discovered in 2010, is the world's fifth species of golden monkeys. Using the tissue materials from a golden monkey individual that died of diseases, 10 somatic cell lines from different tissue materials (the heart, lung, kidney, liver, spleen, muscle, bone, skin, marrow and blood) were established and frozen successfully. The preservation of these cell lines will provide cell materials for the follow-up research.

4.The karyotype analyse of gayals

By means of peripheral blood culture, chromosome preparation and G-banding, we carried out karyotype analysis of gayals for Yunnan Academy of Grassland Animal Science. The chromosomes of thirty-five gayal individuals have been analyzed. Among these individuals, some hybrids between gayals and cattles have been found. This work provides clear genetic information for Yunnan Academy of Grassland Animal Science to carry out artificial reproduction of gayals.

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生命条形码南方中心

生命条形码南方中心，成立于 2011 年 1 月，专门从事 DNA 条形码相关的科学研究、技术革新和应用推广。根据国重室的相关规定，目前生命条形码南方中心的工作任务主要为：与国家重点实验室课题组合作，服务国重室的各项科研任务；开展 DNA 条形码分子实验和数据提交汇总；进行分子鉴定；以及国重室领导交办的其他工作。

South China DNA Barcoding Center

2018 年度，生命条形码南方中心继续发挥支撑作用，积极服务国重室及研究所各研究组，与两栖爬行类多样性与进化组、分子进化与基因组多样性学科组、吴东东组等合作，为其库存样品进行 DNA 条形码测序，数目超过 10000 条。并在云南，广西，贵州等地举行组织 3 次采集蜻蜓样品，以及 2 次蜘蛛样品的采集活动，一共获得 3200 多份无脊椎动物标本，制成蜻蜓标本 500 余份，所获得标本均入到动物遗传资源库。

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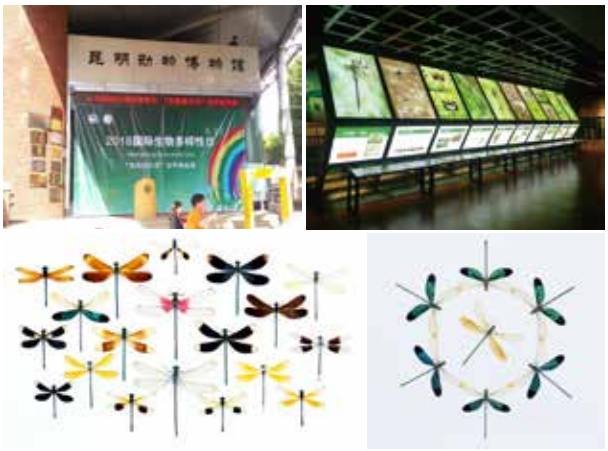
重要成果及产出：

1. **Zhang, HM1**, Hämäläinen, M., & **Wang, WZ*.** Indocypha cyanicauda sp. nov. from southern Yunnan, China (Odonata: Chlorocyphidae). International Journal of Odonatology,2018, 21(1), 71–80.
2. SUWANNAPOOM, C.,Wu YJ, **Chen X**, C. ADEOLA, A., Che J*, & **Wang WZ*.** (2018). Complete mitochondrial genome of the Thai Red Junglefowl (Gallus gallus) and phylogenetic analysis. ZOOLOGICAL RESEARCH, 2018, 39(2), 127–1298
3. Li JT, Gao YD, Xie L, Deng C, Shir P, Guan ML, Huang S, Ren JL, Wu DD, Ding L, Huang ZY, Nie H, Humphreys DP, Hillish DM, **Wang WZ*& Zhang YP*,** Comparative genomic investigation of high-elevation adaptation in ectothermic snakes. PNAS. 2018, pnas.1805348115.
4. Hybridization, C, Dna, L, **Chen, X**, Ni, G, He, K, Ding, Z, Zhang, Y. (2018). Capture Hybridization of Long-Range DNA Fragments for High-Throughput Sequencin. [Methods in Molecular Biology] Computational Systems Biology Volume 1754.
5. Iyiola OA, Nneji LM, Mustapha MK, Nzeh CG, Oladipo SO, Nneji IC, Okeyoyin AO, Nwani CD, Ugwumba OA, Ugwumba AA, Faturoti EO, **Wang WZ, Chen J**, **Wang YY**, Adeola AC. DNA barcoding of economically important freshwater fish species from north-central Nigeria uncovers cryptic diversity. Ecology and Evolution. 2018, 1–20.
6. 张浩淼． 中国蜻蜓大图鉴 Dragonflies and Damselflies of China. 重庆：重庆大学出版社，2018. ISBN 978-7-5689-8.
7. 张浩淼． 新昆虫记—神秘航线． 武汉：湖北科技出版社，2018.（2018 年 12 月印刷）.

1. “色彩的天空”世界蜻蜓展

2018 年 5 月 22 日，国际生物多样日，世界蜻蜓展“色彩的天空”将亮相中科院昆明动物研究所昆明动物博物馆。展览的标本、精美彩照和文字介绍，由“蜻蜓王子”张浩淼博士采集、拍摄并精心设计，和动物博物馆专业的策展团队合作，经过一年多的筹备，即将惊艳登场。此次标本的展出形式，打破原传统的标本展示盒子，简洁、现代的线条，衬托蜻蜓的精美。与原来六边形展区进行结合，不仅图文并茂，而且名副其实的一个“美”字。与 12 年前在大连市举办的“蜻舞菲扬”张浩淼个人蜻蜓作品展相比，此次展览为艺术与专业的更完美结合。展览由中科院昆明动物研究所昆明动物博物馆、生命条形码南方中心、遗传资源与进化国家重点实验室联合推出，自 2018 年 5 月 22 日始将长期展出于昆明动物博物馆二楼昆虫厅（出品／李维薇　策展／吴丽彬 张浩淼　标本捐赠、图片提供、科学指导／张浩淼　标本制作／张浩淼 陈泉燕）。



2. 2018 年第 55 届热带生物学对话会议

应热带生物学保护协会 Ahimsa Campos-Arceiz 博士邀请，生命条形码南方中心王运宇、张浩淼博士参加 2018 年 6 月 30 日至 7 月 6 日在马来西亚砂拉越州古晋举办的 2018 年第 55 届热带生物学对话会议。热带生物学对话协会于 1963 年成立，致力于关于热带生物学相关的研究、教育和交流。年会亮点包括邀请座谈会、系列报告、海报招贴和公共政策会议等。ATBC 成员和来自世界各地的顶尖科学家将在年会上呈现他们最新的研究成果。本届有许多相关领域的著名专家被邀请参加，报告当前的最新研究进展，就热点问题进行集体讨论，探讨今后各方开展国际合作的可能性。世界各国学者共享了最新研究信息，相互交流，促进热带亚热带生物多样性保护，检测的发展。通过参加此类重大国际会议，获得了最新的研究进展，在资源和技术上优势互补，提高本实验室的科研能力，对外宣传研究所的科研平台和科研能力，提升研究所在本领域的国际影响力，增加争取国际项目资助的资历，增进我所与世界各国的技术交流，进而推进云南省乃至全国生物多样性的保护监测水平。此外提升了昆明动物研究所在本领域内的国际影响力，增加了争取国际项目资助的资历，增进了我所与世界各国的技术交流。

