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

2019年报

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

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主任致辞

披荆斩棘，力耕不欺。2019 年，是中华人民共和国成立 70 周年，中国科学院建院 70 周年，也是昆明动物研究所建所 60 周年。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立足于我国西南和东南亚丰富的生物多样性遗传资源，面向战略生物资源的国家需求和世界科技前沿以及国民经济主战场，在任务承担、科研成果、队伍建设、开放交流等各方面工作均取得了可喜进展。

在承担科研项目方面，实验室积极发挥集群优势，组织策划国家、国际重大科技任务，成效显著。2019 年新增科研项目 76 项，包括主持科技部科技基础资源调查项目 1 项，参与科技部国家重点研发计划 2 项并主持其子课题，获基金委优秀青年科学基金资助 1 项，主持中国科学院先导 A 项目多个子课题。在研项目共计 217 项目，其中包括国家级项目 72 项，省部级项目 110 项，国际合作项目 11 项，横向项目 24 项。新增研究经费 7991 万元。在致力于基础研究的同时，实验室也积极结合国家和地区的战略与发展需求，并将基础理论应用于技术创新与推广应用。

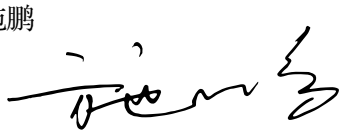
在科研成果产出方面，实验室围绕三大研究方向，继续揭示生物多样性形成与演变的规律及其遗传机制，为遗传资源的保护和可持续利用提供理论依据。2019 年发表 SCI 论文 170 篇，其中以第一完成单位发表论文 69 篇，以第一作者或通讯作者（含并列）在 *Science*、*Cell Research*、*Genome Biology*、*Nature Communications* 等五年影响因子 >9 的国际知名期刊论文 28 篇，中国科学院期刊分区 1 区论文占总论文的 32.35%；合作出版专著 1 部；授权发明专利 5 项；获云南省自然科学一等奖 1 项。

在人才队伍建设方面，2019 年，实验室继续采用“引进加培养”的方式，创新人才机制，激发队伍活力，取得明显成效。实验室新引进学术带头人 1 名。培养新增副研究员 8 人，其中 3 人由研究所破格晋升为副高级专业技术岗位，实现了在学术领域方向研究表现突出的青年人才早挑重担的创新培养政策。在固定人员中，1 人新入选中组部万人计划领军人才，1 人新入选中组部万人计划青年拔尖人才，1 人荣获基金委优秀青年科学基金资助。实验室牵头组织中科院西部之光交叉创新团队 1 个。培养输出博士研究生 19 人，硕士研究生 12 人，出站博士后 1 人。此外，还成功举办 2019 年“进化生物学”暑期班，吸引更多有志青年加入实验室。

实验室长期遵循“交流促进合作”的原则，在 2019 年开展了一系列合作交流活动。定期举办“遗传资源与进化青年学者论坛”共计 4 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。作为主办方之一，成功举办“一带一路”前景聚焦国际研讨会暨“一带一路”高通量条形码国际培训班。邀请 13 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 16 项，并将各科研平台开放共享。

只争朝夕，创新前行！ 2020 年是国家“十三五”规划收官之年，也是中国科学院基本实现“四个率先”的关键年。立足过去，共创未来。我们在学术委员会指导下，力争在 2020 年做出更大贡献！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依托于中国科学院昆明动物研究所，前身为中科院重点实验室“细胞与分子进化重点实验室”。2007 年 11 月经科技部批准筹建，2009 年 9 月通过验收。

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

实验室积极发挥地域优势和资源特色，开展了大量动物和人类遗传资源收集工作，为生物多样性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、过程与人工选择机制方面做出了具有影响力的代表性成果。近五年，实验室承担国家级、省部级、国际合作及横向项目共 361 项，到位研究经费共计 4.05 亿元。发表 SCI 论文共 782 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 109 篇。授权专利 18 项。农业农村部认定水产新品种 1 项。荣获云南省自然科学一等奖、二等奖各 2 项，云南省科技进步三等奖 2 项，云南省专利二等奖、三等各 1 项。

实验室拥有研究组 19 个，支撑部门 3 个。目前固定工作人员 131 人，正高级职称 23 人，副高级职称 30 人。其中 40 岁以下研究骨干占比为 69.23%，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。拥有国家基金委创新群体 1 个，中国科学院院士 1 人，欧洲科学院院士 1 人，人社部百千万人才工程 4 人，中青年科技创新领军人才 3 人，教育部长江学者奖励计划 1 人，国家万人计划领军人才 3 人，国家万人计划青年拔尖人才 1 人，国家海外高层次人才引进计划 1 人，国家杰出青年科学基金获得者 5 人，国家优秀青年科学基金获得者 4 人。目前实验室在站博士后 6 人，在读博士研究生 96 人，硕士研究生 68 人。

实验室目前建设有 7 大平台：分子实验平台、显微影像与操作平台、生物信息学平台、功能基因发掘与分析平台、生物多样性考察平台、生命条形码平台、集成家猪平台。拥有大型仪器设备共计 100 余台 / 套，设备总价值 15861 万元。这些设施除了满足实验室在后基因组时代对基因组进化与基因功能研究的需求以外，所有大型设备还依托于昆明大型仪器区域中心，并通过“仪器设备共享管理网”对实验室内外乃至研究所内外全面开放共享。

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

实验室积极开展与国内外的交流与合作，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

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

2. 基因与基因组的进化

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

3. 遗传发育与进化

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

三、组织结构

1. 现任实验室领导

主　任

施　鹏 研究员

副主任

文建凡 研究员

毛炳宇 研究员

焦保卫 研究员

2. 第三届学术委员会

主　任

张亚平　院　士，中国科学院

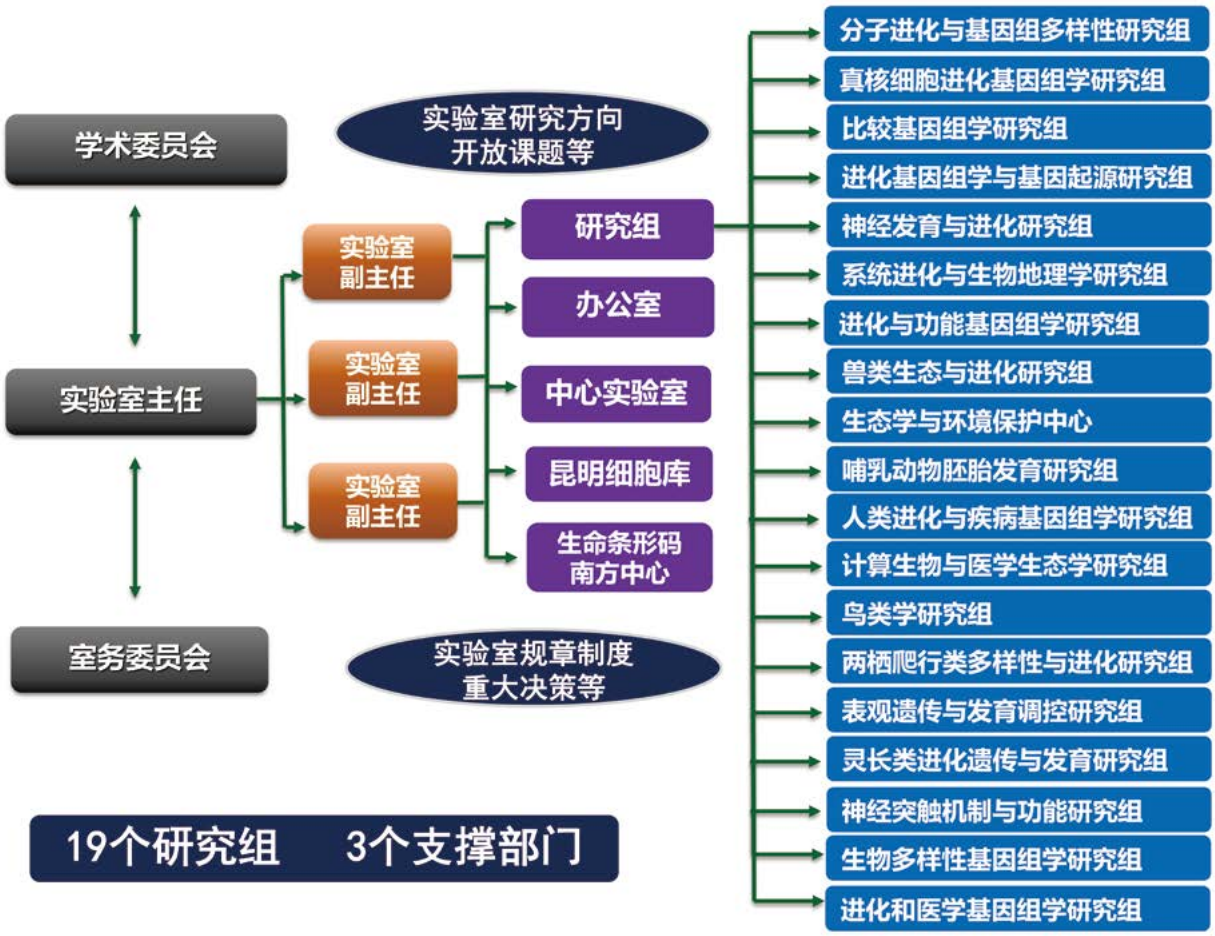
副主任

宿　兵　研究员，中国科学院昆明动物研究所

委　员

桂建芳　院　士，中国科学院水生生物学研究所
金　力　院　士，复旦大学
魏辅文　院　士，中国科学院动物研究所
吴仲义　院　士，中山大学
焦保卫　研究员，中国科学院昆明动物研究所
李德铢　研究员，中国科学院昆明植物研究所
施　鹏　研究员，中国科学院昆明动物研究所
汪小全　研究员，中国科学院植物研究所
王　文　研究员，中国科学院昆明动物研究所
杨　光　教　授，南京师范大学
张克勤　教　授，云南大学

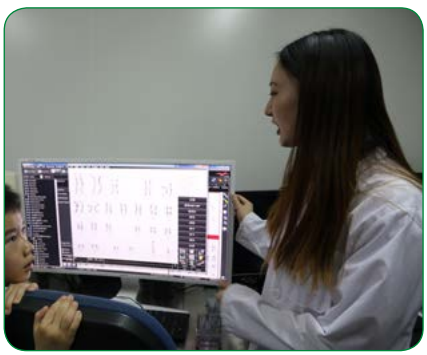
3. 研究队伍



大事记



5 月 15-16 日，实验室第三届学术委员会第二次会议在西南生物多样性实验室报告厅召开。会议由学术委员会主任张亚平院士主持，魏辅文院士、汪小全研究员、李德铢研究员、杨光教授、张克勤教授等 10 位委员出席。研究所姚永刚所长以及实验室学术带头人和青年研究骨干参加会议。会议上，学术委员会在学科团队布局、战略发展、人才队伍建设等方面，对实验室提出了客观中肯的建议和指导。


5 月 18 日中国科学院公众科学日，实验室的三个研究组及支撑部门细胞库分别面向公众开放参观，并举办细胞科普讲座。此次活动针对中小学生，形式多样，内容丰富。体现了国家重点实验室的开放和科教融合的运行特色，旨在提升了广大公众的科学知识和素养，激发了青少年对科学的关注和兴趣。


7 月 22-26 日，实验室与研究生部联合举办 2019 年“进化生物学”暑期班，对 30 余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、学科组研习等活动，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。



12 月 26-27 日，中国科学院遗传与发育生物学研究所分子发育生物学国家重点实验室主任杨维才研究员同该实验室 20 余位学术带头人及青年骨干来到我实验室进行学术访问交流活动。同时还特别邀请到中国科学院动物研究所的刘以训院士出席。双方围绕交叉学科领域进行探讨，促进合作研究，提升资源共享、联合攻关的能力。



2019 年，实验室不定期举办“遗传与进化前沿交叉论坛”共计 13 场，邀请到黄勋研究员、杨振业教授、孟飞龙研究员、周波研究员、王弘毅教授、苏正昌教授、Oyekanmi Nashiru 教授、黄开耀研究员等国内外知名学者到室进行学术报告，积极与国内外一流机构开展学术交流与合作研究。






2019 年，实验室举办上一年度“青年学者论坛”总决赛及新一届论坛共 4 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，并吸引了研究所内及其他科研院校广大师生积极参与。

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

家犬肿瘤活化石揭示郊狼到北美土著家犬的古老渐渗

Canine transmissible venereal tumor genome reveals ancient introgression from coyotes to pre-contact dogs in North America

Xuan Wang, Bo-Wen Zhou, Melinda A. Yang, Ting-Ting Yin, Fang-Liang Chen, Sheila C. Ommeh, Ali Esmailizadeh, Melissa M. Turner, Andrei D. Poyarkov, Peter Savolainen, Guo-Dong Wang, Qiaomei Fu & Ya-Ping Zhang

Canine transmissible venereal tumor (CTVT), the oldest known somatic cell line, is a living fossil of the original founder, transmitted from host's cancer cells to other canids during the mating process.[1] Since it was shown ten years ago that living cells from an ancient host could be transmitted among canids, the origin of CTVT has been studied continuously.[2] Recent comparison of the CTVT genetic data with a more comprehensive canine reference panel including pre-contact dogs (PCDs) from North America argued that the CTVT founder (the original canid infected with CTVT) is the closest detectable lineage to PCDs, and that this clade underwent introgression from wild canids in North America.[3]

Cell Research, 2019, 29(7):592-595

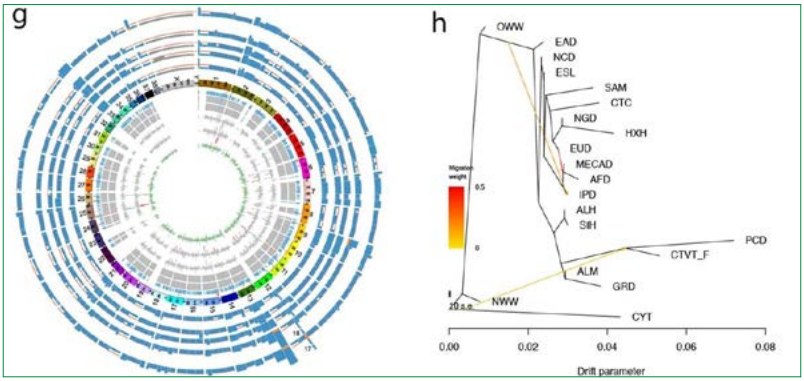


图 1：CTVT 基因组拷贝数变异与郊狼渐渗，全球家犬群体分化与混合结构

犬类生殖器传染性肿瘤（CTVT）是一种可以在犬科动物中传染生存的肿瘤，作为最初患瘤个体（CTVT founder）的活化石，其基因组记录了一只古代犬科动物的遗传信息。近 10 年来，科学家们反复讨论了 CTVT 的起源和肿瘤进化过程。目前，通过对全球范围的现代家犬和部分古代家犬化石的全基因组测序，CTVT 的起源范围已由最初的狼或古老犬种，缩小至与北美洲土著家犬有关的群体。

张亚平研究团队与中科院古脊椎动物与古人类研究所付巧妹研究员团队合作开发了首个犬类生殖器传染性肿瘤（CTVT）专用的基因型检测工具 ttgeno，结合 102 个世界各地的犬科动物的单核苷酸多态（SNPs），获得了可能属于 CTVT founder 的祖先正常多态信息位点。通过系统发育关系和群体遗传结构分析，发现 CTVT 起源于北美土著家犬。此外还发现 CTVT founder 和北美土著家犬具有北美郊狼和北美灰狼的基因流。本研究创新性的将 CTVT 当作活化石来进行群体遗传研究，为家犬迁徙历史和种群间杂交研究提供了新的思路和视角。

研究成果发表在 ***Cell Research*** 上。

研究方向一：遗传资源多样性的演化与保护

代表性成果二

揭示粟黍农业人群介导了大麦农业向青藏高原的传播

Neolithic millet farmers contributed to the permanent settlement of the Tibetan Plateau by adopting barley agriculture

Yu-Chun Li, Jiao-Yang Tian, Feng-Wen Liu, Bin-Yu Yang, Kang-Shu-Yun Gu, Zia Ur Rahman, Li-Qin Yang, Fa-Hu Chen, Guang-Hui Dong, Qing-Peng Kong

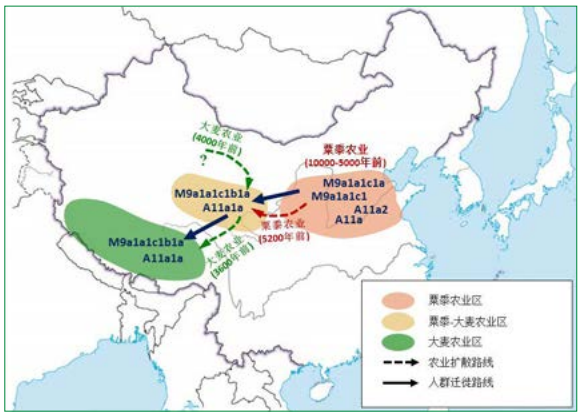
Abstract

The permanent human settlement of the Tibetan Plateau (TP) has been suggested to have been facilitated by the introduction of barley agriculture ~3.6 kilo-years ago (ka). However, how barley agriculture spread onto the TP remains unknown. Given that the lower altitudes in the northeastern TP were occupied by millet cultivators from 5.2 ka, who also adopted barley farming ~4 ka, it is highly possible that it was millet farmers who brought barley agriculture onto the TP ~3.6 ka. To test this hypothesis, we analyzed mitochondrial DNA (mtDNA) from 8277 Tibetans and 58 514 individuals from surrounding populations, including 682 newly sequenced whole mitogenomes. Multiple lines of evidence, together with radiocarbon dating of cereal remains at different elevations, supports the scenario that two haplogroups (M9a1a1c1b1a and A11a1a), which are common in contemporary Tibetans (20.9%) and were probably even more common (40–50%) in early Tibetans prior to historical immigrations to the TP, represent the genetic legacy of the Neolithic millet farmers. Both haplogroups originated in northern China between 10.0–6.0 ka and differentiated in the ancestors of modern Tibetans ~5.2–4.0 ka, matching the dispersal history of millet farming. By showing that substantial genetic components in contemporary Tibetans can trace their ancestry back to the Neolithic millet farmers, our study reveals that millet farmers adopted and brought barley agriculture to the TP ~3.6–3.3 ka, and made an important contribution to the Tibetan gene pool.