South China DNA Barcoding Center

Established in 2011, the Center is the first and only facility focus on DNA barcoding in China. The initialization of SCDBC commercial using DNA barcoding technology and high-throughput barcoding laboratory construction and operation. In the year of 2018, the SCDBC collected more than 3K specimens in wild field, got almost 10K standard DNA barcodes. This year we using DNA Barcoding data to understand the diversity of dragonflies in China, get know Urban butterfly species diversity. And make great progress.

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1. Dragonflies and Damselflies of China

China is home to over 900 species of dragonflies and damselflies, more than any other nation on earth. This splendid, lavishly produced book for the first time provides us with a very thorough identification guide to these gorgeous insects. Multiple high quality photographs of living specimens illustrate almost 90% of known species. Where necessary, these live portraits are augmented by close-up photographs of microscopic diagnostic structures, all clearly and logically presented. With this book the reader can identify most Chinese dragonflies normally encountered. Identification is a vital first step to appreciation, but this book is far more than a mere field guide or photo gallery. It is also a handbook to the biology of Chinese dragonflies. The fascinating life stories of dragonflies, with their many variations, are clearly explained and richly illustrated. Topics covered include detailed information on adult and larval morphology, ecology and behaviour. A well researched and fascinating account of the long history of the study of Chinese dragonflies rounds out the general text. This book will be the standard work on Chinese Odonata for many years to come and will certainly earn its place as a classic among books on the Order.Author: Haomiao Zhang,South China DNA Barcoding Center, Kunming Institute of Zoology, Chinese Academy of Sciences.Publishing House: Publishing House of Chongqing University. Language: Chinese & English. Pages: 1488.The book contains two main parts: “Introduction” and “Dragonflies and Damselflies of China”. The content covers the morphology, biology and taxonomy of dragonflies. A total of 820 species or subspecies, representing three suborders, 23 families and 175 genera are described and illustrated, 83.42 % of the known species-group taxa from China. Of these the Zygoptera includes 293 species in 65 genera and 13 families, Anisozygoptera includes three species (in general introduction), and the Anisoptera includes 524 species in 106 genera and 8 families. More than 3500 color photos are selected to show the charming and gorgeous morphology of dragonflies from the best view, being the largest collection of dragonfly species and the most complete Chinese dragonfly book among the world's dragonfly books. A latest “checklist of Odonata from China” is also attached.

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Yun-yu Wang, Engineer

张浩淼　博士　助理研究员

Hao-miao Zhang, Assistant researcher

中心实验室

中心实验室是隶属于遗传资源与进化国家重点实验室的公共技术服务平台，于 2008 年 11 月正式投入使用。目前，实验室共有基因组学分析平台、蛋白质组学分析平台、高性能计算平台三大技术平台，同时还涵盖一些中小型仪器设备。每个平台都配有专业技术人员，从实验设计，仪器操作，到数据分析，为仪器设备使用者提供全方位的技术支持与服务。

实验室主页：http://www.kiz.cas.cn/gre/gre6/gre61/

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三大技术平台

一、基因组学分析平台

1. Ion Torrent 测序系统

Ion Torrent 测序系统（Ion Proton 与 Ion PGM）主要用于基因组测序、转录组测序、外显子组测序、基因测序、ChIP 测序，线粒体基因组测序、甲基化分析等等。

2. Miseq 测序仪

Miseq 测序仪是 Illumina 公司推出的测序通量最低的仪器，该仪器的主要特点是测序精度高，读长长（测序片段长度最长可达 2 X 300bp），通量灵活，适合靶向和小型基因组测序。

3. 单细胞自动制备

C1™ 单细胞全自动制备系统是基于 Fluidigm 创新的微流体技术，能够让研究者们快速可靠地分离单个细胞并进行基因组分析。前所未有地将分离细胞、提取、逆转录和预放大全过程实现全面自动化，使细胞活性的检测和分析成为可能。

4. 高通量单细胞基因分型系统

BioMark HD 高通量单细胞基因分型系统整合了先进的微流控芯片和 qPCR 技术，通过独立的纳米级微型阀门控制溶液在阵列反应仓（Reaction Chamber）中的流动来实现生物样品的分液、qPCR 体系混合建立、qPCR 扩增。集成流体通路技术极大地简化了生物样品和试剂的分液操作，提高生物分析通量和灵敏度，其纳升级的反应体系为高通量的基因分析应用节省大量成本（试剂用量更少，样品量更少）和劳动力。综合而言，Fluidigm 的微流控 qPCR 芯片融合了芯片的高通量和 qPCR 的准确性。

5. QuantStudio 12K Flex 实时定量 PCR 仪

QuantStudio 12K Flex 实时定量 PCR 仪是新一代荧光定量 PCR 仪。在实现常规定量 PCR 仪功能的基础上，又可以满足 8 连管、96 孔板、384 孔板以及 OpenArray 芯片等不同通量的实验需求。

6. 高端定制型流式细胞仪

BD LSRFortessa™ 流式细胞分析仪兼顾了分析性能和可拓展性，可提供强大的扩展空间以满足不断发展的多色流式细胞仪实验的需求。

二、蛋白质组学分析平台

双向电泳技术是蛋白质组学研究的基础技术平台，是一种分析细胞、组织或其他生物样本提取的蛋白质混合物的有力手段。利用该技术可对一种样本中的许多蛋白质同时进行系统化的分离、鉴定、定量。另外，该技术还可检测翻译后和翻译过程中的蛋白质修饰。

三、显微影像分析平台

透射电子显微镜是观察细胞的超微结构和蛋白等生物大分子的细胞内定位等。在基因组进化的研究中，搞清楚细胞的细胞质、细胞器以及细胞核等超微结构，在重大疾病和新药研究领域中，通过对正常细胞和病变细胞的超微结构的对比观察，在干细胞研究领域中都是必备的研究工具。制样系统可以进行电镜样品前期处理，超薄切片机可以进行半薄和超薄切片，为透射电子显微镜提供较好的切片。

Core Facility

The Core Facility of the State Key Laboratory of Genetic Resources and Evolution is established in November 2008. Currently, the center contains three major technology platforms: Genomic Analysis Platform, Proteomic Analysis Platform, and High Performance Computing Platform. Each platform is supported by professional technicians, from the experimental design, instrument operation, to data analysis.

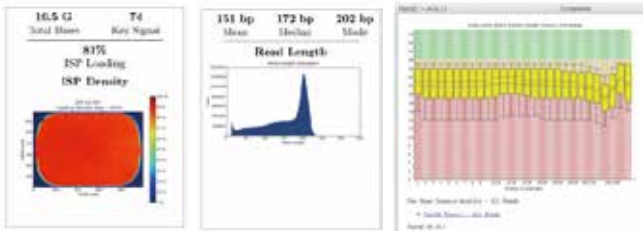
http://www.kiz.cas.cn/gre/gre6/gre61/

The Three Technical Platforms

I. Genomic Analysis Platform

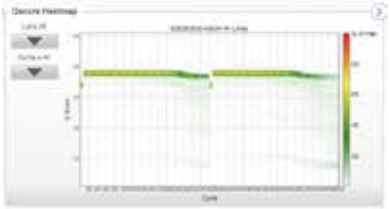
1. Ion Torrent Sequencers

The Key applications of the Ion Torrent Sequencers (Ion Proton and Ion PGM) are genome sequencing, Whole transcriptome sequencing, Exome sequencing, Gene sequencing, ChIP sequencing, Mitochondrial sequencing, Methylation analysis, and so on.



2. Miseq Sequencer

The MiSeq desktop sequencer allows you to access more focused applications such as targeted gene sequencing, metagenomics, small genome sequencing, targeted gene expression, amplicon sequencing, and HLA typing. New MiSeq reagents enable up to 15 Gb of output with 25 M sequencing reads and 2x300 bp read lengths.



3. C1 Single-Cell Preparation System

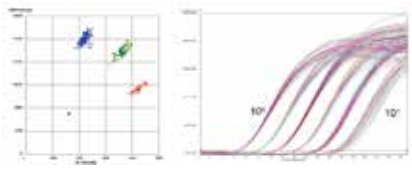
The C1 system enables cell capture, lysis, and preparation of individual cells for genomic applications. The system is an electrically and pneumatically operated desktop instrument. It has a built-in vacuum pump to hold the IFC in position. The embedded PC inside the system regulates all the functions and monitors the performance of the instrument. The system has a touchscreen display. All required user-specific instructions and functions can be controlled through the touch-enabled user interface. C1 uses a thermal stack to provide rapid, accurate, uniform heating and cooling.

4. Biomark HD Real-time PCR System

The BioMark HD System sets a new standard in high-throughput genotyping—it is the only multi-purpose real-time PCR system that performs genotyping, gene signature profiling, quantitative real-time digital PCR (qdPCR), and single-cell analysis. Its integrated fast-capable thermal cycler and four color detection provides even faster time to results and enough throughput for routine genomic testing applications.

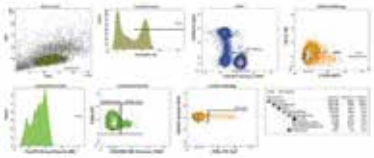
5. QuantStudio 12K Flex Real-Time PCR System

QuantStudio 12K Flex Real-Time PCR System is new level for qPCR, designed for maximum throughput, flexibility, and scalability. You can choose not only OpenArray®, 384-well, 96-well blocks for your experiments, but also digital PCR for high accuracy and sensitivity.



6.Flow Cytometers

The BD LSRFortessa brand provides power, performance and consistency for your research. Designed to be affordable and expandable, BD LSRFortessa cell analyzers have the flexibility to support the growing needs of multicolor flow cytometry assays.

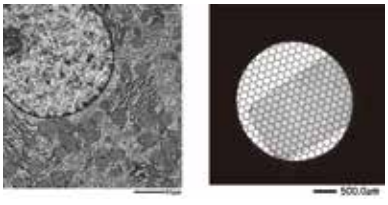


II. Proteomic Analysis Platform

2-D electrophoresis is a powerful and widely used method for the analysis of complex protein mixtures extracted from cells, tissues, or other biological samples. The analysis involves the systematic separation, identification, and quantification of many proteins simultaneously from a single sample. The technique is also unique in its ability to detect post- and co-translational modifications.

III. Micro-imaging Analysis Platform

The JEM-1400Plus is a transmission electron microscope (TEM) developed for application in a wide range of disciplines, from biology to materials researches, such as biological sections, polymers, nanomaterials and so on. With the JEM-1400Plus, images from the ultra LOWMAG mode (min. mag. ×10) to the MAG mode (max. mag. ×1.2 M) can be acquired with only one camera, resulting seamless observation with no switching of cameras or shifting one's gaze to a fluorescent screen. Using the auto montage function (provided as standard) makes it easy to acquire high-precision images of a wide field of view. 8M pixel camera (high-resolution camera) and a 1 M pixel cameras are selectable depending on user's purposes.



重要基金项目

序号	参与类型	项目 / 课题类型	项目 / 课题名称	项目 / 课题负责人	执行期	合同经费（万元）
1	主持	国家重点研发计划 ——“ 主动健康和老龄化科技应对 ” 重点专项	中国健康长寿人群多队列的系统研究	孔庆鹏	2018-2022	2820.0
2	参与	国家重点研发计划 ——“ 典型脆弱生态修复与保护研究 ” 重点专项	动物多样性起源与地理格局形成机制及其进化动力	孙　航	2017-2020	340.0
3	参与	国家重点研发计划 ——“ 干细胞与转化研究 ” 重点专项	代谢、自噬和 DNA 损伤修复协同维持多能干细胞干性和染色体稳定性的机理研究	郑　萍	2016-2021	239.5
4	参与	国家重点研发计划 ——“ 干细胞与转化研究 ” 重点专项	基于多模态分子影像的移植后细胞生物行为的在体研究	焦保卫	2016-2021	175.0
5	参与	国家重点研发计划 ——“ 海洋环境安全保障 ” 重点专项	企鹅物种进化树、进化格局以及对地质环境变迁的响应	张国捷	2018-2021	228.0
6	参与	国家重点研发计划 ——“ 生殖健康及重大出生缺陷防控研究 ” 重点专项	继发性卵巢早衰致病因素及分子机制研究	秦莹莹	2017-2020	153.0
7	参与	国家科技重大专项 —— 农业部转基因生物新品种培育重大专项	猪、牛、羊肌肉生长和脂肪沉积性状重要育种价值基因的克隆及其功能验证	高　云	2016-2020	658.9
8	参与	国家重点基础研究发展计划 (973 计划)	遗忘的生物信息学分析	黄京飞	2013-2018	202.0
9	主持	国家自然科学基金 —— 创新研究群体	基因组中新遗传结构的起源与动物的适应进化（延续）	王　文	2017-2019	525.0
10	主持	国家自然科学基金 —— 重大研究计划	多组学视角下家犬行为微进化的基因相互作用机制	吴东东	2017-2019	883.0
11	主持	国家自然科学基金 —— 重大研究计划	家犬在人工选择下的微进化研究	王国栋	2016-2018	336.0
12	主持	国家自然科学基金 —— 重大研究计划	藏族人群高原低氧适应关键基因 *EPAS1* 和 *EGLN1* 互作的分子机制及功能验证研究	宿　兵	2017-2019	289.0
13	主持	国家自然科学基金 —— 重大研究计划	凸颅鼢鼠属快速物种形成及种间基因交流的基因组机制研究	施　鹏	2017-2019	150.0
14	主持	国家自然科学基金 —— 重点项目	灵长类大脑进化分子机制的转基因猕猴研究	宿　兵	2018-2022	340.0
15	主持	国家自然科学基金 —— 优秀青年科学基金	两栖爬行类多样性与进化	车　静	2017-2019	130.0
16	主持	国家自然科学基金 —— 优秀青年科学基金	进化基因组学	吴东东	2019-2021	130.0