National Science Review, 2019, 6(5):1005-1013

耐寒农作物大麦向青藏高原的传播与利用被认为是促进史前人群大规模永久定居高原高海拔地区的关键因素，但大麦农业向青藏高原传播是人群扩散模式，还是技术交流模式却仍不清楚。

孔庆鹏研究团队与兰州大学董广辉教授合作，基于现代藏族（8277 份）及周边人群（58514 份）线粒体 DNA（mtDNA）数据，深入解析了藏族的遗传结构。结合不同海拔农作物遗存的碳十四测年等数据，发现藏族人群中存在大量的源于中国北方粟黍农业人群的遗传组分（占 ~20%），并且在耐寒作物大麦传播至青藏高原高海拔地区时（3600 BP），高原人群可能以粟黍农业人群组分为主（达 ~50%）。这说明粟黍农业人群可能在到达青藏高原低海拔地区后，采用了耐寒的大麦农业并进一步向高海拔迁徙，最终大规模永久定居青藏高原。



研究成果发表在 ***National Science Review*** 上。工作发表后，该杂志同步刊发了两篇评论文章，专门对此成果进行了评述和介绍。

研究方向一：遗传资源多样性的演化与保护

代表性成果三

大规模 mtDNA 数据揭示汉族人群母系遗传结构的形成机制

River Valleys Shaped the Maternal Genetic Landscape of Han Chinese

Yu-Chun Li, Wei-Jian Ye, Chuan-Gui Jiang, Zhen Zeng, Jiao-Yang Tian, Li-Qin Yang, Kai-Jun Liu, Qing-Peng Kong

Abstract

A general south-north genetic divergence has been observed among Han Chinese in previous studies. However, these studies, especially those on mitochondrial DNA (mtDNA), are based either on partial mtDNA sequences or on limited samples. Given that Han Chinese comprise the world's largest population and reside around the whole China, whether the north-south divergence can be observed after all regional populations are considered remains unknown. Moreover, factors involved in shaping the genetic landscape of Han Chinese need further investigation. In this study, we dissected the matrilineal landscape of Han Chinese by studying 4,004 mtDNA haplogroup-defining variants in 21,668 Han samples from virtually all provinces in China. Our results confirmed the genetic divergence between southern and northern Han populations. However, we found a significant genetic divergence among populations from the three main river systems, that is, the Yangtze, the Yellow, and the Zhujiang (Pearl) rivers, which largely attributed to the prevalent distribution of haplogroups D4, B4, and M7 in these river valleys. Further analyses based on 4,986 mitogenomes, including 218 newly generated sequences, indicated that this divergence was already established during the early Holocene and may have resulted from population expansion facilitated by ancient agricultures along these rivers. These results imply that the maternal gene pools of the contemporary Han populations have retained the genetic imprint of early Neolithic farmers from different river basins, or that river valleys represented relative migration barriers that facilitated genetic differentiation, thus highlighting the importance of the three ancient agricultures in shaping the genetic landscape of the Han Chinese.

Molecular Biology and Evolution, 2019, 36(8):1643-1652

作为世界上人口数量最大的族群，汉族人群的遗传结构及其形成机制一直以来都是不同领域广泛关注的热点问题。以往基于线粒体DNA（mtDNA）的研究提示，汉族人群的母系遗传结构存在南北分化。然而这些研究主要是基于较为有限的样本和低分辨率的数据，导致汉族人群的整体母系遗传结构尚缺乏清晰认识，而促进汉族人群母系遗传结构形成的主要因素迄今亦不清楚。

孔庆鹏研究团队与成都二十三魔方生物科技有限公司合作，通过分析中国 33 个省级行政区 21668 例汉族样本的 mtDNA 突变数据，发现不同水系的汉族人群间的遗传差异较南北差异更为显著，且该差异主要表现为三大水系（黄河、长江和珠江）之间的分化。巧合的是，三大水系也是三大史前农业——粟黍农业（黄河流域）、水稻农业（长江流域）和热带农业（珠江流域）的起源或扩散中心，而不同水系人群在该时期均出现了人口数量急剧增长。因此，汉族人群的母系遗传结构更多地保留了新石器时期早期的遗传印记，不同流域史前农业的起源和扩散则是促进汉族人群母系遗传分化的重要原因。

研究成果发表在***Molecular Biology and Evolution***上。工作发表后，该杂志以 "news" 形式对我们的工作专门进行了宣传报道。

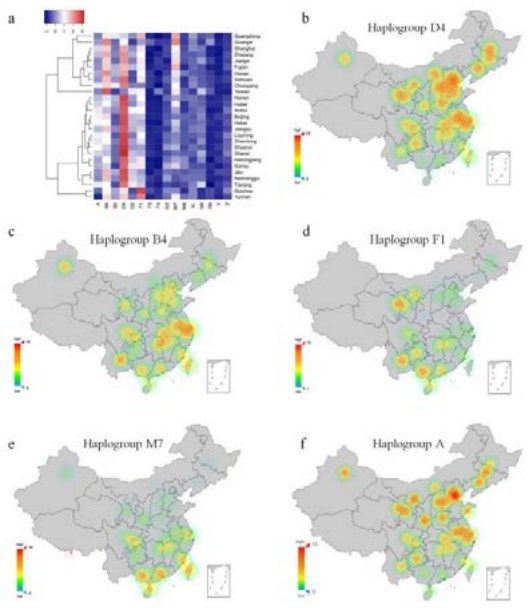


FIG. 1. Regional distributions of mtDNA haplogroups in China

研究方向一：遗传资源多样性的演化与保护

代表性成果四

经典多样性—稳定性关系理论研究取得重要突破

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

Zhanshan (Sam) Ma Aaron M. Ellison

Abstract

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 data sets; 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 data sets, 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: (1) 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); (2) analysis of SDNs based on special trio motifs, core-periphery, rich-club, and nested structures, and high salience skeletons; and (3) 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.

Ecological Monographs, 2019, 89(2)

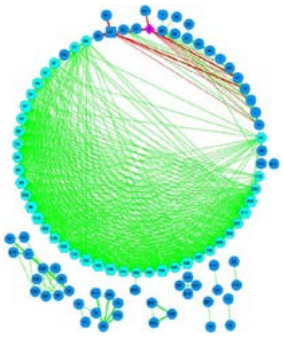
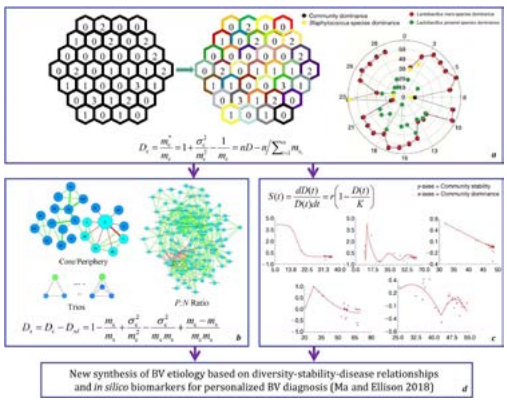


FIG. 1. The SDN (species dominance network) for subject number 424



"多样性—稳定性关系"（也称之为"复杂性—稳定性关系"）被认为是生态学中最重要的核心理论课题之一，并具有极其重要的实际意义。例如：生物多样性保护的最大实际收益其实就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。复杂性—稳定性关系的研究不仅具有有趣的起源，而且也是跨学科研究的重要理论难题之一。

马占山研究员与美国哈佛大学 Aaron Ellison 教授在美生态学会旗舰期刊《***Ecological Monographs***》发表论文，在经典多样性—稳定性关系领域提出系列新概念和方法，主要进展包括：引入了"优势度"（dominance）概念，以"偷换""多样性（复杂性）概念"；提出优势网络概念和分析技术；将其应用于研究菌群稳定性与疾病关系的研究。

Ecological Monographs 是学界为数不多对于稿件长度有下限要求的杂志之一，每年仅发表大约 30-40 篇论文。此次发表的论文也是 *Ecological Monographs* 创刊近一个世纪以来首篇涉及人类疾病的论文。 论文发表后受到科技日报、新华网、美国 NBC， ABC， CBS 等媒体采访和报道。

ECOLOGICAL MONOGRAPHS
ECOLOGICAL SOCIETY OF AMERICA

研究方向二：基因与基因组的进化

代表性成果一

在家养动物高原适应遗传机制方面取得新进展

Convergent genomic signatures of high altitude adaptation among domestic mammals

Dong-Dong Wu, Cui-Ping Yang, Ming-Shan Wang, Kun-Zhe Dong, Da-Wei Yan, Zi-Qian Hao, Song-Qing Fan, Shu-Zhou Chu, Qiu-Shuo Shen, Li-Ping Jiang, Yan Li, Lin Zeng, He-Qun Liu, Hai-Bing Xie, Yun-Fei Ma, Xiao-Yan Kong, Shu-Li Yang, Xin-Xing Dong, Ali Esmailizadeh Koshkoiyeh, David M Irwin, Xiao Xiao, Ming Li, Yang Dong, Wen Wang, Peng Shi, Hai-Peng Li, Yue-Hui Ma, Xiao Gou, Yong-Bin Chen, Ya-Ping Zhang

ABSTRACT

Abundant and diverse domestic mammals living on the Tibetan Plateau provide useful materials for investigating adaptive evolution and genetic convergence. Here, we utilized 327 genomes from horses, sheep, goats, cattle, pigs and dogs living at both high and low altitudes, including 73 genomes generated for this study, to disentangle the genetic mechanisms underlying local adaptation of domestic mammals. Although molecular convergence is comparatively rare at the DNA sequence level, we found convergent signature of positive selection at the gene level, particularly EPAS1 gene in these Tibetan domestic mammals. We also reported a potential function in response to hypoxia for the gene C10orf67, which underwent positive selection in three of the domestic mammals. Our data provides insight into adaptive evolution of high-altitude domestic mammals, and should facilitate the search for additional novel genes involved in the hypoxia response pathway.

National Science Review, 2019, doi.org/10.1093/nsr/nwz213

张亚平和吴东东研究团队利用大规模基因组学数据，利用各种群体遗传学方法揭示了青藏高原家养动物（如藏獒、藏鸡、藏黄牛等）的高原适应性遗传机制（*Mol Biol Evol* 2014；*Mol Biol Evol* 2015; *Nature Genetics* 2016；*Cell Res* 2017；*Nat Ecol Evol* 2018），鉴定出一批以 HIF 缺氧诱导通路为代表的高原适应候选基因，揭示了基因交流在家养动物高原适应中的重要作用，为高原家养动物物品种资源保护提供了重要信息。

研究人员进一步综合比较分析了多个家养动物（包括藏獒、藏猪、藏绵羊、藏山羊、藏马、藏黄牛等）适应青藏高原遗传机制的个性和共性特征，发现这些家养动物在基因水平发生显著的趋同进化，尤其是 *EPAS1* 基因，它是人类以及多个家养动物适应青藏高原的关键基因。另外，研究人员从这些快速进化基因中，鉴定出一个新的低氧通路基因 *C10orf67*。

研究成果发表在 ***National Science Review*** 上。

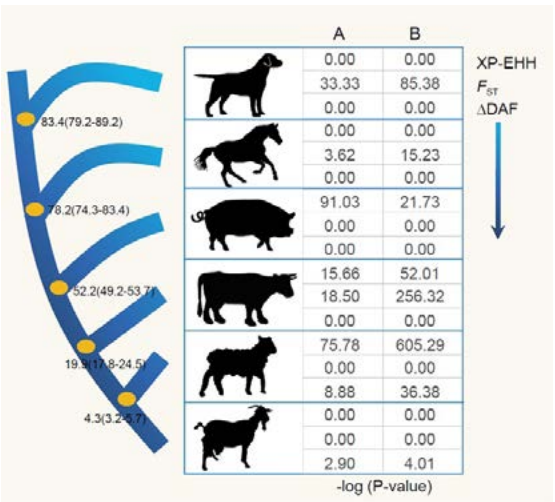


Figure 1: Rapid evolution of hypoxia response genes in six Tibetan domestic mammals.

研究方向二：基因与基因组的进化

代表性成果二

发布高质量中国恒河猴参考基因组并解析猿类特异的结构变异

Long-read assembly of the Chinese rhesus macaque genome and identification of ape-specific structural variants

Yaoxi He, Xin Luo, Bin Zhou, Ting Hu, Xiaoyu Meng, Peter A. Audano, Zev N. Kronenberg, Evan E. Eichler, Jie Jin, Yongbo Guo, Yanan Yang, Xuebin Qi & Bing Su

Abstract

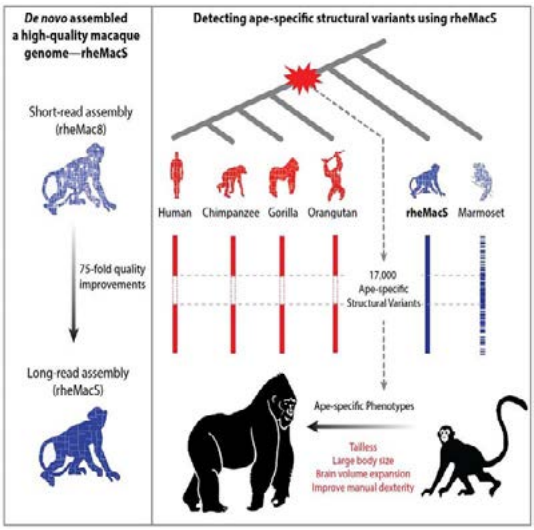
We present a high-quality de novo genome assembly (rheMacS) of the Chinese rhesus macaque (Macaca mulatta) using long-read sequencing and multiplatform scaffolding approaches. Compared to the current Indian rhesus macaque reference genome (rheMac8), rheMacS increases sequence contiguity 75-fold, closing 21,940 of the remaining assembly gaps (60.8 Mbp). We improve gene annotation by generating more than two million full-length transcripts from ten different tissues by long-read RNA sequencing. We sequence resolve 53,916 structural variants (96% novel) and identify 17,000 ape-specific structural variants (ASSVs) based on comparison to ape genomes. Many ASSVs map within ChIP-seq predicted enhancer regions where apes and macaque show diverged enhancer activity and gene expression. We further characterize a subset that may contribute to ape- or great-ape-specific phenotypic traits, including taillessness, brain volume expansion, improved manual dexterity, and large body size. The rheMacS genome assembly serves as an ideal reference for future biomedical and evolutionary studies.

Nature Communications, 2019, 10, 4233

恒河猴（*Macaca mulatta*）是生物科学研究和新药研发广泛应用的非人灵长类实验动物。构建一个高质量的恒河猴基因组是开展相关研究的重要基础。当前国际上广泛使用的是印度恒河猴的参考基因组，但这个主要基于二代测序的恒河猴参考基因组组装质量较差，序列碎片化和缺失严重，极大地限制了它的应用，特别是无法用于对基因组结构变异（Structural Variant，SV）的解析。

宿兵研究团队利用三代长读长的测序数据，结合多层次的基因组组装手段，从头组装了一个中国恒河猴的全基因组 ——rheMacS。利用高质量的中国恒河猴基因组，识别到了 17,000 个猿共有的结构变异（ape-shared structural variants，ASSVs）。这些结构变异是造成猿特有表型的重要潜在因子。另外，研究找到了一系列可能与猿的重要特征相关的 ASSVs。该研究发布的中国恒河猴基因组将对未来的生物医学研究提供重要的基础数据，并为解析包括人类在内的灵长类表型进化的遗传基础提供新的思路。

研究成果发表在 ***Nature Communications*** 上。



研究方向二：基因与基因组的进化

代表性成果三

发现 CRISPR-Cas9 基因编辑系统在灵长类中不会导致明显的脱靶效应

Trio deep-sequencing does not reveal unexpected off-target and on-target mutations in Cas9-edited rhesus monkeys

Xin Luo, Yaoxi He, Chao Zhang, Xiechao He, Lanzhen Yan, Min Li, Ting Hu, Yan Hu, Jin Jiang, Xiaoyu Meng, Weizhi Ji, Xudong Zhao, Ping Zheng, Shuhua Xu & Bing Su

Abstract

CRISPR-Cas9 is a widely-used genome editing tool, but its off-target effect and on-target complex mutations remain a concern, especially in view of future clinical applications. Non-human primates (NHPs) share close genetic and physiological similarities with humans, making them an ideal preclinical model for developing Cas9-based therapies. However, to our knowledge no comprehensive in vivo off-target and on-target assessment has been conducted in NHPs. Here, we perform whole genome trio sequencing of Cas9-treated rhesus monkeys. We only find a small number of de novo mutations that can be explained by expected spontaneous mutations, and no unexpected off-target mutations (OTMs) were detected. Furthermore, the long-read sequencing data does not detect large structural variants in the target region.