序号	参与类型	项目 / 课题类型	项目 / 课题名称	项目 / 课题负责人	执行期	合同经费（万元）
17	主持	国家自然科学基金 —— 国际（地区）合作与交流项目	基于线粒体基因组和 Y 染色体遗传信息追溯美洲印第安人的源流历史	孔庆鹏	2017-2021	235.0
18	主持	国家自然科学基金 —— 国际（地区）合作与交流项目	棘皮动物及脊索动物发育进程中的进化遗传程度的研究	王　文	2015-2018	199.0
19	主持	国家自然科学基金 —— 国际（地区）合作与交流项目	气候变化下山地森林树木枯死现象对生态和社会经济的影响	Douglas W Yu	2016-2019	161.0
20	主持	国家自然科学基金 —— 云南联合基金	阿尔茨海默症（AD）转基因树鼩模型的创建及有效性评价	郑　萍	2018-2021	204.0
21	主持	国家自然科学基金 —— 云南联合基金	鲤科鱼类肌间刺系统演化及其在滇池金线鲃遗传机制	杨君兴	2018-2021	200.0
22	主持	中国科学院 B 类战略性先导科技专项	动物复杂性状的进化解析与调控	施　鹏 王　文	2014-2019	22260.0
23	参与	中国科学院 A 类战略性先导科技专项（泛第三极环境变化与绿色丝绸之路建设）	人类早期活动及其对高寒环境的适应策略	孔庆鹏	2018-2022	3242.1
24	参与	中国科学院 A 类战略性先导科技专项（泛第三极环境变化与绿色丝绸之路建设）	驯化动植物对高寒环境的适应及基因资源利用	彭旻晟	2018-2022	1160.0
25	参与	中国科学院 A 类战略性先导科技专项（泛第三极环境变化与绿色丝绸之路建设）	关键区域的高通量、连续覆盖生物多样性监测与评估	Douglas Yu	2018-2023	1094.2
26	参与	中国科学院 A 类战略性先导科技专项（泛第三极环境变化与绿色丝绸之路建设）	气候环境变化对典型动物及种群的影响	车　静	2018-2023	1060.3
27	参与	中国科学院 A 类战略性先导科技专项（泛第三极环境变化与绿色丝绸之路建设）	高原人群适应高寒环境的遗传资源发掘	孔庆鹏	2018-2022	686.3
28	参与	中国科学院 A 类战略性先导科技专项	重要生物 DNA 条形码数据平台	车　静	2018-2023	92.0
29	主持	中国科学院前沿科学重点研究项目	建立哀牢山自然保护区快速生物多样性监测方法	Douglas W Yu	2017-2019	400.0
30	主持	中国科学院前沿科学重点研究项目	健康长寿人群基因组表观修饰模式及功能利用研究	孔庆鹏	2016-2020	250.0
31	主持	中国科学院重大科技基础设施维修改造项目	中国西南野生生物种质资源库动物分库信息化管理系统的升级改造	高　云	2017-2019	223.0
32	主持	中国科学院重点部署项目	西南地区动物实物标本库、快速鉴定技术集成与应用示范	王文智	2017-2018	180.0
33	主持	中国科学院中 - 非联合研究中心国际合作项目	东非动物多样性格局	蒋学龙	2016-2020	500.0

序号	参与类型	项目 / 课题类型	项目 / 课题名称	项目 / 课题负责人	执行期	合同经费（万元）
34	主持	中国科学院海外科教基地建设计划	东非重要动物类群系统发育与进化	彭旻晟	2016-2020	400.0
35	主持	中国科学院东南亚生物多样性研究中心国际合作项目	基于角蟾科生命之树研究东南亚物种多样性格局的形成	周炜帏	2017-2019	100.0
36	主持	中国科学院国际合作局对外重点项目	全球范围内超蛙科 (Natatanura) 物种遗传资源收集、物种多样性研究、同时基于大规模二代测序数据探讨其起源和时空演化	车　静	2018-2020	100.0
37	主持	中国科学院国际合作局对外重点项目	健康长寿人群维持良好线粒体功能的分子机制研究	孔庆鹏	2016-2018	100.0
38	主持	中央引导地方科技发展专项	生命条形码技术创新中心	王文智	2017-2018	100.0
39	主持	中组部青年千人计划	青年千人计划经费 —— 焦保卫	焦保卫	2014-2019	300.0
40	主持	云岭学者	云岭学者 —— 宿兵	宿　兵	2015-2019	200.0
41	主持	云南省创新团队	云南省创新团队 —— 孔庆鹏	孔庆鹏	2018-2022	100.0
42	主持	云南省高端科技人才项目	云南省高端科技人才项目 —— 焦保卫	焦保卫	2014-2019	210.0
43	主持	云南省高端科技人才项目	云南省高端科技人才项目 —— 施鹏	施　鹏	2013-2019	200.0
44	主持	云南省高端科技人才项目	云南省高端科技人才项目 —— 郑萍	郑　萍	2015-2019	160.0
45	主持	云南省科技入滇专项	基因大数据信息技术及其应用研究	马占山	2017-2019	120.0
46	主持	云南省云岭产业技术领军人才	云岭产业技术领军人才基金 —— 马占山	马占山	2015-2019	100.0
47	主持	版纳州政府横向项目	滇南小耳猪分子育种及产业化	高　云	2017-2018	261.9
48	主持	瑞士 Ferring 公司横向项目	Are germ stem cells present in ovaries and required for maintenance of normal ovarian function?	郑　萍	2018-2021	200.0
49	主持	大理州环保局横向项目	云南洱海珍稀特有鱼类大理弓鱼保育与种群恢复研究	杨君兴	2017-2019	100.0
50	主持	云南省水利厅横向项目	牛栏江珍稀鱼类繁殖研究及放流	杨君兴	2017-2018	84.0