Nature Communications, 2019, 10, 5525

CRISPR-Cas9基因编辑系统已被广泛应用于生物和医学研究，然而，其在临床前的安全性却缺少全面的评估。猕猴（*Macaca mulatta*）作为与人类进化关系最近的可进行遗传操作的非人灵长类，在大脑发育以及脑结构上都与人类具有高度的相似性。因此，在猕猴疾病模型上探索 Cas9 基因编辑的脱靶效应对未来的临床应用至关重要。

为了系统评估 CRISPR-Cas9 在灵长类基因编辑中的脱靶效应，宿兵和郑萍研究团队等多个团队合作，利用 CRISPR-Cas9 系统构建了小头症基因 -*MCPH1* 敲除的猕猴模型。通过对多只基因敲除猴及其野生型父母本进行深度二代测序和分析，发现 Cas9 在灵长类基因组中并不会造成大量的新生突变。此外，利用长片段测序技（PacBio），也对 *MCPH1* 基因的打靶区域进行了深度测序和分析，发现打靶区域并不存在大片段的结构变异。该成果首次表明 CRISPR-Cas9 基因编辑系统在灵长类中并不会造成明显的脱靶效应，具有比较高的安全性。

研究结果发表在 ***Nature Communications*** 上。

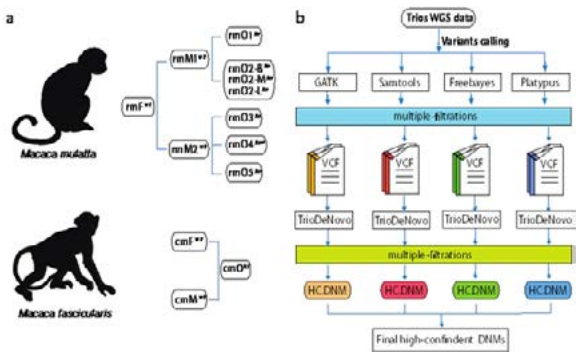


Fig. 1 Detecting de novo mutations (DNMs) in the Cas9-treated monkeys

研究方向二：基因与基因组的进化

代表性成果四

家犬基因组研究国际联盟发表 dog10K 计划白皮书

Dog10K: an international sequencing effort to advance studies of canine domestication, phenotypes and health

Elaine A Ostrander, Guo-Dong Wang, Greger Larson, Bridgett M vonHoldt, Brian W Davis, Vidhya Jagannathan, Christophe Hitte, Robert K Wayne, Ya-Ping Zhang, Dog10K Consortium

Abstract

Dogs are the most phenotypically diverse mammalian species, and they possess more known heritable disorders than any other non-human mammal. Efforts to catalog and characterize genetic variation across well-chosen populations of canines are necessary to advance our understanding of their evolutionary history and genetic architecture. To date, no organized effort has been undertaken to sequence the world's canid populations. The Dog10K Consortium (http://www.dog10kgenomes.org) is an international collaboration of researchers from across the globe who will generate 20× whole genomes from 10 000 canids in 5 years. This effort will capture the genetic diversity that underlies the phenotypic and geographical variability of modern canids worldwide. Breeds, village dogs, niche populations and extended pedigrees are currently being sequenced, and de novo assemblies of multiple canids are being constructed. This unprecedented dataset will address the genetic underpinnings of domestication, breed formation, aging, behavior and morphological variation. More generally, this effort will advance our understanding of human and canine health.

National Science Review, 2019, 6(4):810-824

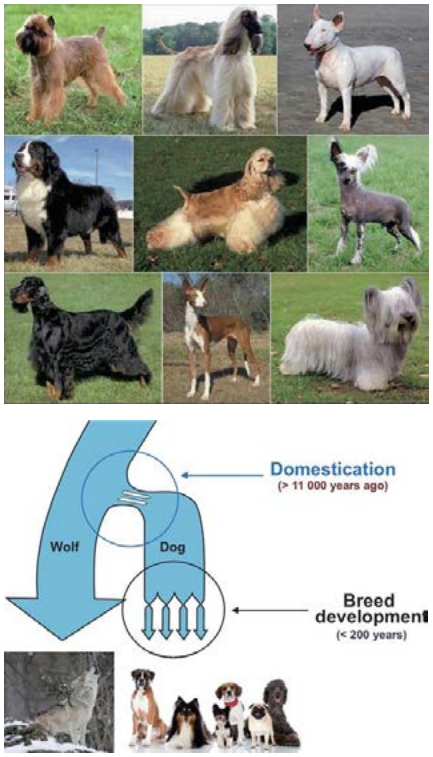


Figure 1. Multiple bottlenecks have shaped the structure of haplotypes and LD observed in modern breeds.

2016 年在北京来自世界各地的 20 多位科学家成立家犬基因组联盟，全面深度探讨家犬起源与驯化、人工选择、疾病机制、医学模型等问题重大科学问题。研究联盟指出，家犬是行为和表型最为多样的哺乳动物，并且比其它任何非人类哺乳动物都具有更多已知的遗传性疾病。对精选的犬科动物、家犬品种、土狗进行基因组变异的分析和描述，有助于加深我们对犬科动物进化历史和遗传结构的理解。

张亚平研究团队作为家犬基因组研究国际联盟的主要发起人，发表了 Dog10K 计划白皮书，综述了当前家犬的研究现状以及研究联盟的计划、目的和意义。联盟计划在 5 年内对 1 万只犬科动物进行基因组高覆盖度测序，并建立一个与人类基因组计划水平相当的资源平台，整合所有研究团队提供的宝贵数据，与北京基因组所联合开发 iDog 数据库并以开放的形式迎接合作（*Nucleic Acids Research* 2019）。旨在获取世界范围内的犬科动物表型以及地理差异上的遗传多样性信息，揭示家犬的驯化、品种犬育种、行为和表型的遗传机制。

同期在 ***National Science Review*** 发表了 Prospective。

NSR National Science Review

研究方向二：基因与基因组的进化

代表性成果五

揭示中国南方灰狼为独立支系

Genomic Approaches Reveal an Endemic Subpopulation of Gray Wolves in Southern China

Guo-Dong Wang,1,2,9 Ming Zhang,3,4,5,9 Xuan Wang,1,2,5 Melinda A. Yang,3,4 Peng Cao,3 Feng Liu,3 Heng Lu,6Xiaotian Feng,3 Pontus Skoglund,7 Lu Wang,8 Qiaomei Fu,3,4,5,* and Ya-Ping Zhang1,2,10,*

SUMMARY

Although gray wolves (Canis lupus) are one of the most widely distributed terrestrial mammals, their origins in China are not well understood. We sequenced six specimens from wolf skins, showing that gray wolves from Southern China (SC) derive from a single lineage, distinct from gray wolves from the Tibetan Plateau and Northern China, suggesting that SC gray wolves may form a distinct subpopulation. Of SC gray wolves, one wolf from Zhejiang carries a genetic component from a canid and had gene flow from a population related to or further diverged from wolves than the dhole. This may indicate that interspecific gene flow likely played an important role in shaping the speciation patterns and population structure in the genus Canis. Our study is the first to survey museum gray wolves' genomes from Southern China, highlighting how sequencing the paleogenome from museum specimens can help us to study extinct species.

iScience, 2019, 10.1016/j.isci.2019.09.008

狼（*Canis lupus*）是家犬的野生祖先，是广泛分布的陆生哺乳动物，占据了欧亚大陆、北美、乃至北非等地。前人的研究表明狼具有复杂的系统发育和群体历史，不仅受地理和生态环境影响存在群体结构，而且和家犬、郊狼（Coyote）、乃至豺存在明显的、长期的基因交流和群体混合现象。在中国，狼不仅生活在青藏高原、东北、新疆、内蒙等地，而且在中国的南方也有分布。

张亚平研究团队与中国科学院古脊椎所合作，提取了从博物馆获得的皮张样本 DNA 并全基因组测序。群体遗传学分析发现中国南方的狼是一个单独的群体，和中国北方、青藏高原狼有差异且关系最近。其次，研究发现采自浙江的狼个体基因组中存在一种遗传组分，可能来自于犬科的另一个物种，且分歧时间大于狼和亚洲豺犬（*Cuon alpinus*）。研究结果亦揭示犬科物种间的基因交流在物种形成过程中扮演了重要的作用，也提示古 DNA 的研究方法对动物博物馆馆藏样本有显著的研究意义。

研究成果发表在 ***iScience*** 上。

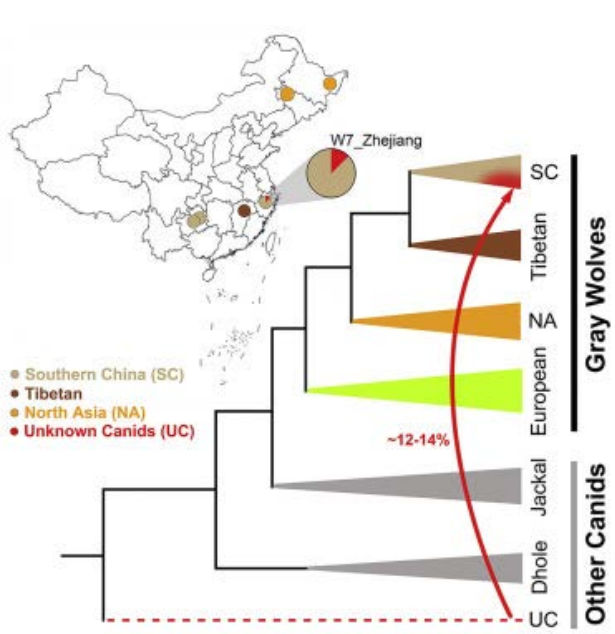


图 1. 中国南方狼的系统发育关系和基因交流

研究方向三： 遗传、发育与进化

代表性成果一

首次在体外重现非人灵长类动物胚胎原肠运动的发生

In vitro culture of cynomolgus monkey embryos beyond early gastrulation

Huaixiao Ma1,2,3,*, Jinglei Zhai1,3,4,*, Haifeng Wan1,3,*, Xiangxiang Jiang1,3,*, Xiaoxiao Wang1,3,4, Lin Wang2, Yunlong Xiang1, Xiechao He5, Zhen-Ao Zhao1, Bo Zhao2, Ping Zheng2,5,6,†, Lei Li1,3,4,†, Hongmei Wang1,3,4,†

Abstract

Gastrulation is a key event in embryonic development when the germ layers are specified and the basic animal body plan is established. The complexities of primate gastrulation remain a mystery because of the difficulties in accessing primate embryos at this stage. Here, we report the establishment of an in vitro culture (IVC) system that supports the continuous development of cynomolgus monkey blastocysts beyond early gastrulation up to 20 days after fertilization. The IVC embryos highly recapitulated the key events of in vivo early postimplantation development, including segregation of the epiblast and hypoblast, formation of the amniotic and yolk sac cavities, appearance of the primordial germ cells, and establishment of the anterior-posterior axis. Single-cell RNA-sequencing analyses of the IVC embryos provide information about lineage specification during primate early postimplantation development. This system provides a platform with which to explore the characteristics and mechanisms of early postimplantation embryogenesis in primates with possible conservation of cell movements and lineages in human embryogenesis.

Science, 2019, 366(6467), 836

受限于伦理和研究技术，灵长类早期胚胎发育的研究非常有限，特别是着床后的早期发育。目前，人类对灵长类胚胎内、中、外三个胚层的分化及胚胎体轴的建立等关键发育事件仍知之甚少。

郑萍研究团队与中科院动物研究所合作研究建立了猴胚胎体外培养系统，可以将食蟹猴囊胚体外培养至原肠运动出现，并进一步发育至受精后 20 天。并且，从形态学、标记分子染色和单细胞转录组等多个角度提供了充分的证据，证明体外发育的食蟹猴胚胎高度重现体内胚胎发育包括原肠运动在内的多个重要事件。本研究以与人遗传与进化较为接近的食蟹猴作为模式动物，避免了人类胚胎培养 14 天的伦理限制，首次证明灵长类动物胚胎可以在没有母体支撑的情况下体外发育至原肠运动，并重现了灵长类动物早期胚胎发育的几个关键事件。为探索灵长类早期胚胎发育和原肠运动开辟了崭新研究平台，也为人类深入认识胚胎发育机制和体外孕育生命（非人）探索提供了重要数据。

研究成果发表国际知名期刊 ***Science*** 上。

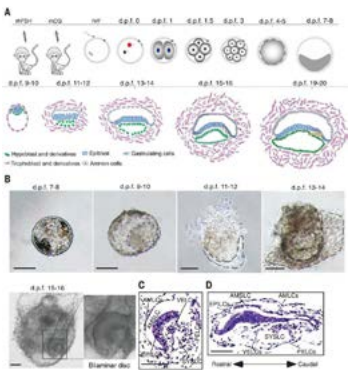


Fig. 1 Establishment of the IVC system for monkey embryos.

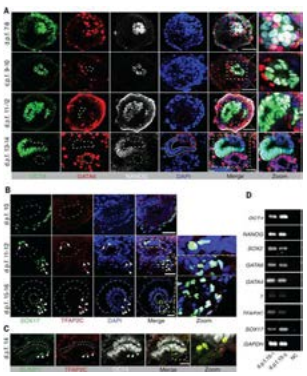


Fig. 2 Recapitulation of monkey early postimplantation development in IVC embryos.

Science

研究方向三： 遗传、发育与进化

代表性成果二

发现 *KHDC3L* 突变可导致复发性流产

KHDC3L mutation causes recurrent pregnancy loss by inducing genomic instability of human early embryonic cells

Weidao Zhang1,2,3, Zhongliang Chen1,2,3, Dengfeng Zhang4, Bo Zhao1, Lu Liu5,Zhengyuan Xie6, Yonggang Yao3,4,7, Ping ZhengID1,2,7,8*

Abstract

Recurrent pregnancy loss (RPL) is an important complication in reproductive health. About 50% of RPL cases are unexplained, and understanding the genetic basis is essential for its diagnosis and prognosis. Herein, we report causal KH domain containing 3 like (KHDC3L) mutations in RPL. KHDC3L is expressed in human epiblast cells and ensures their genome stability and viability. Mechanistically, KHDC3L binds to poly(ADP-ribose) polymerase 1 (PARP1) to stimulate its activity. In response to DNA damage, KHDC3L also localizes to DNA damage sites and facilitates homologous recombination (HR)-mediated DNA repair. KHDC3L dysfunction causes PARP1 inhibition and HR repair deficiency, which is synthetically lethal. Notably, we identified two critical residues, Thr145 and Thr156, whose phosphorylation by Ataxia-telangiectasia mutated (ATM) is essential for KHDC3L's functions. Importantly, two deletions of KHDC3L (p.E150_V160del and p.E150_V172del) were detected in female RPL patients, both of which harbor a common loss of Thr156 and are impaired in PARP1 activation and HR repair. In summary, our study reveals both KHDC3L as a new RPL risk gene and its critical function in DNA damage repair pathways.

PLOS Biology, 2019, 17(10)

维持基因组稳定是细胞的基本功能，这对早期胚胎发育的奠基石细胞尤为重要，基因组不稳定可导致胚胎发育异常甚至失败。

郑萍研究团队以胚胎干细胞为模型，研究早期发育阶段的多能细胞如何维持基因组稳定性从而保障胚胎正常发育。前期，课题组在小鼠胚胎干细胞中鉴定了一个重要调控蛋白Filia，Filia 缺失使胚胎干细胞产生严重的基因组不稳定性，并可导致着床后胚胎发育失败（*Cell stem cell 2015, 16: 684-698; Cell Research 2018, 28:69-89*）。人类早期胚胎多能细胞表达小鼠 Filia 的同源蛋白 *KHDC3L*，但其氨基酸序列保守性低，功能也不清楚。我们通过与医院合作，收集了 29 例不明原因的复发性流产病人以及 205 例健康女性血样，对 *KHDC3L* 进行测序，筛选到病人特异性的两个片段缺失突变。并利用人胚胎干细胞研究体系，详细阐述了 *KHDC3L* 维持早期胚胎基因组稳定性的功能和突变致病机制，并寻找到两个关键的磷酸化功能调控位点，可作为临床诊断复发性流产遗传病因的靶点。

该研究成果发表在 ***PLOS Biology*** 上。

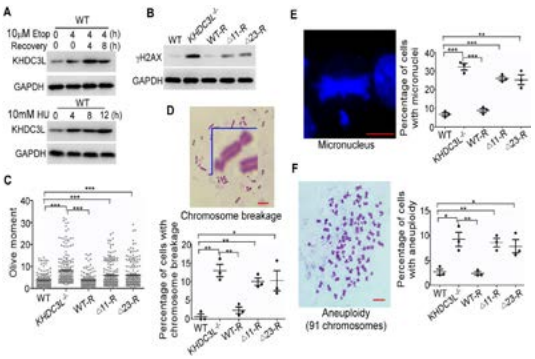


Fig 1. KHDC3L preserves genomic stability of hESCs

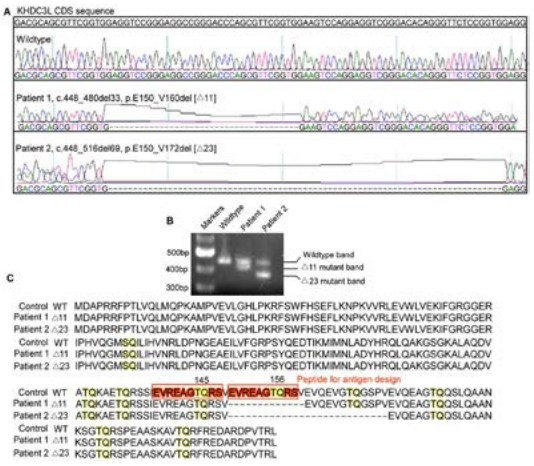


Fig. 2. KHDC3L is mutated in patients with recurrent pregnancy loss (RPL).

研究方向三： 遗传、发育与进化

代表性成果三

发现人类大脑进化幼态持续现象的分子机制

Transgenic rhesus monkeys carrying the human MCPH1 gene copies show human-like neoteny of brain development

Lei Shi, Xin Luo, Jin Jiang, Yongchang Chen, Cirong Liu, Ting Hu, Min Li, Qiang Lin, Yanjiao Li, Jun Huang, Hong Wang, Yuyu Niu, Yundi Shi, Martin Styner, Jianhong Wang, Yi Lu, Xuejin Sun, Hualin Yu, Weizhi Ji, Bing Su

Abstract

Brain size and cognitive skills are the most dramatically changed traits in humans during evolution and yet the genetic mechanisms underlying these human-specific changes remain elusive. Here, we successfully generated 11 transgenic rhesus monkeys (8 first-generation and 3 second-generation) carrying human copies of MCPH1, an important gene for brain development and brain evolution. Brain-image and tissue-section analyses indicated an altered pattern of neural-cell differentiation, resulting in a delayed neuronal maturation and neural-fiber myelination of the transgenic monkeys, similar to the known evolutionary change of developmental delay (neoteny) in humans. Further brain-transcriptome and tissue-section analyses of major developmental stages showed a marked human-like expression delay of neuron differentiation and synaptic-signaling genes, providing a molecular explanation for the observed brain-developmental delay of the transgenic monkeys. More importantly, the transgenic monkeys exhibited better short-term memory and shorter reaction time compared with the wild-type controls in the delayed-matching-to-sample task. The presented data represent the first attempt to experimentally interrogate the genetic basis of human brain origin using a transgenic monkey model and it values the use of non-human primates in understanding unique human traits.

National Science Review, 2019, 6, 480-493

幼态持续（neoteny）是人类进化中发生的独特现象。与我们的近亲非人灵长类相比，人类的发育速度变慢，发育过程延缓。人类的幼态持续在进化上的重要性在于为大脑发育和神经网络的可塑性提供了更长的时间窗口，是人类智力形成的关键因素。

宿兵研究团队一直从事灵长类大脑功能演化及其进化调控的研究。在前期研究的基础上，首次构建了携带人源 *MCPH1* 基因拷贝的转基因恒河猴模型，成功获得了 8 个 F0 代和 3 个 F1 代转基因猴，通过核磁共振脑影像分析对大脑发育不同时间点的脑影像动态图谱进行了跟踪分析，发现转基因猴存在明显的神经细胞与神经网络成熟延迟的现象。进一步对大脑发育不同时间点的脑组织学与转录组学的动态图谱的分析表明，转基因猴大脑中许多与神经元分化与成熟相关基因的表达受到了抑制，其表达峰值明显延后，这可能是导致转基因猴大脑发育延缓的分子基础。尤为重要的是，对转基因猴的认知能力进行了检测，发现与野生型对照猴相比转基因猴的工作记忆能力明显提高，说明大脑发育的延缓对转基因猴的智力提升可能是有益的，类似于人类大脑发育过程中的幼态持续现象。

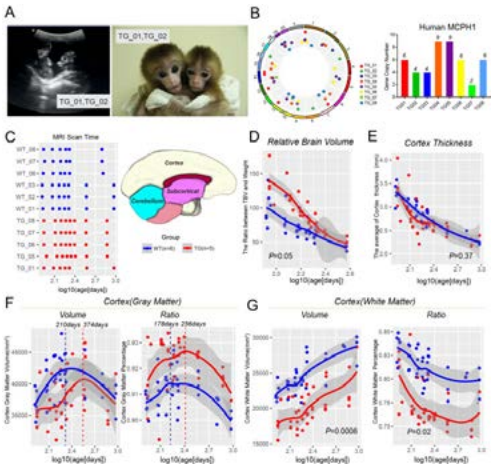


Fig 1. Brain-developmental tracking of the TG monkeys via structural MRI.

该项研究成果是首次利用非人灵长类转基因模型研究人类特异的遗传变异对人类智力起源的贡献及其分子机制，显示了转基因猴模型对研究人类起源以及人类特有脑疾病（如老年痴呆等）的重要价值。

研究成果发表 ***National Science Review*** 上。

研究方向三： 遗传、发育与进化

代表性成果四

基于大规模转录组数据解析非人灵长类大脑衰老潜在机制

547 transcriptomes from 44 brain areas reveal features of the aging brain in non-human primates

Ming-Li Li, Shi-Hao Wu, Jin-Jin Zhang, Hang-Yu Tian, Yong Shao, Zheng-Bo Wang, David M. Irwin, Jia-Li Li, Xin-Tian Hu & Dong-Dong Wu

Abstract

Background

Brain aging is a complex process that depends on the precise regulation of multiple brain regions; however, the underlying molecular mechanisms behind this process remain to be clarified in non-human primates.

Results

Here, we explore non-human primate brain aging using 547 transcriptomes originating from 44 brain areas in rhesus macaques (Macaca mulatta). We show that expression connectivity between pairs of cerebral cortex areas as well as expression symmetry between the left and right hemispheres both decrease after aging. Although the aging mechanisms across different brain areas are largely convergent, changes in gene expression and alternative splicing vary at diverse genes, reinforcing the complex multifactorial basis of aging. Through gene co-expression network analysis, we identify nine modules that exhibit gain of connectivity in the aged brain and uncovered a hub gene, PGLS, underlying brain aging. We further confirm the functional significance of PGLS in mice at the gene transcription, molecular, and behavioral levels.

Conclusions

Taken together, our study provides comprehensive transcriptomes on multiple brain regions in non-human primates and provides novel insights into the molecular mechanism of healthy brain aging.

Genome Biology, 2019, 20(1)

随着老龄化社会的发展，大脑衰老成为大家日益关系的话题。大脑衰老会带来记忆力减退，认知能力下降，并且与很多神经退行性疾病密切相关。大脑衰老是一个复杂的过程，它依赖于多个脑区的精确调控，而以往的研究通常集中于少数脑区。我们缺乏一个涵盖多个脑区的转录图谱来解析大脑衰老背后的分子机制。

吴东东研究团队基于大规模转录组数据分析发现，随着年龄的增长，皮质内脑区之间的表达连接性以及皮质内左右脑半球之间的表达连接性都发生了明显的下降。在各个脑区中，基因表达和选择性剪接通过不同的机制来调控大脑衰老，而不同脑区之间老化的分子机制大同小异。通过对老年猕猴的转录组数据基因共表达网络分析，研究人员发现了九个在老年猴中表现出连接性增强的模块，并解析出一个网络关键驱动基因 *PGLS*，在老年猴中表达上调，可能对大脑衰老有重要作用。通过在小鼠体内过表达 *PGLS*, 发现 *PGLS* 过表达导致小鼠出现衰老的表型，例如认知能力下降，运动能力下降和厌食等等。 进一步的生物学实验也证明 *PGLS* 过表达导致突触的丢失和细胞的凋亡。因此，研究推断 *PGLS* 很可能是大脑衰老的一个新的标记基因。

研究成果发表在 ***Genome Biology*** 上。

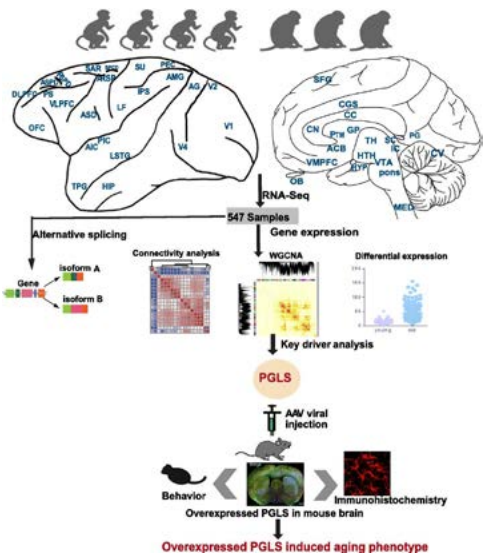


Fig. 1 Schematic view of this study

Genome Biology

研究方向三： 遗传、发育与进化

代表性成果五

揭示爬行动物卵生和胎生繁殖模式进化的遗传机制

Genomic and transcriptomic investigations of the evolutionary transition from oviparity to viviparity

Wei Gao, Yan-Bo Sun, Wei-Wei Zhou, Zi-Jun Xiong, Luonan Chen, View ORCID ProfileHong Li, Ting-Ting Fu, Kai Xu, Wei Xu, Li Ma, Yi-Jing Chen, Xue-Yan Xiang, Long Zhou, Tao Zeng, Si Zhang, Jie-Qiong Jin, Hong-Man Chen, Guojie Zhang, David M. Hillis, Xiang Ji, Ya-Ping Zhang, and Jing Che

Abstract

Viviparous (live-bearing) vertebrates have evolved repeatedly within otherwise oviparous (egg-laying) clades. Over two-thirds of these changes in vertebrate reproductive parity mode happened in squamate reptiles, where the transition has happened between 98 and 129 times. The transition from oviparity to viviparity requires numerous physiological, morphological, and immunological changes to the female reproductive tract, including eggshell reduction, delayed oviposition, placental development for supply of water and nutrition to the embryo by the mother, enhanced gas exchange, and suppression of maternal immune rejection of the embryo. We performed genomic and transcriptomic analyses of a closely related oviparous–viviparous pair of lizards (Phrynocephalus przewalskii and Phrynocephalus vlangalii) to examine these transitions. Expression patterns of maternal oviduct through reproductive development of the egg and embryo differ markedly between the two species. We found changes in expression patterns of appropriate genes that account for each of the major aspects of the oviparity to viviparity transition. In addition, we compared the gene sequences in transcriptomes of four oviparous–viviparous pairs of lizards in different genera (Phrynocephalus, Eremias, Scincella, and Sphenomorphus) to look for possible gene convergence at the sequence level. We discovered low levels of convergence in both amino acid replacement and evolutionary rate shift. This suggests that most of the changes that produce the oviparity–viviparity transition are changes in gene expression, so occasional reversals to oviparity from viviparity may not be as difficult to achieve as has been previously suggested.

PNAS, 2019, 116(9):3646-3655

脊椎动物繁殖模式主要分为两种：卵生（oviparity）和胎生（viviparity）。有鳞类爬行动物（包括蜥蜴、蛇和蚓蜥）约有 20% 的胎生物种，为研究胎生繁殖模式的进化提供了一个重要的模型。

车静研究团队挑选了沙蜥属物种作为研究对象探讨胎生形成的分子机制。生活在青藏高原地区的青海沙蜥（*Phrynocephalus vlangalii*）进化出了典型的胎生繁殖模式，而低海拔地区荒漠沙蜥（*P. przewalskii*）等则具有卵生繁殖模式。

在建立两种沙蜥室内繁殖体系及明确物种不同繁殖时期性状对比的基础上，研究人员成功获得两物种主要繁殖差异时期输卵管及子宫转录组样品收集。在成功解析了青海沙蜥和荒漠沙蜥全基因组数据的基础上，构建了两物种不同时期体输卵管 / 子宫组织的基因表达谱。通过基因的进化分析和表达分析，鉴定出了控制诸如卵壳退化、延迟产卵等一系列性状的关键候选基因 / 通路。此外，通过与有鳞类中其它胎生物种的比较研究，从序列和表达调控两个层面对胎生进化的遗传机制及其相对贡献进行了分析。

研究成果发表在 ***Proceedings of the National Academy of Sciences of the United States of America***。

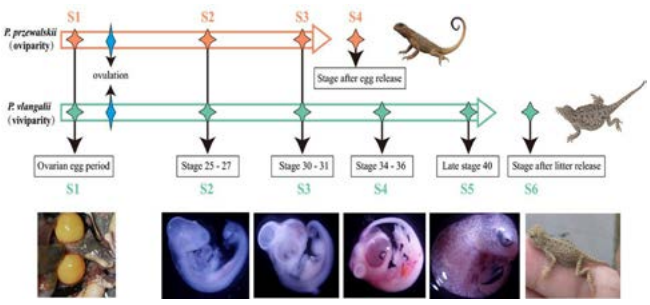


图 1. 卵壳腺退化相关基因的表达模式。

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。至今已主持项目 40 余项，发表论文 160 余篇，其中 SCI 论文 100 余篇，获得国家授权专利 20 项，云南省省级奖励 6 项。

重要成果及产出：

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2. **Jiang WS**[1], **Guo YC**[1], **Yang KF,** Shi Q*, **Yang JX***. 2019. Insights into body size evolution: a comparative transcriptome study on three species of Asian Sisoridae catfish. International Journal of Molecular Sciences, 20(944): 1-23.
3. **Jiang WS**[1], Lv YY[1], Cheng L[1], **Yang KF**, Bian C, **Wang XA**, Li YP, **Pan XF**, You XX, **Zhang YW**, Yang JL, Li J, Zhang XH, **Liu SW**, **Sun C**, **Yang JX***, Shi Q*. 2019. Whole genome sequencing of the giant devil catfish, Bagarius yarrelli. Genome Biology and Evolution, 11(8): 2071-2077.
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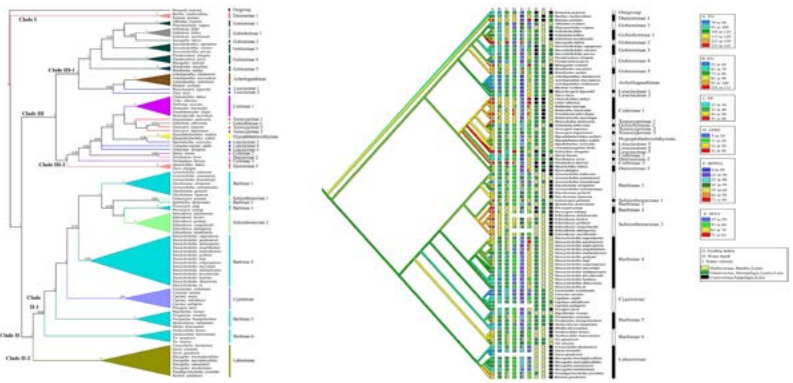
6. 张春光、**杨君兴**、赵亚辉、**潘晓赋**.2019. 金沙江流域鱼类 . 科学出版社 .
7. **王晓爱，潘晓赋，杨君兴，杨坤凤，刘倩** . 一种犀角金线鲃心脏细胞系的构建方法 . 专利号：201510864325.9
8. **潘晓赋，王晓爱，杨君兴，刘倩** . 一种安水金线鲃脾脏细胞系的构建方法 . 专利号：201510860377.9
9. **王晓爱，潘晓赋，杨君兴，**范伟，**刘倩** . 一种大理裂腹鱼肾脏细胞系的构建方法 . 专利号：201610976570.3

1. 鲤科鱼类肌间刺演化

肌间刺广泛存在于鲤科鱼类中，因其小、多、尖、硬而严重影响了鱼肉品质及其经济价值，而对于肌间刺的成因及其演化机制尚不清楚。我们从系统进化的角度出发，首次利用 592 个鲤科鱼类样本探索肌间刺的系统演化。采用 X 光拍摄法及传统解剖法，确定鲤科鱼类肌间刺数量为 73-169，肌间刺类型分为髓弓小骨和脉弓小骨两种，大部分的肌间刺分布在臀鳍第一鳍担骨之后的区域，这个区域可能会成为未来育种的目标区域。同时，肌间刺与脊椎骨数量呈正相关，因此，可以通过脊椎骨数量预测肌间刺数量。基于肌间刺构建的系统发育关系中，虽然有些分支显示肌间刺数量变化与一些物种系统地位的变化具有一定的相关性，但总体来看，鲤科鱼类肌间刺演化方向是多变的，因此，鲤科鱼类肌间刺数量和类型的演变可能反应了其系统发育的历史，但也是多种环境因素共同作用的结果。



2. 鱼类体型大小的演化（以鮡科鱼类为例）

体型大小作为物种的重要特征之一，一直存在一个基本生物学问题，即各个物种如何进化出相应的体型。通过对鮡科鱼类中亲缘关系近、但体型差异距大的三个物种（体型巨大的巨鲇、体型中等的大斑纹胸鮡和穗缘异齿鳅）的转录组进行比较，每个物种大约注释出编码蛋白基因 17000 个，其中 9509 个为置信度较高的同源基因。巨鲇各组织均上调表达的基因主要富集于核糖体生物合成通路。此外，差异表达基因和正选择基因揭示该物种在糖酵解 / 丙酮酸代谢、细胞周期通路上得到强化。通过多重比较分析和基因功能扫描，发现 20 个体型相关候选基因（主要包含 2 个生长模块，AKT3/SH2B1 和 PKM2A 模块），这些基因可能在巨鲇体型形成中起着至关重要的作用。该研究为体型大小进化提供了新的视角。

3. 云南珍稀特有鱼类的人工繁殖、养殖推广和野外种群复壮

目前，珍稀鱼类保育基地饲养有土著鱼类 60 余种，50 余万尾，无重大鱼病出现。单位养殖水体的养殖密度逐年提高。对西畴、曲靖、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。

2019 年度在昆明晋宁古滇艺码头放流滇池金线 12 万余尾，牛栏江放流滇池金线 4 万尾，短须裂腹鱼 2 万尾，金沙鲈鲤 2 万尾，云南光唇鱼 2 万尾。

Phylogenetics and Biogeography

Dr. 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. Till now, total of 160 papers have been published which more than 100 of them are SCI papers, and 6 books and 20 national invention patent have been published.

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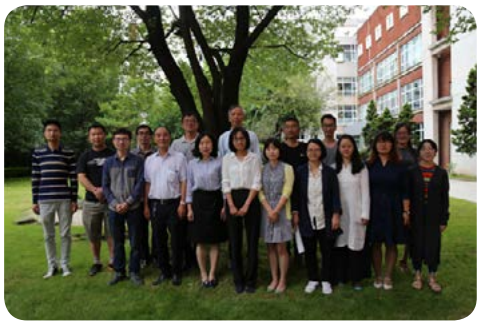

1. Evolution of the intermuscular bones in the Cyprinidae (Pisces) from a phylogenetic perspective

Intermuscular bones (IBs) are widely present in morphologically generalized teleost fishes and are commonly found in the Cyprinidae. Intermuscular bones are small, hard spicules of bone that are formed by ossification in the myosepta between neighboring myomeres. Why fish have IBs, and whether there is any evolutionary pattern to their occurrence, has been poorly understood. However, the presence of IBs does substantially affect the meat quality and commercial values of many cyprinid fishes in aquaculture. In this study, we sampled 592 individuals of cyprinid fishes to systematically investigate the evolution of IBs from a phylogenetic point of view. We found that the total number of IBs in the Cyprinidae ranged from 73 to 169, and we clarified that only two categories of IBs (epineural and epipleural) were present in all examined cyprinids. Most of the IBs were distributed in the posterior region of the fish, which might be an optimal target for selecting fewer IB strains in aquaculture. There was a positive correlation between IBs and the number of vertebrae, thus making it possible to predict the approximate number of IBs by counting the number of vertebrae. Although the IBs displayed some correlation with phylogenetic relationships in some lineages and to ecological factors such as diet (especially carnivore), in an overall view the variations of IBs in cyprinids were extremely diverse. The number and patterns of IBs in these fishes may reflect their phylogenetic history, but have been shaped by multiple environment factors.