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说明：“[1]” 为并列第一作者，“*” 为通讯作者

专利及新品种

授权专利

1. **潘晓赋**，**王晓爱**，**杨君兴**，**刘倩**，**杨坤凤**. 一种短须裂腹鱼人工繁殖方法. 专利号：ZL 2015 1 0863420.7 申请日期：2015 年 12 月 01 日，授权日期：2018 年 09 月 11 日

2. **潘晓赋**，**王晓爱**，**杨君兴**，**刘倩**. 一种暗色唇鱼肝脏细胞系的构建方法. 专利号：ZL 2015 1 0204441.8 申请日期：2015 年 04 月 27 日，授权日期：2018 年 10 月 26 日。

农业新品种

水产新品种 滇池金线鲃 “ 鲃优 1 号 ”(2018) 新品种证字第 2 号，品种登记号：GS-01-002-2017。

获 奖

序号	成果名称	成果类型	等级	完成人	排名
1	一种暗色唇鱼的人工繁殖方法	云南省专利奖	二等	杨君兴，潘晓赋，李再云，陈小勇	1
2	肠道微生物组与肠肝疾病关系及作用机制研究	云南省自然科学奖	一等	耿嘉蔚，张志刚，柳陈坚等	2

第二章 开放合作交流

开放课题

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）
GREKF18-01	张明旺	副教授	四川农业大学	胫腺侧褶蛙分子谱系地理学研究	7
GREKF18-02	陈自明	副教授	云南大学	餐 (Hemiculter leucisculus) 的群体遗传学及生物地理学研究	7
GREKF18-03	黄勋和	副教授	嘉应学院	群体基因组分析揭示中国乌骨鸡黑色素沉积分子机制及其育种历史	7
GREKF18-04	才旺计美	副研究员	西藏自治区林木科学研究院	气候变化对西藏墨脱甲虫谱系多样性随海拔梯度变化丧失程度的影响评估	7
GREKF18-05	陈　兵	讲　师	昆明学院	衣藻混合营养方式形成机制的研究	7
GREKF18-06	Barrett Rowan	助　教	McGill University	中国西南边境地区泡酒 metabarcoding 研究	7
GREKF18-07	白彩娟	讲　师	西藏大学	藏族人群在高原低氧环境中的生殖适合度及其对高原低氧适应的分子机制	7
GREKF18-08	张　锐	教　授	中山大学	RNA 编辑在藏族人群高原适应中的作用	7
GREKF18-09	阚显照	教　授	安徽师范大学	雀形目 NADH 家族及 NUMT 的进化研究	7
GREKF18-10	向　阳	教　授	南昌大学	滇产野菊花防治皮肤光损伤的有效成分分离及机制研究	7
GREKF18-11	李志鹏	副研究员	中国农业科学院特产研究所	梅花鹿消化道甲烷菌演替与生态位变化研究	7
GREKF18-12	李　艳	研究员	中国科学院昆明植物研究所	泛素连接酶 RNF220 调控 Shh 信号通路的机制及其在 Shh 型髓母细胞瘤发生中的功能	7
GREKF18-13	解　萌	副教授	四川农业大学	枯叶蛱蝶拟态进化的遗传和基因组机制	7
GREKF18-14	邹　权	研究员	天津大学	肥胖相关肠道菌群宏基因组学及菌群生态学探究	7
GREKF18-15	袁智勇	讲　师	西南林业大学	超蛙科物种系统地理学研究	7
GREKF18-16	曹祖兵	副教授	安徽农业大学	mRNA m6A 甲基化修饰在猪卵母细胞成熟及早期胚胎发育中的功能研究	7
GREKF18-17	陈立畅	讲　师	云南农业大学	健康衰老多组学大数据分析平台的构建与研究	7

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）
GREKF18-18	李 琳	助理研究员	昆明市延安医院	FKBP9 在脑胶质瘤发展中的作用及机制研究	7
GREKF18-19	石 云	教 授	南京大学模式动物研究所	信号肽在红藻氨酸受体突触转运中的功能机制	7

参加学术会议

序号	报告名称	报告人	会议名称	地点	会议时间
1	泰国中、北部两栖类多样性及代表物种的分子资源挖掘	陈进民	2018 年东南亚中心学术年会	缅甸内比都	1 月 30-2 月 2 日
2	灵长类动物高原适应及药物干预分子机制	张国捷	2018 动物学前沿论坛	昆明	2 月 26 日
3	Selection and environmental adaptation along a path to speciation in the Tibetan frog Nanorana parkeri	张宝林	第一届亚洲演化生物学大会	深圳	4 月 18-20 日
4	A Parallel Mechanism Underlying Frizzle in Chickens	彭旻晟	第一届亚洲演化生物学大会	深圳	4 月 18-20 日
5	Genetics of Lactase Persistence in Iranian Populations	Hadi Charati	第一届亚洲演化生物学大会	深圳	4 月 18-20 日
6	Whole-genome Resequencing and Phenotypic Analyses Reveal Adaptation to Unique Tropical Environmental Stressors in African Indigenous Chickens	Newton Otieno Otecko	第一届亚洲演化生物学大会	深圳	4 月 18-20 日
7	Whole genome resequencing reveals population structure and genetic mechanism of body size variation in Chinese pigs	杨 阳	第一届亚洲演化生物学大会	深圳	4 月 18-20 日
8	A genomic perspective on evo-devo of ant superorganisms	张国捷	Biology & Genomics of Social Insects	美国冷泉港	5 月 5-8 日
9	A proposed guide for flying squirrel taxonomy research	李 权	2018-International Squirrel Colloquium	昆明	6 月 4-8 日
10	Demic diffusion of millet agriculture facilitated the formation of genetic landscape of the Tibetans	李玉春	第八届东亚考古学大会	南京	6 月 8 日