2. Insights into Body Size Evolution: A Comparative Transcriptome Study on Three Species of Asian Sisoridae Catfish

Body size is one of the most important attributes of a species, but the basic question of why and how each species reaches a different “right size” is still largely unknown. Herein, three phylogenetically closely related catfishes from Sisoridae, including one extraordinarily large-sized *Bagarius yarrelli* and two average-sized *Glyptothorax macromaculatus* and *Oreoglanis setiger*, were comparatively studied using RNA-Seq. Approximately 17,000 protein-coding genes were annotated for each of the three fishes, and 9509 genes were identified as high-confidence orthologous gene pairs. Comparative expressions uncovered a similar functional cluster about ribosome biogenesis was enriched in different tissues of the upregulated genes of Bagarius yarrelli. Moreover, differentially expressed genes and positively selected genes revealed that the glycolysis/pyruvate metabolism and cell cycle pathways have also greatly enhanced in this large-sized species. In total, 20 size-related candidate genes (including two growth modulators: the serine/threonine-protein kinases 3 (AKT3) and adaptor protein 1 (SH2B1), and a crucial pyruvate kinase (PKM2A)) were identified by multiplying comparative analyses along with gene functional screening, which would play major roles in enabling the large body size associated with Bagarius yarrelli and provide new insights into body size evolution. In conjunction with field observations and morphological comparisons, we hypothesize that habitat preferences promote size divergence of sisorids.

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

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 0.2 million individuals were released in wild to rebuilt and restore the wild population of these fishes.

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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：

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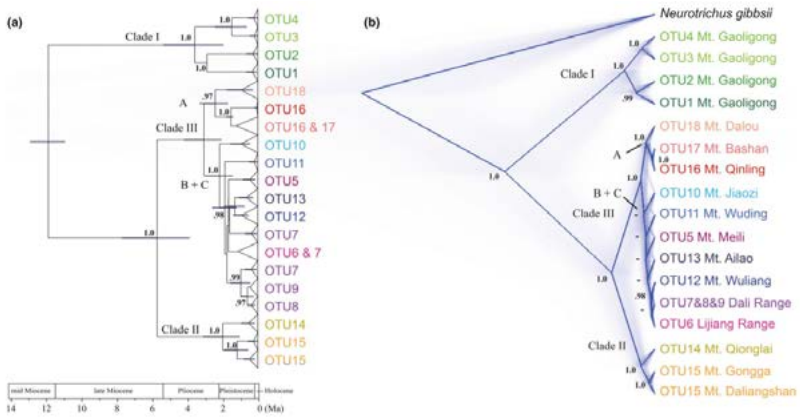
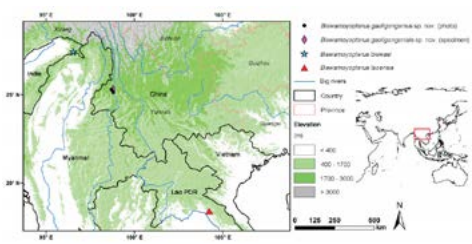
1. 西南山地“空岛”生态 - 环境保守性与地形复杂性对长尾鼩分化的影响

生物多样性热点地区丰富的多样性与特有性形成的驱动因子还不清楚，特别是栖息于高山亚高山的物种，为检验地形地貌与气候因子在多大程度上影响高山物种的分化与扩散，通过测定高山亚高山物种 - 长尾鼩全域范围内 113 个样品的 1 个线粒体和 6 个核基因序列，进行系统发育地理和种群动态分析，评估了系统发育关系与分歧时间、种群遗传结构和物种界定，检验了潜在的基因流，并预测了现今、末次盛冰期、末次间冰期潜在分布区。结果显示：长尾鼩至少可划分为 17 个分隔在不同山系的分类单元，低山和大型河流是其扩散的障碍，但末次间冰期的适宜性气候仅对少数几个点有影响。因此，西南山地“空岛”复杂的地形地貌通过生态 - 环境的稳定性和地理的片断化，促进了扩散力较低的物种独特的分化，山地环境发挥着对气候变化的缓冲作用，为长尾鼩提供了自晚中新世旱期以来持续适宜的生境，狭谷阻碍着基因交流，而山体则提供促进物种扩散的垫脚石。

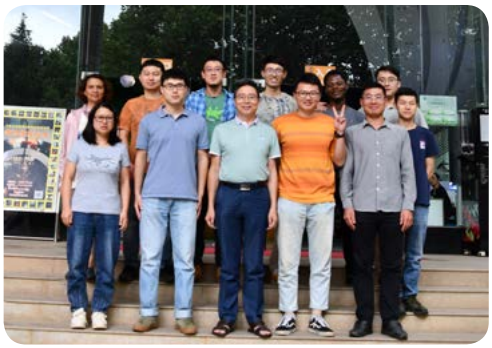


2. 高黎贡山发现世界最稀有的哺乳动物之一比氏鼯鼠属新物种

发现并命名了高黎贡比氏鼯鼠（*Biswamoyopterus gaoligongensis*），并进行了详细形态描记，填补了印度比氏鼯鼠和老挝比氏鼯鼠分布区之间宽达 1250 km 的空隙，暗示比氏鼯鼠的分布范围远比之前学界认为的广阔，为比氏鼯鼠这一世界珍稀兽类的研究和保护提供了新的认识。该研究结果被国内外多家媒体报道。



Mammal Ecology and Evolution



Prof. Xuelong Jiang, Professor, The laboratory is mainly interested in specimen-based investigations of biodiversity inventory, taxonomy and systematics, phylogenetics and phylogeography of small mammals with a special focus in the 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. Diversity and distribution patterns of non-volant small mammals along different elevation gradients on Mt. Kenya, Kenya

The distribution of small mammals in mountainous environments across different elevations can provide important information on the effects of climate change on the dispersal of species. However, few studies conducted on Afromontane ecosystems have compared the altitudinal patterns of small mammal diversity. We investigated the species diversity and abundance of non-volant small mammals (hereafter 'small mammals') on Mt. Kenya, the second tallest mountain in Africa, using a standard sampling scheme. Nine sampling transects were established at intervals of 200 m on the eastern (Chogoria) and western (Sirimon) slopes. A total of 1905 individuals representing 25 species of small mammals were trapped after 12240 trap-nights. Abundance was highest at mid-elevations on both slopes. However, species richness and their distribution patterns differed between the two slopes. There were more species were recorded on Chogoria (24) than on Sirimon (17). On Chogoria, species richness was higher at mid-high elevations, with a peak at mid-elevation (2800 m a.s.l.), whereas species richness showed little variationon the Sirimon slope. These results indicate that patterns of species diversity can differ between slopes on the samemountain. In addition, we extensively reviewed literature on Mt. Kenya's mammals and compiled a comprehensive checklist of 76 mammalian species. However, additional research is required to improve our understanding of small mammal diversity in mountain habitats in Africa.

2. Habitat suitability and connectivity inform a co-management policy of protected area network for Asian elephants in China

Enlarging protected area networks (PANs) is critical to ensure the long-term population viability of Asian elephants (Elephas maximus), which are threatened by habitat loss and fragmentation. Strict policies of PAN enlargement that focus on wildlife conservation have failed largely due to difficulties in encouraging stakeholder participation and meeting the elephant habitat requirement. A co-management policy that promotes sustainable resource use, wildlife conservation, and stakeholder participation may have greater feasibility than the strict policies in a developing world. Here, we identified the suitable habitat of elephants using maximum entropy models and examined whether habitat suitability is indirectly associated with local economic development in human-dominated landscapes. We found that (1) the suitable habitat was mainly in areas of forest matrix (50% natural forest cover) with multiple land-use practices rather than relatively intact forest and near communities (mean distance two km) and (2) habitat suitability was negatively associated with local economic development (rP ¼ -0.37, P ¼ 0.04). From the standpoint of elephant habitat and its socio-economic background, our results indicate that co-management will be more effective than the currently strict approaches of enlarging PAN. Additionally, our results provide on-ground information for elephant corridor design in southern China.

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鸟类学研究组

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

重要成果及产出：

1. **Dong F**, Hung CM, **Yang XJ***. Secondary contact after allopatric divergence explains avian speciation and high species diversity in the Himalayan-Hengduan Mountains. Molecular Phylogenetics and Evolution 143 (2020) 106671.
2. **Wu F**, Kong DJ, **Shan PF**, **Wang J**, **Kungu GN**, Lu GY, **Yang XJ***. Ongoing green peafowl protection in China.Zoological Research 40(6): 588-590, 2019.
3. Bi D, Ding HW, Wang QQ, Jiang L, Lu WK, Zhu R, Zeng JH, Zhou SB, **Yang XJ***, Kan XZ*. Two new mitogenomes of Picidae (Aves, Piciformes): Sequence, structure and phylogenetic analy. International Journal of Biological Macromolecules 133 (2019) 683–692.
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1. 正在进行的中国绿孔雀（Pavo muticus）保护

作为主要的绿色的孔雀在中国研究团队，我们于 1990 年代及 2014-2018 年进行了两次全面的绿孔雀调查，了解绿孔雀的生存现状。

除了基础设施，栖息地改变、毒杀和偷猎是影响中国绿孔雀生存的主要威胁。我们在 2018 年的调查显示，超过 65% 的绿孔雀种群分布在中国的保护区之外，这使得它们更容易受到上述威胁。然而，中国的生态文明计划为我国的绿孔雀及其他濒危物种和生态系统的保护带来了新的希望。2012 年底以来，环境保护成为中国政府工作的核心内容。为了实现生态文明，中国政府采取了生态红线（ERL）战略。ERL 是指对生态功能或生态敏感性的关键领域进行严格控制和依法划定的边界。这些 ERL 区域现在正式受中国 2015 年新修订的环境保护法的规定保护。值得庆幸的是，云南省人民政府于 2018 年 6 月 29 日正式划定并公布的云南省 ERL 区域，覆盖了我国绿孔雀种群的全部分布范围。保护区内和保护区外的绿孔雀栖息地。

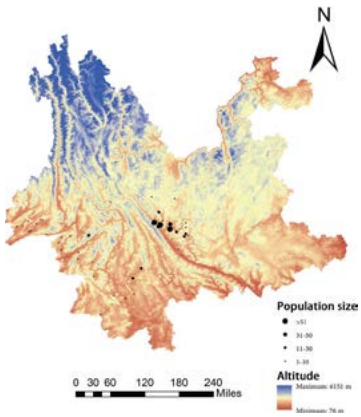

图 中国云南绿孔雀分布及种群大小

2. 异域辐散后的二次接触解释了喜马拉雅—横断山脉鸟类的物种形成和高物种多样性

物种形成的地理环境对理解物种形成和群落聚集很重要。然而，喜马拉雅 - 横断山脉 (HHMs) 是一个全球生物多样性热点地区，其主要的物种形成模式仍然未知。在这里，我们用四对目前同时出现在 HHMs 中的姐妹或密切相关的鸟类物种来研究地理和物种形成的作用。虽然基于 9 至 11 个基因的多位点网络分析揭示了这些物种之间的深度分裂，但基于个别位点的几个等位基因网络提示了系统发育旁枝暗示了最近的分化历史。在这些物种对的接触区进行了广泛的采样后，基于聚结的近似贝叶斯计算方法在它们的差异期间不支持基因流动，并且与异地物种形成模型相一致。我们进一步估算了这四对物种在中更新世和晚更新世时期的差异时间，其特征是冰川变化幅度的增大。我们发现它们的散度时间与当前同域水平之间存在正相关关系，这支持了异域物种形成后的二次接触情况。更新世冰期 - 间冰期旋回可能导致了最初的地理种群隔离；生态分化或择偶可能进一步加速其在二次接触过程中的分化，促进其在山地景观中的形成和物种积累。我们的发现揭示了 HHMs 中地理隔离在物种形成中的关键作用，并阐明了这一生物多样性热点是如何聚集众多物种的。

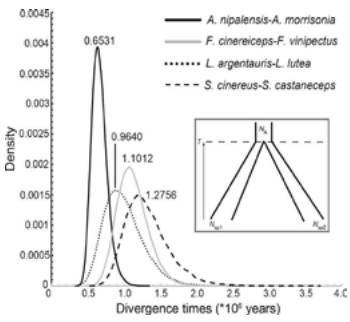

图 后验概率密度散度时间估计 *BEAST 分析。给出了各近缘种对发散时间的中值。

Ornithology

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1. Ongoing green peafowl protection in China

As the main green peafowl research team in China (Ornithology Group of the Kunming Institute of Zoology, Chinese Academy of Sciences), we have conducted several green peafowl surveys, including two comprehensive surveys in the 1990s (Wen et al., 1995) and 2014–2018 (Kong et al., 2018), to clarify the status and trends of this species in China.

In addition to infrastructure projects, habitat conversion, poisoning, and poaching are also major threats affecting the survival of the green peafowl in China (Kong et al., 2018). Our surveys in 2018 showed that over 65% of the green peafowl population occurs outside protected reserves in China, making this species even more vulnerable to the aforementioned threats.

However, China's ambitious Ecological Civilization Plan (UNEP, 2016; Xiao & Zhao, 2017) brings new hope for the conservation of the green peafowl and the other threatened species and ecosystems in the country. Since late 2012, environmental protection has become the core element in Chinese governmental work.To achieve an ecological civilization, the Chinese government has adopted an Ecological Redline (ERL) strategy. The ERL refers to the strictly controlled and legally drawn boundaries for key areas of ecological functions or ecological sensitivity (UNEP, 2016). These ERL areas are now formally protected by provisions within China's newly revised Environmental Protection Law of 2015 (Bai et al., 2016). Fortunately, the ERL zones in Yunnan Province, demarcated and formally announced on 29 June 2018 (The People's Government of Yunnan Province, 2018), cover the entire distribution range of the green peafowl population in China. Most green peafowl habitats inside and outside protected reserves, including those within the RRUD, are now incorporated into the ERL of Yunnan.

2. Secondary contact after allopatric divergence explains avian speciation and high species diversity in the Himalayan-Hengduan Mountains

The geographical context of speciation is important for understanding speciation and community assembly. However, the predominant mode of speciation in the Himalayan-Hengduan Mountains (HHMs), a global biodiversity hotspot, remains unknown. Here, we examined the role of geography in speciation using four pairs of sister or closely related avian species that currently co-occur in the HHMs. While multilocus network analyses based on nine to eleven genes revealed deep splits between these species, several allelic networks based on individual loci suggested phylogenetic paraphyly implying a recent history of divergence. Following extensive sampling in the contact zones of these species pairs, the coalescence-based approximate Bayesian computation approach supported no gene flow during their divergence and was consistent with an allopatric speciation model. We further estimated the divergence times of the four species pairs during the middle and late Pleistocene, which were characterized by increased amplitudes of glacial variability. We found a positive relationship between their divergence times and current sympatry levels, supporting a scenario of secondary contact following allopatric speciation. The Pleistocene glacial-interglacial cycles may have led to the initial geographic population isolation; ecological divergence or mate choice might further accelerate their differentiation during secondary contact, facilitating their speciation and species accumulation in the mountainous landscape. Our findings reveal the critical role of geographic isolation in speciation in the HHMs and shed light on how this biodiversity hotspot aggregates numerous species.

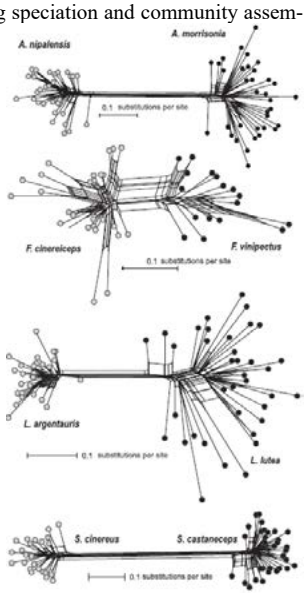

Fig. Multilocus networks based on standardized matrices of nuclear genetic distances between closely related species.

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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. **Wang XY**[1], Hua FY, Wang L, Wilcove DS, **Yu DW***. The biodiversity benefit of native forests and mixed-pecies plantations over monoculture plantations. ***Diversity and Distributions***, 2019, 00:1–15, IF4.93.
2. **Ji YQ**[1], Huotari T[1], Roslin T, Schmidt NM, **Wang JX, Yu DW*,** Ovaskainen O*. SPIKEPIPE: A metagenomic pipeline for the accurate quantification of eukaryotic species occurrences and intraspecific abundance change using DNA barcodes or mitogenomes. ***Molecular Ecology Resources***, 2019, 00:1–12, IF7.049.
3. Peel N[1], Dicks LV, Clark MD, Heavens D, Percival-Alwyn L, Cooper C, Davies RG, Richard M. Leggett RM, **Yu DW***. Semi-quantitative characterisation of mixed pollen samples using MinION sequencing and Reverse Metagenomics (RevMet). ***Methods in Ecology and Evolution***, 2019, 10:1690–1701, IF7.099.
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6. Boza G[1]*, Worsley SF, **Yu DW**[1], Scheuring I[1]*. Efficient assembly and long-term stability of defensive microbiomes via private resources and community bistability. ***PLOS Computational Biology***, 2019, doi.org/10.1371/journal.pcbi.1007109, IF4.428.

1. 原生林和混合种植林的生物多样性优于单一种植林

我们选取四川中南部地区的退耕还林为研究目标，讨论不同的退耕还林类型对生物多样性的影响。本研究中主要选取了 4 种退耕还林种植林：3 种单一种植林（竹林，桉树林和柳杉林）和 1 种混合种植林（由 2 种以上的单一种植林树种简单混合种植），和 2 种参考对照的生境类型：原生林和农田。首次运用 DNA 条形码、高通量条形码（Metabarcoding）等技术对退耕还林不同种植搭配类型中昆虫的 alpha 和 beta 多样性监测和分析，同时与鸟类多样性监测结果进行了比对，得出了一致的结论：退耕还林时应优先进行自然林的恢复，生物多样性将会得到更好的恢复；其次是将两种以上的树种混合种植，也能获得较高的生物多样性。我们的结果从生物多样性保护角度为退耕还林提出了科学依据，对退耕还林的实施具有较高的参考价值。

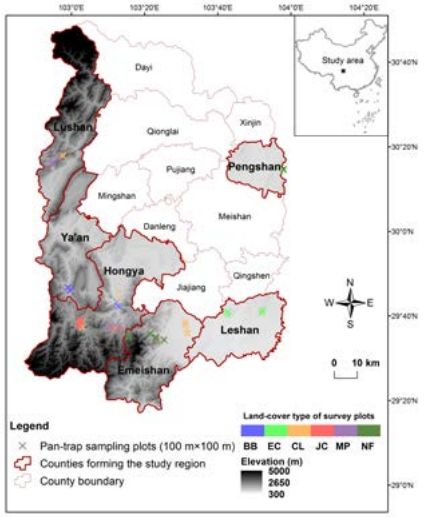

图 1. 研究区位于四川省中南部

2. SPIKEPIPE：用于准确定量真核物种的宏基因组方法 -- 使用 DNA 条形码或线粒体基因组测量种内丰度变化

真核生物丰度的准确定量仍然是群落生态学和环境生物监测的关键挑战。本项目为北极格陵兰岛萨肯博格地区建立了一个含有 308 个节肢动物物种的线粒体基因组参考数据库，对 492 份时间尺度的生态学样本进行了宏基因组测序（其中部分样本经过重复测序），得到总共 728 份宏基因组数据。本项目完善改进了线粒体宏基因组学，为准确定量真核生物的群落组成和生物量建立了一个新的基于 DNA 的方法 ——SPIKEPIPE，这种方法提供了成本效益和可靠的真核生物群落的定量。

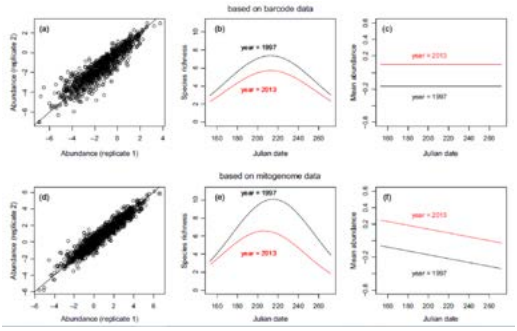

图 2. 1997 年和 2013 年利用黄色陷阱盘采集的 Zackenberg 地区节肢动物标本，用 SPIKEPIPE 方法进行处理

Ecology, Conservation, & Environment Center(ECEC)

Dr. Douglas W. Yu. Yu's research covers two fields, (1) game-theoretical models of symbiosis, and (2) rapid biodiversity assessment using genomics. In the first area, we have developed new genomics methods for biodiversity rapid assessment. In the second, we have been elucidating the mechanisms stabilizing cooperation among species, using in fig-wasp and ant-plant mutualisms as experimental models. Yu has 90 publications, including in Nature, Science, PNAS, PLoS Biology, Ecology Letters, Ecological Monographs, Ecology.
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1. The biodiversity benefit of native forests and mixed-species plantations over monoculture plantations

We sampled arthropod communities using pan traps in the land cover types concerned under the GFGP. These land use types include croplands, native forests and the dominant GFGP reforest- ation outcomes: monoculture and mixed-species plantations. We used COI-amplicon sequencing ("metabarcoding") of the arthropod samples to quantify and assess the arthropod community profiles associated with each land cover type. We found that native forests support the highest overall levels of arthropod species diversity, followed by mixed-species plantations, followed by bamboo and other monocultures. Also, the arthropod community in native forests shares more species with mixed-species plantations than it does with any of the monocultures. Together, these results broadly corroborate our previous conclusions on birds and bees but show a higher arthropod biodiversity value of mixed-species plantations than previously indicated by bees alone.

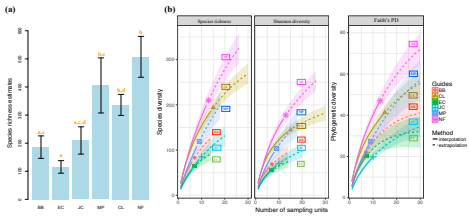

Figure 3. Species richness estimates across land-cover type.

2. SPIKEPIPE: A metagenomic pipeline for the accurate quantification of eukaryotic species occurrences an intraspecific abundance change using DNA barcodes or mitogenomes

The accurate quantification of eukaryotic species abundances from bulk samples remains a key challenge for community ecology and environmental biomonitoring. We resolve this challenge by combining shotgun sequencing, mapping to reference DNA barcodes or to mitogenomes, and three correction factors: (a) a percent-coverage threshold to filter out false positives, (b) an internal-standard DNA spike-in to correct for stochasticity during sequencing, and (c) technical replicates to correct for stochasticity across sequencing runs. The SPIKEPIPE pipeline achieves a strikingly high accuracy of intraspecific abundance estimates (in terms of DNA mass) from samples of known composition (mapping to barcodes R2 = .93, mitogenomes R2 = .95) and a high repeatability across environmental-sample replicates (barcodes R2 = .94, mitogenomes R2 = .93). As proof of concept, we sequence arthropod samples from the High Arctic, systematically collected over 17 years, detecting changes in species richness, species-specific abundances, and phenology. SPIKEPIPE provides cost-efficient and reliable quantification of eukaryotic communities.

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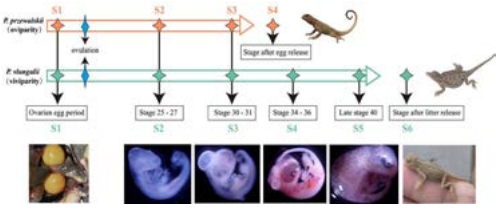
两栖爬行类多样性与进化

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. **Gao Wei[1], Sun YB[1], Zhou WW**[1], Xiong ZJ[1], Chen LN, Li H, **Fu TT, Xu K, Xu W,** Ma L, Chen YJ, Xiang XY, Zhou L, Zeng T, Zhang S, **Jin JQ, Chen HM,** Zhang GJ, Hillis DM*, Ji X*, Zhang YP*, **Che J***. 2019. Genomic and transcriptomic investigations of the evolutionary transition from oviparity to viviparity. ***Proc Natl Acad Sci USA***. 116(9): 3646–3655.
2. Yuan Zhiyong[1], **Zhang BL**[1], Raxworthy CJ, Weisrock DW, Hime PM, Jin JQ, Lemmon EM, Lemmon AR, Holland SD, Kortyna ML, **Zhou WW**, Peng MS, . **Che J***, Prendini E. 2019. Natatanuran frogs used the Indian Plate to step-stone disperse and radiate across the Indian Ocean. ***National Science Review***. 6(1): 240–252.
3. Wang Kai[1], **Che J***, Lin SM, Deepak V, Aniruddha DR, Jiang K, **Jin JQ, Chen HM**, Siler CD. 2019. Multilocus phylogeny and revised classification for mountain dragons of the genus *Japalura s.l.* (Reptilia: Agamidae: Draconinae) from Asia. ***Zoological Journal of the Linnean Society***. 185(1): 246–267.
4. **Wu YH**[1], Suwannapoom C[1], Poyarkov, Jr. NA, Paawangkhanant P, **Xu K, Jin JQ**, Murphy RW, **Che J***. 2019. A new species of the genus *Xenophrys* (Anura:Megophryidae) from northern Thailand. ***Zoological Research.*** 40 (6): 564–574.
5. **Wu YH**[1], Suwannapoom C[1], **Xu K, Chen JM, Jin JQ, Chen HM,** Murphy RW, **Che J***. 2019. A new species of the genus *Raorchestes* (Anura: Rhacophoridae) from Yunnan Province, China ***Zoological Research***. 40 (6): 558–563.

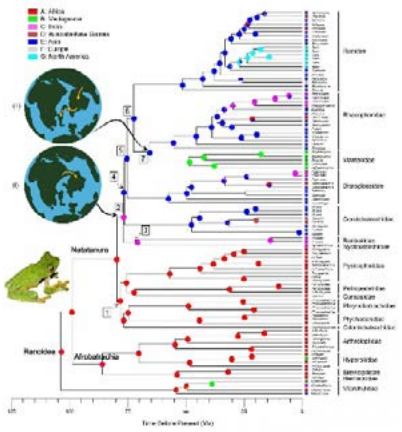
1. 爬行动物卵生和胎生繁殖模式进化的遗传机制



脊椎动物繁殖模式主要分为两种：卵生（oviparity）和胎生（viviparity）。有鳞类爬行动物（包括蜥蜴、蛇和蚓蜥）约有 20% 的胎生物种，为研究胎生繁殖模式的进化提供了一个重要的模型。课题组挑选了沙蜥属物种作为研究对象探讨胎生形成的分子机制。生活在青藏高原地区的青海沙蜥（*Phrynocephalus vlangalii*）进化出了典型的胎生繁殖模式，而低海拔地区荒漠沙蜥（*P. przewalskii*）等则具有卵生繁殖模式。

在建立两种沙蜥室内繁殖体系及明确物种不同繁殖时期性状对比的基础上，我们成功获得两物种主要繁殖差异时期输卵管及子宫转录组样品收集。在成功解析了青海沙蜥和荒漠沙蜥全基因组数据的基础上，构建了两物种不同时期体输卵管 / 子宫组织的基因表达谱。通过基因的进化分析和表达分析，鉴定出了控制诸如卵壳退化、延迟产卵等一系列性状的关键候选基因 / 通路。此外，通过与有鳞类中其它胎生物种的比较研究，从序列和表达调控两个层面对胎生进化的遗传机制及其相对贡献进行了分析。**(Gao, et al. 2019 *PNAS*)**

2. 蛙超科起源及扩散进程



生物的地理分布与地球演化历史紧密相关。冈瓦纳古陆的解体以及后期各大陆之间的重组如何影响生物的迁移和扩散，如何重塑当今物种全球的地理分布格局，是地质学家和生物学家长期关注的科学问题。从白垩纪末期至第三纪时期，印度板块和南极 – 澳大利亚 – 新几内亚板块对生物在冈瓦纳古陆和劳亚古陆间的交流起到了关键性作用，但是这两个板块的地理位置长期存在争议，科学家提出了“方舟”和“踏脚石”两个假说。

两栖类是进行生物地理学研究的理想对象。我们以各大陆蛙超科主要代表类群物种为研究对象，构建了 21 个科的系统发育关系，重建了该类群在全球尺度的时空演化树。结果显示蛙超科起源于非洲，通过印度板块扩散到了亚洲，随后（经历了一次从亚洲通过印度板块至马达加斯加的扩散事件，演化出了现今马达加斯加主要的树栖型蛙类。因此，中生代晚期印度板块从冈瓦纳古陆分离后，在亚洲、非洲和马达加斯加之间充当着“脚踏板”的角色，促进了各大陆间生物的扩散与交流。我们的研究推翻了传统观点认为的印度板块在向北漂移过程中只扮演着一个孤立的“方舟”角色的假说。**(Yuan, et al. 2019 *National Science Review*)**

Herpetological Diversity and Evolution

Dr. 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. Molecular Mechanism of Evolutionary Transition from Egg-laying to Live Birth in Reptiles

Vertebrates have two reproductive strategies: viviparity and oviparity. Viviparous species provide an environment for embryonic development and protect the embryo from environmental threats. It is an important basic biological question of how oviparity evolved to viviparity.

We sequenced the genomes of viviparous *Phrynocephalus vlangalii* and oviparous *P. przewalskii*, and compared the transcriptomes of maternal oviducts through the development of eggs and embryos of both species. We also compared the transcriptomes of three other pairs of closely related oviparous and viviparous species of the genera *Eremias*, *Scincella*, and *Sphenomorphus*, to examine potential sequence convergence associated with viviparity across independent origins of this transition.

The comparative analysis of stage-specific highly expressed genes (HEGs) in Stage 1 (S1), when an eggshell gland is expressed in egg-laying species, suggested a clear mechanism for eggshell degeneration in viviparous species. Most of S1-specific HEGs in *P. przewalskii* (oviparous), which involved in uterine cell differentiation, proliferation and morphogenesis, gland development, were not highly expressed at S1 in viviparous *P. vlangalii*. And genes in estrogen receptor (ESR) pathway which were reported related to shell gland formation highly expressed at S1 in *P. przewalskii*, but reverse in viviparous species.These specific expression pattern changes appeared to be among the changes associated with the loss of eggshell formation in the viviparous species. Differential expression pattern were also found between two species at S3, which is soon before egg-laying in oviparous *P. przewalskii.* Estrogen receptor (ESR1) and other growth factor receptor (GHR and IGF1R) may play an important role in placenta development in viviparous species. Besides, the down-regulation of PTGS2 at S4 and sustained highly expression of ADRB2 may promote the egg retention in viviparous *P. vlangalii*.

At last, four genes (C7, NKTR, NBEAL2, PTX2) were detected that experienced amino acid replacements at same position across four viviparous lizards. And they are all related to immune regulation. But this level was not significantly higher than by chance, which suggests that most of the changes that produce the oviparity–viviparity transition are changes in gene expression. (**Gao, et al. 2019 *PNAS***)

2. Natatanuran frogs used the Indian Plate to step-stone disperse and radiate across the Indian Ocean

The Late Mesozoic breakup of Gondwana triggered major biotic exchanges between Laurasia and Gondwanan landmasses that continue to influence modern distributions of many taxa. Concerning tectonic drifting of the Indian Plate, the traditional view was that this landmass acted as an isolated biotic ferry in the Indian Ocean, carrying Gondwanan biodiversity to Asia in the Early Tertiary; many biogeographic studies have relied on this assumption.

Our study comprehensively rejects this traditional view. Using the near-cosmopolitan distributed Natatanuran frogs, we integrated phylogenomic data, biogeographic reconstruction, and molecular dating methods to resolve the spatiotemporal diversification of ranoid frogs between Laurasia and Gondwana, and examine support for alternative biogeographic hypotheses. Unexpectedly, no biotic exchanges dated between 88 and 55 Ma when the Indian Plate broke away from other Gondwanan landmasses, and ultimately collided with Asia. In contrast, results found two major stepping-stone dispersals via the Indian Plate: 1) from Africa into Asia, and 2) from Asia into Madagascar. This is the first demonstrated case of extant taxa having using the Indian Plate as a stepping stone to disperse between Africa, Asia and Madagascar; the results point to a close biogeographic association between Africa and the Indian Plate. Further, no evidence supported Natatanuran exchanges between Antarctica-Australia-New Guinea and either India or Madagascar before the Eocene, arguing against hypothetical landbridges. In contrast, two lineages appeared to have dispersed independently from Asia to Australia-New Guineaduring the Neogene. This study not only identifies clear routes for these frogs' dispersals around the Indian Ocean, but also provides novel insights into the Earth's geological history. (**Yuan, et al. 2019 *National Science Review***).