序号	报告名称	报告人	会议名称	地点	会议时间
11	Odonata fauna of Yunnan Province, China	张浩淼	第 55 届热带生物学对话会议	马来西亚古晋	7 月 1-5 日
12	How climate change impacts on beetle diversity in a natural reserve area in Southernwest China?	王运宇	第 55 届热带生物学对话会议	马来西亚古晋	7 月 1-5 日
13	粟黍农业扩张促进藏族人群遗传结构的形成	李玉春	第五届地球系统科学大会	上海	7 月 2-4 日
14	Transcriptomic Landscape of von Economo Neurons in Human Anterior Cingulate Cortex Revealed by Microdissected-Cell RNA Sequencing	宿　兵	2018 年分子生物学与进化年会	日本横滨	7 月 8-12 日
15	The transcriptomic landscape of yaks reveals molecular pathways for high altitude adaptation	祁学斌	2018 年分子生物学与进化年会	日本横滨	7 月 8-12 日
16	De Novo assembly of Tibetan genome	和耀喜	2018 年分子生物学与进化年会	日本横滨	7 月 8-12 日
17	高山倭蛙适应高原极端环境皮肤基础表型研究	杨春华	中国动物学会两栖爬行动物学分会	兰州	8 月 14-17 日
18	高原适应的进化历史及趋同性 —— 通过海拔呈梯度分布的不同类群比较研究	付婷婷	中国动物学会两栖爬行动物学分会	兰州	8 月 14-17 日
19	A Global Standard for the Identification of Key Biodiversity Areas	张浩淼	Freshwater Key Biodiversity Areas in the Lower Mekong River Basin	泰国曼谷	9 月 3-8 日
20	Filia is an ESC-specific guardian of genomic stability	郑　萍	中国干细胞第八届年会	济南	9 月 14-16 日
21	The Lophuromys aquilus species complex	Kenneth Otieno Onditi	92nd Annual Meeting of the German Society for Mammalian Biology	德国波恩	9 月 17-20 日
22	蜻蜓目昆虫应用于环境评价的研究方法及应用	张浩淼	水生昆虫应用于环境评价的研究方法讨论会	北京	9 月 26-29 日
23	藏族人群中 EGLN1 基因的适应性进化及其功能解析	张　慧	2018 年美国人类遗传学会年会	美国圣地亚哥	10 月 16-19 日

序号	报告名称	报告人	会议名称	地点	会议时间
24	东亚人群的史前人类定居历史	李春梅	2018 年美国人类遗传学会年会	美国圣地亚哥	10 月 16-19 日
25	MCPH1 转基因猴的认识能力分析	姜　瑾	2018 年美国人类遗传学会年会	美国圣地亚哥	10 月 16-19 日
26	History, selection, and genomic basis of complex traits of dogs	王国栋	世界生命科学大会	北京	10 月 27-29 日
27	Stem cell-specific protein Filia plays key roles in preserving genomic stability	郑　萍	9th international symposium on DNA Damage Response & Human Disease	深圳	11 月 1-4 日
28	Mammary gland development and breast cancer	杨　星	2018 年 “ 香港中文大学生物医学学院研究生日 ”	香港	11 月 9 日
29	萤火虫分类与系统研究	李学燕	中国南方八省昆虫学会热带南亚热带昆虫资源与害虫防治第二届学术研讨会	西双版纳	11 月 18 日
30	国家 II 保护动物滇池金线鲃的保育与利用	潘晓赋	第十四届全国野生动物生态与资源保护学术研讨会	昆明	11 月 21-23 日
31	基于形态和遗传特征的鳡 白鱼增殖放流合理性评价	张源伟	第十四届全国野生动物生态与资源保护学术研讨会	昆明	11 月 21-23 日
32	鮡科鱼类体型大小进化的比较转录组研究	蒋万胜	第十四届全国野生动物生态与资源保护学术研讨会	昆明	11 月 21-23 日
33	李氏小飞鼠（Hylopetes leonardi）种级地位的恢复	李　权	第十四届全国野生动物生态与资源保护学术研讨会	昆明	11 月 21-23 日
34	动物高原适应的动态进化历程及趋同性研究	孙艳波	第十四届全国野生动物生态与资源保护学术研讨会	昆明	11 月 21-23 日
35	Natatanuran frogs used the Indian Plate to step-stone disperse and radiate across the Indian Ocean	张宝林	第十四届全国野生动物生态与资源保护学术研讨会	昆明	11 月 21-23 日
36	藏族人群对高原低氧环境的适应机制	宿　兵	第 29 届国际高原医学会议	尼泊尔加德满都	11 月 21-25 日

序号	报告名称	报告人	会议名称	地点	会议时间
37	Cross-altitude Analysis Suggests a Turning Point at the Elevation of 4,500 m for Polycythemia Prevalence in Tibetans	祁学斌	第 29 届国际高原医学会议	尼泊尔加德满都	11 月 21-25 日
38	Blunted nitric oxide regulation and high altitude adaptation in Tibetans	和耀喜	第 29 届国际高原医学会议	尼泊尔加德满都	11 月 21-25 日
39	大尺度、跨物种的动物进化基因组研究	王　文	中国遗传学会第十次全国会员代表大会暨学术讨论会	南京	11 月 26-29 日
40	Population Genomic Insights into High Altitude Adaptation in Pamirs	希尔扎提江 · 苏来曼	中国遗传学会第十次全国会员代表大会暨学术讨论会	南京	11 月 26-29 日
41	Identity-by-descent analysis reveals novel susceptibility loci for severe acne in Chinese Han coho	杨兴艳	中国遗传学会第十次全国会员代表大会暨学术讨论会	南京	11 月 26-29 日
42	非洲珍珠鸡的遗传多样性及环境适应	沈全宽	中国遗传学会第十次全国会员代表大会暨学术讨论会	南京	11 月 26-29 日
43	Canine transmissible venereal tumor genome reveals ancient introgression from coyotes to pre-contact dogs in North America	汪　轩	中国遗传学会第十次全国会员代表大会暨学术讨论会	南京	11 月 26-29 日
44	干细胞基因组不稳定性与发育异常	郑　萍	中国遗传学会第十次全国会员代表大会暨学术讨论会	南京	11 月 26-29 日

邀请学术报告

序号	专家姓名	单位	报告日期	报告题目
1	余正涛	昆明理工大学	1 月 18 日	机器翻译发展前沿及东南亚语言机器翻译
2	石　云	南京农业大学	1 月 24 日	谷氨酸受体与兴奋性神经突触传递