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分子进化与基因组多样性研究

张亚平，博士，研究员，中国科学院院士，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，牵头组织的家犬基因组研究国际联盟（Dog10K）于 2019 年发表了 Dog10K 计划白皮书，并联合开发 iDog 数据库；采用古 DNA 的研究方法，揭示了中国南方存在狼的地方性群体以及犬类生殖器传染性肿瘤的起源问题。比较基因组学研究揭示了爬行动物卵生和胎生繁殖模式进化的遗传机制、欧亚大陆和北美洲通过白令海峡大陆桥的不对称生物交换事件；揭示了濒危物种金丝猴的起源和群体历史。在国际权威杂志上发表了 SCI 论文 21 篇，其中 IF>10 的 7 篇，包括 ***PNAS*** (1), ***Nucl Acids Res*** (1), ***Nat Sci Rev*** (3), ***Mol Biol Evol*** (1)，***Cell Res*** (1) 等。

重要成果及产出：

1. Dinerstein E, Vynne C, Sala E, Joshi AR, Fernando S, Lovejoy TE, Mayorga J, Olson D, Asner GP, Baillie JEM, Burgess ND, Burkart K, Noss RF, **Zhang YP**, Baccini A, Birch T, Hahn N, Joppa LN, Wikramanayake E. A Global Deal For Nature: Guiding principles, milestones, and targets. ***Science Advances***, 2019, 5(4). IF13.293
2. **Gao W**[1], **Sun YB**[1], **Zhou WW**[1], **Xiong ZJ**[1], Chen LN, Li H, **Fu TT**, **Xu K**, **Xu W**, Ma L, Chen YJ, Xiang XY, Zhou L, Zeng T, Zhang S, **Jin JQ**, **Chen HM**, **Zhang GJ**, Hillis DM*, Ji X*, **Zhang YP***, **Che J***. Genomic and transcriptomic investigations of the evolutionary transition from oviparity to viviparity. ***PNAS***, 2019, 116(9): 3646-3655. IF10.6
3. Ostrander EA, **Wang GD**, Larson G, vonHoldt BM, Davis BM, Jagannathan V, Hitte C, Wayne RK, **Zhang YP***. Dog10K: An international sequencing effort to advance studies of canine domestication, phenotypes, and health, ***National Science Review***, 2019, 6(4):810–824. IF13.833
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5. **Wang GD**, Larson G, Kidd JM, vonHoldt BM, Ostrander EA*, **Zhang YP***. Dog10K: the International Consortium of Canine Genome Sequencing. ***National Science Review***, 2019, 6(4): 611-613. IF13.833
6. **Wang GD**[1], Shao XJ[1], Bai B[1], Wang JL, Wang XB, Cao X, Liu YH, **Wang X**, **Yin TT**, Zhang SJ, Lu Y, Wang ZC, Wang L, Zhao WM, Zhang B, Ruan J*, **Zhang YP***. Structural variation during dog domestication: insights from gray wolf and dhole genomes. ***National Science Review***, 2019, 6(1): 110-122. IF13.833
7. **Wang X**[1], **Zhou BW**[1], Yang MA[1], **Yin TT**, Chen FL, Ommeh SC, Esmailizadeh A, Turner MM, Poyarkov AD, Savolainen P, **Wang GD***, Fu QM*, **Zhang YP***. Canine transmissible venereal tumor genome reveals ancient introgression from coyotes to pre-contact dogs in North America. ***Cell Research***, 2019, 29(7): 592-595. IF18.448

1. 家犬基因组研究国际联盟发表 Dog10K 计划白皮书

作为家犬基因组研究国际联盟的主要发起人，本研究团队发表了 Dog10K 计划白皮书，综述了当前家犬的研究现状以及研究联盟的计划、目的和意义。联盟计划在 5 年内对 1 万只犬科动物进行基因组高覆盖度测序，并建立一个与人类基因组计划水平相当的资源平台，整合所有研究团队提供的宝贵数据，与北京基因组所联合开发 iDog 数据库并以开放的形式迎接合作。旨在获取世界范围内的犬科动物表型以及地理差异上的遗传多样性信息，揭示家犬的驯化、品种犬育种、行为和表型的遗传机制。同期《***National Science Review***》还发表了 Prospective。

【Ostrander EA et al. 2019 ***National Science Review***, IF= 13.222；
Tang BX et al. 2019 ***Nucleic Acids Research***, IF =10.727;
Wang GD et al. 2019 ***National Science Review***, IF= 13.222 】

2. 家犬肿瘤活化石揭示郊狼到北美土著家犬的古老渐渗

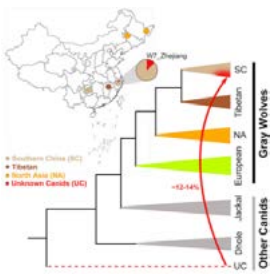
开发了首个犬类生殖器传染性肿瘤（CTVT）专用的基因型检测工具 ttgeno，结合 102 个世界各地的犬科动物的单核苷酸多态（SNPs），获得了可能属于 CTVT founder 的祖先正常多态信息位点。通过系统发育关系和群体遗传结构分析，发现 CTVT 起源于北美土著家犬。此外还发现 CTVT founder 和北美土著家犬具有北美郊狼和北美灰狼的基因流。本研究创新性的将 CTVT 当作活化石来进行群体遗传研究，为家犬迁徙历史和种群间杂交研究提供了新的思路和视角。

【Wang X et al. 2019 ***Cell Research***, IF= 17.848 】

3. 中国南方灰狼为独立支系

采用古 DNA 的研究方法对动物博物馆馆藏样本群体基因组学分析发现中国南方的狼是一个单独的群体，证实了中国南方存在狼的地方性群体。

【Wang GD et al. 2019 iScience】



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 2019, as one of the sponsors of the Dog10K Consortium, we reviewed the current research status and the plan, purpose, and significance of consortium. Then jointly developed iDog. Using the methods of ancient DNA revealed that an Endemic Subpopulation of Gray Wolves in Southern China, and CTVT originated from North American dogs. We also revealed the evolutionary transition from oviparity to viviparity. The above research progresses were published in 21 SCI-indexed papers, including ***PNAS*** **(1),** ***Nucl Acids Res*** **(1),** ***Nat Sci Rev*** **(3),** ***Mol Biol Evol*** **(1),** ***Cell Res*** **(1).**

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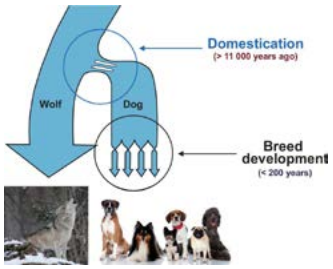
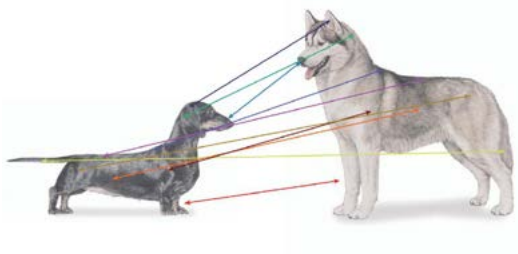
1.Dog10K advance studies of canine domestication, phenotypes and health

As one of the sponsors of the Dog10K Consortium, we reviewed the current research status and the plan, purpose, and significance of consortium. The consortium plans to sequence the genome ~10,000 canines in five years. The diversity of worldwide canine phenotypes and geography will be obtained. At present, a large number of modern breeds, native dogs, and outgroups have been subjected to whole-genome sequencing, and a *de novo* assembly of some canines completed. These unprecedented datasets will help solve some genetic problems such as domestication, breed formation, and behavior and morphological changes in canines. In addition, the consortium will establish a resource platform comparable to the human genome project. Integrated, valuable data will be publicly accessible by all research teams. In this regard, cooperation will be welcome in an open forum. This work will improve our understanding of human and canine health.



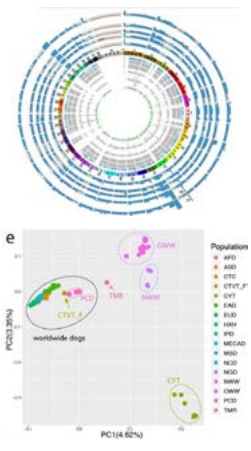


【Ostrander EA et al. 2019 ***National Science Review***, IF= 13.222;
Tang BX et al. 2019 ***Nucleic Acids Research,*** IF =10.727;
Wang GD et al. 2019 ***National Science Review***, IF= 13.222 】

2.CTVT revealed the ancient introgression from coyote to North American indigenous dogs (PCDs)

We developed a transmissible tumor genotyper (ttgeno), Combining 102 worldwide canis SNPs, we found that CTVT founders were more closely related to PCDs than to any other population. This confirms that CTVT originated from North American dogs. Furthermore, gene flows and introgression regions between CTVT founder/ PCDs and North American coyotes and grey wolves were detected. This research not only developed a method for detecting genotypes of CTVT, but it also used CTVT founders to do a population genetics study that provides a new insight into migration and admixture of dogs.

【Wang X et al. 2019 ***Cell Research***, IF= 17.848 】



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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。长期以来一直致力于进化基因组学的研究。目前已经在 *Science*、 *Nature Biotechnology*、*Nature Communications*、 *Nature ecology & evolution*、*Molecular plant* 等重要学术杂志上发表论文 170 余篇，2019 年在国际权威杂志上发表了 SCI 论文 18 篇，其中 IF>10 的有 4 篇，包括 ***Science*** (2), ***Nature ecology & evolution*** (1), ***Molecular plant*** (1) 等。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“国家自然科学奖二等奖”（第一完成人），2017 年获得两项“云南省自然科学奖二等奖”（分别为第一完成人和第二完成人），**2019 年获得“云南省自然科学奖一等奖” （第三完成人）**。

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

重要成果及产出：

1. Chen L[1], Qiu Q[1], Jiang Y[1] , Wang K[1], Lin ZS[1], Li ZP[1], …**Liu GC**, **Liu W**, **Wang B**, **Zeng Y**, **Zhao RP,** Zhang GJ*, Heller R*, **Wang W***: Large-scale ruminant genome sequencing provides insights into their evolution and distinct traits. ***Science*** 2019, **364**(6446).
2. Lin ZS[1], Chen L[1], Chen XQ[1], Zhong Y[1], Yang Y[1], Xia W[1]… Qiu Q*, **Wang W***, Li ZP*: Biological adaptations in the Arctic cervid, the reindeer (Rangifer tarandus). ***Science*** 2019, **364**(6446).
3. **Liu GC**[1], **Chang Z**[1], Chen L[1], **He JW**[1], **Dong ZW**, Yang J, Lu SH**, Zhao RP**, **Wan WT**, Zhang R**, Wang W***, **Li XY***. 2019. Genome size variation in butterflies (Insecta, Lepidotera, Papilionoidea): A thorough phylogenetic comparison. ***Systematic Entomology***. (DOI: 10.1111/syen.12417)
4. **Lu SH**[1], Yang J[1], Dai XL[1], Xie FA , **He JW**, **Dong ZW**, Mao JL, **Liu GC**, **Chang Z**, **Zhao RP**, **Wan WT**, Zhang R, **Wang W*, Li XY***: Chromosomal-level reference genome of Chinese peacock butterfly (*Papilio bianor*) based on third-generation DNA sequencing and Hi-C analysis. ***GigaScience*** 2019, **8**(11).
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6. **Liu GC**[1], Zhang R[1], **Hou QB**, He JW, **Dong ZW**, **Zhao RP**, **Wang W**, **Li XY***: Cloning and Characterization of Luciferase from the Chinese Firefly Lamprigera yunnana. ***Photochem Photobiol*** 2019, **95**(5):1186-1194.
7. **Liu GC**[1], **Dong ZW**[1], **Hou QB**[1], He JW, **Zhao RP**, **Wang W**, **Li XY***: Second Rhagophthalmid Luciferase Cloned from Chinese Glow-worm Menghuoius giganteus (Rhagophthalmidae: Elateroidea). ***Photochem Photobiol*** 2019.
8. **Chen X**[1], **Dong ZW**[1], **Liu GC**[1], He JW, **Zhao RP**, **Wang W***, Peng YQ*, **Li XY***: Phylogenetic analysis provides insights into the evolution of Asian fireflies and adult bioluminescence. ***Molecular phylogenetics and evolution*** 2019, **140**:106600.
9. **Wang B**, Chen L*, **Wang W***: Genomic insights into ruminant evolution: from past to future prospects. ***Zoological Research*** 2019, **40**(6).
10. **Liu W**[1], Chen L[1], Zhang SL[1], **Wang B**, **Zhao RP**, Tian ZX*, Ge S*, **Wang W***. Decrease of gene expression diversity during domestication of animals and plants. ***BMC Evolutionary Biology*** 2019, 19(1):19

1. 反刍动物系统基因组学研究

反刍动物是大型陆地哺乳动物中最成功的一类，具有非常丰富的生物多样性，能够适应多样化的生存环境，并演化出极为特殊的生物性状和新器官。然而，反刍动物的系统发育关系存在诸多争议，其独特的进化特征也未得到进一步解析。我们通过大尺度、跨物种、大数据创新思路和手段，系统阐明了长期有争议的反刍动物进化历史，发现人类对包括反刍动物在内的哺乳动物的种群衰减甚至绝灭可能有重要影响；阐明了反刍动物鹿角快速再生和鹿抗癌能力的遗传基础，发现鹿角的快速再生招募了大量原癌基因，同时，鹿类的抗癌基因特别 p53 是抑癌基因通路受到强烈的正选择。这一发现首次在分子水平将鹿角快速再生与鹿低癌发生率联系起来，对再生和肿瘤医学有重要启示意义；阐明驯鹿适应北极极端环境的机制，揭示了驯鹿昼夜节律丧失、高效维素 D 和钙代谢等的分子机制，为睡眠障碍和骨质疏松等的防治提了新启示。【Chen et al, 2019 ***Science***; Lin et al, 2019 ***Science*** 】

2. 蝴蝶系统生物学研究

蝴蝶因其丰富的形态多样性，自达尔文时代就作为研究物种适应性进化的重要类群之一，近几年更被认为是研究形态遗传、进化和发育的理想模型。在我们前期建立的蝴蝶基因组学和基因编辑平台上，我们于 2017 年启动了蝴蝶系谱基因组计划，旨在系统发育框架下获得一些具有重要表型特征的代表种类的高质量基因组，并进一步探索表型特征进化的分子遗传机制。为此，我们测定了 6 科 67 种蝴蝶的 C 值并组装了其线粒体基因组，结合已知的线粒体基因组数据和基因组大小的数据，在 264 种蝴蝶的系统发育框架下探讨了 106 种蝴蝶的基因组大小进化，发现尽管现生蝴蝶的基因组大小变异达 6.4 倍，所有蝴蝶的祖先基因组都在 0.5pg 左右，为蝴蝶基因组测序提供了有价值的参考。在此基础上，以碧凤蝶 (*Papilio bianor*) 为例，我们获得了首个利用三代和 Hi-C 技术 组装的蝴蝶染色体水平的参考基因组，为研究碧凤蝶特殊生物学特性的遗传和分子机制奠定了基础，也为凤蝶乃至整个蝴蝶资源开发和生物多样性保护提供了基础资料。【Liu et al, 2019 ***Systematic Entomology***; Lu et al, 2019 ***GigaScience***】

3. 萤火虫等甲虫发光系统探索

自 2002 年开始以萤火虫等发光甲虫为研究对象，我们一直循着物种分类、系统发育、发光基因和发光的分子体系展开了相关的研究。我们发现了亚洲首例发光叩甲，组装了其线粒体基因组，综合分子和形态数据确立该种作为叩甲科的一个新亚科新属新种，为甲虫生物荧光的多次起源提供了重要的证据；利用线粒体基因组数据和核基因标记，探讨了亚洲 15 属 23 种萤火虫的系统发育关系，其中 11 属 22 种萤火虫的线粒体基因组和核糖体 DNA 均为首次报道，明确了这些萤火虫属的系统发育地位，揭示了萤火虫的共同祖先具有成虫生物荧光，该研究成果完善了亚洲萤火虫的系统发育研究，并为进一步揭示全世界萤火虫的系统发育关系提供了重要的数据资源。为了进一步探讨发生物荧光分子机制，我们克隆了中国分布的一些萤火虫物种的荧光酶基因并分析了酶学特征【He et al., 2019, ***Mitochondrial DNA-B***; Bi et al., 2019, ***Zookeys***; Chen et al., 2019, ***Molecular phylogenetics and evolution***; Liu et al., 2019, ***Photochem Photobiol***】

Evolutionary Genomics and Origin of New Genes

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1. Systematic genomics of ruminants

The ruminants are one of the most successful mammalian lineages, exhibiting morphological and habitat diversity. However, the phylogenetic relationship of ruminants is controversial and its unique evolutionary characteristics have not been further analyzed. To better understand their evolution, we conducted a system study of ruminant genomes. We constructed a time-calibrated phylogenetic tree of the group, analyzed species population histories, and investigated the genomic evolution of these species. We reveal the genetic basis of rapid regeneration of antler and low cancer rate of deer. The rapid regenerative properties of antler tissue involve exploitation of oncogenetic pathways, and at the same time some tumor suppressor genes are under strong selection in deer. This discovery has important implications for regeneration and oncology in future. We also elucidates the mechanisms of how reindeer adapt to the extreme environment in Arctic, including the molecular mechanisms of the circadian rhythm loss the highly effective metabolism of vitamin D and calcium, which provided prospects for the prevention and treatment of sleep disorders and osteoporosis of human.

2. Systems biology study of butterflies

Due to its rich morphological diversity, butterflies have been one of the important groups for studying the adaptive evolution of species since the Darwin era. Butterflies have been considered as an ideal model for studying morphological diversity evolution and development recently. Our butterfly genome project aims to obtain high-quality genomes of some representative species with important phenotypic characteristics and then further explore the genetic mechanism of these phenotypes. As the first step of this project, we measured the C value of 67 butterflies in 6 families and assembled their mitochondrial genomes. Combining known mitochondrial genomic data and genome size data, we constructed a phylogenetic tree with 264 species. Our results show that butterflies have a 6.4-fold variation of genome size, and their ancestral genomes were about 0.5pg. This research provides a valuable reference for the sequencing butterfly genomes. Then, a chromosomal-level reference genome was obtained for *Papilio bianor* using Pacbio and Hi-C. This study provide important data resource for studying the genetic and molecular mechanisms of butterfly diversity.

3. Systems biology study of luminous beetles and their bioluminescence

Since 2002, we have been researching luminous beetles including their and phylogeny, luciferase, and bioluminescence origin and evolution. We discovered the first case of luminescent beetle in Asia and assembled its mitochondrial genome. Our data indicate this species should be placed in a new subfamily of Elateridae. This new species provides important evidence for the multiple origins of beetle bioluminescence. With mitochondrial genomic data and nuclear gene markers, we explored the phylogenetic relationship of 23 fireflies in 15 genera from Asia. Among them, the mitochondrial genomes and ribosomal DNA of 22 fireflies in 11 genera were reported for the first time. Our data suggest that the common ancestor of Lampyridae possessed adult bioluminescence, with a higher loss rate than gain rate of bioluminescence during its lineage evolution. Our results provide insight into Asian firefly phylogeny, and also enrich mitogenome and rDNA data resources for further study. In order to explore the molecular mechanism of the fluorescence of the organism, we cloned the luciferase genes of some firefly species distributed in China and analyzed the enzymatic characteristics.