序号	专家姓名	单位	报告日期	报告题目
3	杨　光	南京师范大学	1月29日	适应性进化驱动鲸类物种形成
4	桂建芳	中国科学院水生生物研究所	1月29日	从单性生殖银鲫雄性发生与决定机制的发现谈脊椎动物性别演化的多样性与可塑性
5	曹　丰	中国人民解放军总医院	2月10日	心脏干细胞的在体分子影像研究
6	Chew Soo Hong	National University of Singapore	3月7日	Neurogenetics of Decision Making under Risk and Uncertainty
7	贾洪涛	Ohio State University	3月27日	NGS在转化医学中的应用
8	Julian Kerbis	Roosevelt University	3月28日	A review of current Field Museum programs in Mammalogy and Ornithology in Africa
9	吴仲义	中山大学	4月3日	What are microRNAs good for? The May-Wigner theory offers a new perspective
10	Christos Mammides	广西大学	4月3日	1. 人类活动对自然保护地区的影响：来自塞浦路斯、肯尼亚和斯里兰卡的例子；2. 利用结构方程模型（SEM）来测量人类对鸟类的影响
11	Jacobus Jan Boomsma	University of Copenhagen	4月23日	Social Adaptation, Natural Selection and Genomics
12	Albert S. Feng	University of Illinois	4月23日	Evolution of Hearing: Insights from studies in Odorrana tormota
13	惠静毅	中国科学院生物化学与细胞生物学研究所	5月14日	Understanding the crosstalk between alternative splicing and signal transduction
14	冯　英	中国科学院上海营养科学研究所	5月14日	Role of alternative splicing in development and diseases
15	杨运桂	中国科学院北京基因组研究所	5月14日	RNA Methylation Code：Regulations and Mechanisms
16	Nyaga Mugao Mzalendo Kibunjia	National Museums of Kenya	5月16日	The National Museums of Kenya : A Center of Excellence for Research and Conservation of Kenya's Cultural and Natural Heritage

序号	专家姓名	单位	报告日期	报告题目
17	David M. Hillis	University of Texas at Austin	8 月 3 日	Species delimitation in geographically variable taxa: Problems with multispecies coalescent approaches
18	王源昌	云南师范大学	8 月 15 日	金融数学原理对生物统计学中小概率事件发生研究的启示
19	Joost Gribnau	Erasmus University Rotterdam	8 月 16 日	Dosage compensation, the X-factor unveiled
20	David C. Blackburn	Florida Museum of Natural History	9 月 6 日	Diversity and Evolution of Frogs, with insights from Africa, fossils and 3D phenotypes
21	王　军	中国科学院微生物研究所	9 月 6 日	微生物组研究技术在不同领域的应用
22	Axel Krings	University of Idaho	10 月 2 日	Recent advances in fault tolerance theories for networked systems
23	景乃禾	中国科学院生物化学与细胞生物学研究所	10 月 12 日	Developmental spatial transcriptome reveals lineage segregation of three germ layers in post-implantation mouse embryos
24	赵　扬	北京大学	10 月 16 日	Harnessing small molecules and direct reprogramming strategy in heart regeneration
25	斋藤成也	National Institute of Genetics, Mishima, Japan	10 月 31 日	Evolutionarily conserved nonconding sequences (CNSs) may bridge gap between DNA and morphology
26	杨　力	中国科学院上海生命科学研究院计算生物学研究所	12 月 4 日	Genome-wide analysis of nucleotide editing modification and the development of targeted base editing
27	周　勇	the University of Alabama	12 月 5 日	The Mechanobiology of Lung Fibrosis and Glaucoma

第三章 人才队伍建议

新增人才称号

序号	姓名	入选年度	人才项目名称	项目来源
1	张亚平	2018 年	欧洲科学院院士	欧洲科学院
2	车　静	2018 年	中青年科技创新领军人才	科技部
3	吴东东	2018 年	优秀青年基金	基金委
4	吴东东	2018 年	优秀青促会会员	中国科学院
5	李学燕	2018 年	西部之光 A 类	中国科学院
6	王明山	2018 年	西部之光 A 类	中国科学院
7	王明山	2018 年	青促会会员	中国科学院
8	宿　兵	2018 年	" 万人计划 " 科技领军人才	云南省
9	孙艳波	2018 年	" 万人计划 " 青年拔尖人才	云南省
10	吴东东	2018 年	" 万人计划 " 青年拔尖人才	云南省
11	张志刚	2018 年	" 万人计划 " 青年拔尖人才	云南省
12	刘　振	2018 年	" 万人计划 " 青年拔尖人才	云南省
13	王国栋	2018 年	" 万人计划 " 青年拔尖人才	云南省

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	罗明洁、徐　凯	蔡　望、李宗煦、杨　洋、王晓阳	李沅衡
2	车　静	徐　伟、余传鑫、董文捷、曹如君、杨春华、ALEX PLIMO KARUNO	陈进民、张宝林、高　伟、付婷婷、吴云鹤、张　毅、侯绍兵、MD MIZANUR RAHMAN、FELISTA KASYOKA KILUNDA	
3	佴文惠	吴甜甜		
4	蒋学龙	于秋鹏、胡文强、胡哲畅、成　市、ALOIS WAMBUA MWEU	宋文宇、牛晓炜、李　权、宁文鹤、黄　程、KENNETH OTIENO ONDITI	陈顺德

序号	导师	硕士生	博士生	博士后
5	焦保卫	成　美、杨　旭、刁显红、李玲玲	赵丽敏、杨　星、郭　璐、赵丽娜、徐海波	
6	孔庆鹏	董　蕾、王昊天、郭荣慧、顾康蜀云、郜宗亮 、邱　考、郭丽云	余　琴、夏王晓、葛明侠、江建军、ZIA RAHMAN	
7	马占山	肖琬蒙	夏　尧、李连伟、李文迪、MD MOTIUR RAHMAN	
8	毛炳宇	朱　良、李雨薇、茶靖美	张龙龙、王绘山	
9	盛能印	唐　杰、万　梨、易雅星、卜宇飞、马可汉	叶雅馨	
10	施　鹏	雷孟龙、杨丽丽、陶乐、吴群富、华　绒、杨　陆、姚晓晴	陈艳艳 (云大合培、有我所学籍) 、祁飞燕、刘　奇、张　涛、白　婧、陈　杰、郭媛婷、罗　杰、郑智中、朱　磊、李媛媛	刘广帅
11	王　文	李　冀	曾　严、陈海涛、刘　威、王　宝	
12	文建凡	邱　兰、邓　琪、薛　敏	吕章夏、程姣妮	
13	吴东东	任小蝶、庄晓琳	李明莉、田航宇、ADEOLA OLUWAKEMI AYOOLA	王　胜
14	宿　兵	胡　艳、胡　庭、周　斌、曾雪芮张凤云、王永琴、周亚楠、李丽雅	和耀喜、姜瑾、袁佳妙、郑王山、孟晓宇、郭永博、杨晏冬、罗鑫	
15	祁学斌	岳　天、黄家卉		
16	杨君兴	吴安丽、殷艳慧、黄新迪	杜丽娜、孙　超、潘晓赋	
17	杨晓君	何书航、黎思涵、陈逸林、袁兴海、姚舜禹、赵　岩、GLADYS NYAKERU KUNG'U	王　洁、单鹏飞、王继山	
18	张亚平	周其俊、伍胤桥、周博闻、刘　行、王　蓉、 DAVID HERIEL MAUKI、刘　露	耿伟航、马云飞、沈全宽、戴珊珊胡靖扬、尹婷婷、黄翠萍、李建波黎武略、颜　晨、许明敏、马　成张越东 NEWTON OTIENO OTECKOHADI CHARATI SABER KHEDERZADEH	
19	王国栋	张湘泉、林　娜		
20	高　云	施　贤		
21	彭旻晟	王雪琪、SAID ISMAIL NGANGA		
22	郑　萍	李　聪、李秀峰、宁雨琪、唐　敏、谢　恒	张伟道、李竞争、姜方洁、孙春丽、龚道华、陈忠良	Larbi
23	张国捷			高琼华

毕业研究生

序号	姓名	攻读专业	学位	导师姓名	毕业日期
1	FELISTA KASYOKA KILUNDA	遗传学	硕士	彭旻晟	2018.6
2	KENNETH OTIENO ONDITI	动物学	硕士	蒋学龙	2018.6
3	LAXMAN KHANAL	动物学	博士	蒋学龙	2018.6
4	LOTANNA MICAH NNEJI	动物学	博士	车　静	2018.6
5	MAHADEV	遗传学	博士	姚永刚	2018.6
6	MARCO ENDRUWEIT	动物学	博士	杨君兴	2018.6
7	MURIITHI JACINTA MURINGI	动物学	硕士	杨晓君	2018.6
8	曾　琳	遗传学	博士	张亚平	2018.1
9	范　闯	动物学	硕士	杨晓君	2018.6
10	甘　霖	动物学	硕士	蒋学龙	2018.6
11	何大健	细胞生物学	博士	郑　萍	2018.6
12	何金武	生物工程	硕士	王　文	2018.6
13	黄　俊	遗传学	硕士	宿　兵	2018.1
14	柯　浩	细胞生物学	博士	焦保卫	2018.6
15	奎　玲	遗传学	博士	王　文	2018.1
16	李永鑫	遗传学	博士	王　文	2018.6
17	刘耀文	遗传学	博士	孔庆鹏	2018.6
18	卢光义	动物学	博士	杨晓君	2018.6
19	吕梦蝶	遗传学	博士	张亚平	2018.6
20	马　成	生物工程	硕士	张亚平	2018.6
21	马玉洁	细胞生物学	硕士	焦保卫	2018.6
22	米　雪	遗传学	硕士	车　静	2018.6
23	牛诚祎	动物学	硕士	杨君兴	2018.6

序号	姓名	攻读专业	学位	导师姓名	毕业日期
24	任彦栋	遗传学	博士	王　文	2018.6
25	苏敬冉	生物工程	硕士	姚永刚	2018.6
26	田娇阳	遗传学	博士	孔庆鹏	2018.6
27	田天祺	动物学	硕士	杨晓君	2018.6
28	汪　轩	遗传学	硕士	张亚平	2018.6
29	王　筱	遗传学	博士	王　文	2018.6
30	王运梅	遗传学	博士	张亚平	2018.6
31	吴　焕	遗传学	博士	孔庆鹏	2018.6
32	向志丹	遗传学	博士	王　文	2018.6
33	杨坤凤	动物学	博士	杨君兴	2018.1
34	杨杏丽	遗传学	硕士	孔庆鹏	2018.6
35	杨　阳	遗传学	博士	张亚平	2018.6
36	叶青青	细胞生物学	博士	文建凡	2018.1
37	张源伟	动物学	博士	杨君兴	2018.6

研究生优秀论文奖

姓名	获奖等级	期刊	IF	作者排序
和耀喜	一等奖	National Science Review	10.973	第一作者
张宝林	二等奖	National Science Review	10.973	并列一作第二
付婷婷	二等奖	Proceedings of the National Academy of Sciences of the United States of America	10.359	并列一作第二
张宝林	二等奖	Proceedings of the National Academy of Sciences of the United States of America	10.359	并列一作第二
陈进民	三等奖	Molecular Phylogenetics and Evolution	4.294	第一作者
杨晏冬	三等奖	Cerebral Cortex	6.8	并列一作第二

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	俱文惠	蒋学龙	焦保卫	孔庆鹏
马占山	毛炳宇	盛能印	施　鹏	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

Adeola Charles	白慧掀	曾　琳	常云艳	陈宏满	陈　鹏
陈　兴	程乐华	丁　果	董　锋	董志巍	付吉东
高建云	高　云	郭　琨	郭　彦	郝军军	何　锴
何水旺	何永捍	和协超	黄岩淦	辉　洪	季吟秋
蒋万胜	金洁琼	柯　浩	李朝翠	李春梅	李功华
李桂梅	李京璘	李兴统	李学燕	李学友	李玉春
李毓劲	廖爱文	刘传发	刘贵春	刘　倩	刘淑伟
刘薇薇	刘心武	刘　振	柳延虎	马怀孝	马鹏程
马夕尧	马玉洁	闵　锐	潘晓赋	彭旻晟	彭　忆
彭　云	浦绍艳	祁学斌	冉　浩	饶定齐	邵　永
石　磊	舒树森	苏伟婷	孙艳波	唐　嘉	田航宇
田骄阳	万　韬	汪嘉欣	王国栋	王洪娇	王　慧
王　洁	王金焕	王　林	王林（郑萍组）	王明山	王荣兴
王晓爱	王运宇	卫小娟	吴春莹	吴　飞	吴　焕
吴汝念	吴世芳	伍和启	肖富辉	谢海兵	熊子军
徐　沙	许绍斌	岩　道	杨滨宇	杨春燕	杨　晖
杨坤凤	杨立新	杨利琴	杨敏敏	杨　钦	杨双娟
叶青青	余国华	余　琴	余　蕊	张栋儒	张海林
张浩淼	张洪磊	张　慧	张锦锦	张树润	张伟道
张晓明	张　洋	张业胜	张源伟	张志刚	赵　博
赵　洁	赵若含	赵若苹	赵士萍	赵亚鹏	郑兰平
周炜帏	周　鑫	周中银	朱春玲	朱建国	朱玮璟
邹　丽					

2018年报

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