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比较基因组学

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实验室主页：http://159.226.149.45/compgenegroup/compgenegroup.htm

重要成果及产出：

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1. 首次用动物模型实验呈现了人类大脑进化过程中幼态持续现象

幼态持续（neoteny）是人类进化中发生的独特现象。与我们的近亲非人灵长类相比，人类的发育速度变慢，发育过程延缓。人类的幼态持续在进化上的重要性在于为大脑发育和神经网络的可塑性提供了更长的时间窗口，是人类智力形成的关键因素。然而，我们对人类幼态持续的遗传基础尚不清楚。宿兵课题组一直从事灵长类大脑功能演化及其进化调控的研究，早在 2004 年通过对人类大脑容量发育关键基因 MCPH1 的分子进化研究首次发现该基因的蛋白序列在人类起源中发生了多个位点的人类特有变异（Wang and Su,2004）。通过细胞功能实验进一步证实这些人类特异的序列变异会改变 MCPH1 对下游基因的调控模式，在细胞水平证实了 MCPH1 人类特异突变具有功能效应（Shi 等，2013）。在此基础上，首次构建了携带人源 MCPH1 基因拷贝的转基因恒河猴模型，成功获得了 8 个 F0 代和 3 个 F1 代转基因猴，通过核磁共振脑影像分析对大脑发育不同时间点的脑影像动态图谱进行了跟踪分析，发现转基因猴存在明显的神经细胞与神经网络成熟延迟的现象。进一步对大脑发育不同时间点的脑组织学与转录组学的动态图谱的分析表明，转基因猴大脑中许多与神经元分化与成熟相关基因的表达受到了抑制，其表达峰值明显延后，这可能是导致转基因猴大脑发育延缓的分子基础。尤为重要的是，对转基因猴的认知能力进行了检测，发现与野生型对照猴相比转基因猴的工作记忆能力明显提高，说明大脑发育的延缓对转基因猴的智力提升可能是有益的，类似于人类大脑发育过程中的幼态持续现象。该项研究成果是首次利用非人灵长类转基因模型研究人类特异的遗传变异对人类智力起源的贡献及其分子机制，显示了转基因猴模型对研究人类起源以及人类特有脑疾病（如老年痴呆等）的重要价值。研究结果发表在国际知名刊物《国家科学评论》National Science Review 6:480-493，2019。

2. 利用三代长读长测序技术解析中国猕猴的完整参考基因组以及猿类特异的结构变异

猕猴是非人灵长类中的重要物种，作为的跟人类亲缘关系最近的关键模式物种，一个高质量的猕猴基因组将极大的促进生物医学和基因编辑的研究，并增进对灵长类物种重要进化事件的理解。本研究我们利用三代长读长的测序数据，结合多层次的基因组组装手段，从头组装了一个中国猕猴的全基因组——rheMacS。rheMacS 总长 2.95 Gbp，cotig N50 和 scaffold N50 分别达到了 8.19 Mbp 和 13.64 Mbp，相比于现有的猕猴参考基因组版本提高了 75 倍的序列连续性和 15 倍的序列完整性。其中，共有 21,940 个参考基因组中存在的 gap 被我们新的猕猴基因组版本填补，填补总长度达到 60.81Mbp。同时，我们利用长读长序列比对的策略识别了 53,916 个 rheMacS 中存在的结构变异（SV，structural variants），其中绝大部分（98%）的 SV 都没有在之前的基于芯片和二代测序的 SV 识别中被发现。进一步地，我们利用高质量的猕猴和猿的基因组，识别到了 17,000 个猿共有的结构变异（ape-shared structural variants，ASSVs）这些结构变异是造成猿特有表型的重要潜在因子。特别地，111 个 ASSVs 发生在猿和猴差异的八个脑区的增强子（ape-monkey differential enhancers，ADE）上。 另外，我们找到了一系列可能与猿的重要特征相关的 ASSVs，比如跟猿的尾巴缺失和更好的手指灵活性，以及跟大猿的更大的脑容量和更大的躯体相关的 ASSVs。该成果首次从头组装了一个高质量的猕猴基因组，并利用该基因组找到了一系列跟猿的进化特征相关的结构变异，是目前为止最完整的猕猴基因组，为灵长类进化的研究提供了新的数据资源。研究成果发表在 Nature Communications 10, 4233 (2019)。

3. 发现 CRISPR-Cas9 基因编辑系统在灵长类中不会导致明显的脱靶效应

CRISPR-Cas9 基因编辑系统已被广泛应用于生物和医学研究，然而，其在临床前的安全性却缺少全面的评估。为了系统评估 CRISPR-Cas9 在灵长类基因编辑中的脱靶效应，我们利用 CRISPR-Cas9 系统构建了小头症基因 -MCPH1 敲除的猕猴模型。通过对多只基因敲除猴及其野生型父母本进行深度二代测序和分析，发现 Cas9 在灵长类基因组中并不会造成大量的新生突变。研究结果发表在 Nature Communications 10, 4233 (2019)。该成果首次表明 CRISPR-Cas9 基因编辑系统在灵长类中并不会造成明显的脱靶效应，具有比较高的安全性。

Comparative Genomics

Dr. 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. Transgenic rhesus monkeys carrying the human MCPH1 gene copies show human-like neoteny of brain development

Brain size and cognitive skills are the most dramatically changed traits in humans during evolution and yet the genetic mechanisms underlying these human-specific changes remain elusive. Here, we successfully generated 11 transgenic rhesus monkeys (8 first-generation and 3 second-generation) carrying human copies of MCPH1, an important gene for brain development and brain evolution. Brain-image and tissue-section analyses indicated an altered pattern of neural-cell differentiation, resulting in a delayed neuronal maturation and neural-fiber myelination of the transgenic monkeys, similar to the known evolutionary change of developmental delay (neoteny) in humans. Further brain-transcriptome and tissue-section analyses of major developmental stages showed a marked human-like expression delay of neuron differentiation and synaptic-signaling genes, providing a molecular explanation for the observed brain-developmental delay of the transgenic monkeys. More importantly, the transgenic monkeys exhibited better short-term memory and shorter reaction time compared with the wild-type controls in the delayed-matching-to-sample task. The presented data represent the first attempt to experimentally interrogate the genetic basis of human brain origin using a transgenic monkey model and it values the use of non-human primates in understanding unique human traits. ***Shi et al. National Science Review*** 6, 480-493 (2019)

2. Long-read assembly of the Chinese rhesus macaque genome and identification of ape-specific structural variants

We present a high-quality de novo genome assembly (rheMacS) of the Chinese rhesus macaque (*Macaca mulatta*) using long-read sequencing and multiplatform scaffolding approaches. Compared to the current Indian rhesus macaque reference genome (rheMac8), rheMacS increases sequence contiguity 75-fold, closing 21,940 of the remaining assembly gaps (60.8 Mbp). We improve gene annotation by generating more than two million full length transcripts from ten different tissues by long-read RNA sequencing. We sequence resolve 53,916 structural variants (96% novel) and identify 17,000 ape-specific structural variants (ASSVs) based on comparison to ape genomes. Many ASSVs map within ChIP-seq predicted enhancer regions where apes and macaque show diverged enhancer activity and gene expression. We further characterize a subset that may contribute to ape- or great-ape specific phenotypic traits, including taillessness, brain volume expansion, improved manual dexterity, and large body size. The rheMacS genome assembly serves as an ideal reference for future biomedical and evolutionary studies. ***He et al. Nature Communications, 10, 4233 (2019).***

3. Trio deep-sequencing does not reveal unexpected off-target and on-target mutations in Cas9-edited rhesus monkeys

CRISPR-Cas9 is a widely-used genome editing tool, but its off-target effect and on-target complex mutations remain a concern, especially in view of future clinical applications. Non-human primates (NHPs) share close genetic and physiological similarities with humans, making them an ideal preclinical model for developing Cas9-based therapies. However, to our knowledge no comprehensive in vivo off-target and on-target assessment has been conducted in NHPs. Here, we perform whole genome trio sequencing of Cas9-treated rhesus monkeys. We only find a small number of de novo mutations that can be explained by expected spontaneous mutations, and no unexpected off-target mutations (OTMs) were detected. Furthermore, the long-read sequencing data does not detect large structural variants in the target region.. ***Luo et al. Nature Communications, 10, 5525 (2019).***

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进化与功能基因组学

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5. **刘振，白婧，施鹏** * (2019). 动物趋同表型分子遗传和演化机制的研究进展．中国科学：生命科学，**49**(1674-7232): 338.

1. 肠道微生物动态变化对宿主重要生命阶段的影响

肠道微生物已被证明对宿主生理、行为等各方面都有重要作用，但其是否影响宿主的性成熟并不清楚。对兰州熊蜂蜂王不同生命阶段的肠道微生物进行研究发现，在未交配 (UQs)、交配 (MQs) 和产卵 (OQs) 三种不同生殖生理状态下肠道微生物的类群丰度和构成显著不同，并且各个状态下具有其独特的优势菌群，其中在未交配 (UQs) 和产卵蜂王 (OQs) 的肠道菌群较为相似，主要优势菌为 *Gilliamella*，*Snodgrassella* 和 *Lactobacillus*，但 *Bifidobacterium* 则只在产卵蜂王 (OQs) 中含量相对较高，而在交配蜂王 (MQs) 的肠道中优势菌属则为 *Bacillus*，*Lactococcus* 和 *Pseudomonas*。该研究不仅首次阐明熊蜂蜂王的重要生命阶段的肠道菌群及优势菌群的变化与其生殖健康的关系，也首次揭示了熊蜂是除果蝇之外研究肠道微生物与生殖行为关系的良好的模式昆虫。

【Wang L et al., 2019, mSystems, IF 6.519】

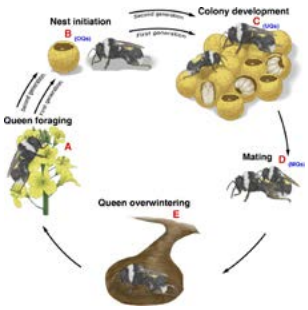

图 1 熊蜂的生命周期

2. 检测谱系特异正选择基因的新方法

目前广泛使用的比较基因组学方法仅分析多个物种的单一序列和分歧位点信息，如果能将多物种群体水平的遗传多态和物种水平的进化相结合进行分析，将有助于解析物种（尤其是近缘种）产生过程中适应性进化和特有表型形成的机制。我们与北京基因组所合作，首次开发了能够同时分析多个物种的群体基因组数据的方法 HDMKPRF。该方法以泊松随机场模型和 McDonald-Kreitman 检验为框架，通过多个物种的联合等位基因频谱理论构建群体遗传学模型，有效整合了微进化与宏观进化过程；很大程度提高了对自然选择基因的检测功效；通过多个物种的群体基因组比较分析，能够有效地把自然选择发生时间定位在多物种进化树的具体某个阶段（分支）上。该方法还提供了对各个物种的群体大小、物种分化时间以及自然选择强度等参数的后验概率分布。

【Zhao S et al., 2019, Molecular Biology and Evolution, IF 14.797】

3. 动物趋同表型分子遗传和演化机制

趋同表型的发生被广泛认为是通过提高适合度促进了远缘物种对所处相同或相似环境的适应性。越来越多的研究表明，相似或相同的遗传变异对趋同表型的起源和演化起了关键性作用。我们以哺乳动物的回声定位这一趋同表型为研究模型，从单基因和基因组层面，结合功能实验系统全面分析了趋同表型与趋同的分子变异之间的关系，鉴定出了多个可能与趋同表型密切相关的经历趋同演化的基因。尽管如此，从严格意义上检测分子水平的趋同变异是否受到达尔文自然选择的作用还是非常困难的。因此，我们进一步提出，除了需要满足趋同位点能够导致基因功能的趋同变化以外，更为关键的是需要证明这些分子的趋同变异确实能够导致趋同表型的产生，并显著增加经历趋同演化物种的适合度。

【刘振 等，2019，中国科学：生命科学】

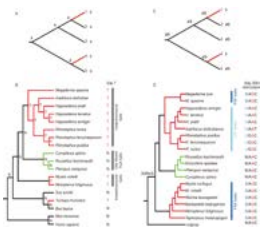

图 2 趋同进化示意图及实例

4. 中国白蜡虫基因组测序与解析

我们与中国林业科学研究院资源昆虫研究所合作，对中国白蜡虫基因组进行了测序、组装和解析，鉴定出 26 个脂肪酰辅酶 A 还原酶基因和 35 个酰基转移酶基因。进化分析显示，白蜡虫与蚜虫形成姊妹群，分歧于大约 2.411 亿年前。白蜡虫中发现 214 个扩张的基因家族和 2219 个收缩的基因家族。这些结果将有助于加深对白蜡虫独特进化特征的理解，并为进一步的研究提供了重要的遗传信息。

【Yang P et al., 2019, GigaScience, IF 4.688】

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.The impact of gut microbiome dynamics to the development of the host

Bumble bees are important pollinators of agricultural crops and wild plants in natural and agricultural ecosystems. Like other animals, bumble bees harbor a characteristic microbial community that plays an important role for their health. However, there is limited information about the composition of the gut microbial community associated with bumble bee queens, which are the sole founding reproductive female of a colony. In the present study, we investigated the diversity of gut bacteria in bumble bee queens, (*Bombus lantschouensis*), of different physiological states, including Unmated Queens, Mated Queens, and Ovipositing Queens. Our results revealed that there were significant shifts in the composition and copy numbers of microbiome members as queens underwent transitioned through these states. Unmated and ovipositing queens showed the greatest similarity in community composition, with mated queens being distinct. *Gilliamella*, *Snodgrassella*, *Lactobacillus* were the relatively dominant bacterial genera in both unmated and ovipositing queens, with *Bifidobacterium* additionally dominant in ovipositing queens. *Bacillus*, *Lactococcus* and *Pseudomonas* increased following queen mating. However, further analysis of unmated queens covering the ages of the mated queen group showed the differences seen in mated queens occurred independent of the occurrence of mating. Our results suggest a relationship between bumble bee queen gut bacteria and their development stage and physiological status. Our study is the first to explore the gut microbiome of bumble bee queens and provides useful information for future studies of the function of gut bacteria in queen development and colony's performance.

2.New methods for identifying lineage-specific targets of natural selection

Previous methods that detect the signals of natural selection in comparative genomics only include divergence sites of several species. With the increasing availability of next-generation and long-reads sequencing, reference genomes of many species had been de novo assembled, as well as the intra-species polymorphisms. By combining intra-species polymorphic sites and inter-species divergence sites, the genetic mechanisms of adaptive evolution and phenotypic specificity in many species will be well investigated. For this purpose, we developed a new method (HDMK-PRF) that can analyze population genomics of several species to identify lineage-specific targets of natural selection. This method is based on the Poisson random field framework and McDonald-Kreitman test. The population genetic model of this method effectively integrates the processes of microevolution and macroevolution by applying the joint allele frequency spectrum of several species. Compared to previous methods, this method boosts the power for detecting selection and can pinpoint the occurrence time of selection to a specific lineage of the species phylogeny. This method also provides posterior distributions of the fitness effects of each gene along with parameters associated with the evolutionary history, including the species divergence time and effective population size of external species.

3.Genetic and evolutionary mechanisms of convergent phenotypes in animals

It is not uncommon that similar phenotypes independently evolved in species of evolutionarily distant lineages, known as convergent evolution. The occurrence of convergent phenotypes is widely believed to promote adaptations to the same or similar environments of evolutionarily distant species by increasing their fitness. More and more studies show that similar or same genetic variations play key roles in the origination and evolution of convergent phenotypes. We set up a research model of the mammalian echolocation to systematically explore the relationships between convergent phenotypes and convergent genetic variations on a genome-wide scale by combining with functional experiments. We revealed molecular bases in genetics and evolution of the convergent phenotype of echolocation and identified many genes undergoing convergent evolution that are closely related to convergent phenotypes. Nevertheless, it is difficult to verify strictly whether convergent variations at the molecular level are under Darwinian natural selection. Except for convergent variations satisfying functional convergence of the related genes, we further proposed that it is more important to demonstrate molecular convergences leading to the occurrence of convergent phenotypes and significantly increasing the fitness of the species undergoing convergent evolution.

4.Genome sequence of the Chinese white wax scale insect

The Chinese white wax scale insect, *Ericerus pela*, is best known for producing wax, which has been widely used in candle production, casting, Chinese medicine, and wax printing products for thousands of years. The secretion of wax, and other unusual features of scale insects, is thought to be an adaptation to their change from an ancestral ground-dwelling lifestyle to a sedentary lifestyle on the higher parts of plants. However, no genomic data are currently available for *E. pela*. To assemble the *E. pela* genome, 303.92 Gb of data were generated using Illumina and Pacific Biosciences sequencing, producing 277.22 Gb of clean data for assembly. The assembled genome size was 0.66 Gb, with 1,979 scaffolds and a scaffold N50 of 735 kb. 26 fatty acyl-CoA reductase genes and 35 acyltransferase genes were identified. Evolutionary analysis revealed that *E. pela* and aphids formed a sister group and split ~241.1 million years ago. There were 214 expanded gene families and 2,219 contracted gene families in *E. pela*. These results will help to increase our understanding of the evolution of unique features in scale insects, and provide important genetic information for further research.

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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. **Li Y-J, Ye Q-Q**, He D, **Bai H-X, Wen J-F*.** The ubiquity of the coexistence of two FBPases in chloroplasts of photosynthetic eukaryotes and its evolutionary and functional implications. ***Plant Diversity***. 2019, https://doi.org/10.1016/j.pld.2019.09.002
2. **Feng J-M**, Jiang C-Q, Sun Z-Y, Hua C-J, **Wen J-F**, Miao W*, Xiong J*. Single-cell transcriptome sequencing of rumen ciliates provides insight into their molecular adaptations to the anaerobic and carbohydrate-rich rumen microenvironment. ***Molecular Phylogenetics and Evolution***. 2019. 143:106687.
3. **Lyu Z-X, Cheng J-N, Shao J-R, Ye Q-Q , Bai H-X**, Wang J-X and **Wen J-F** *. An Investigation of the Prevalence of *Giardia agilis* in Anuran Amphibians Reveals Special Parasitic Adaptations of this *Giardia* Species. ***Parasites & Vectors*** (submitted).
4. **Feng J-M**, **Yang C-L, Tian H-F, Wang J-X, Wen J-F***. Identification and Evolutionary Analysis of the Nucleolar Proteome of *Giardia lamblia*. *BMC Genomics* (submitted).

1. 原生生物首个核仁蛋白质组的构建与核仁的进化探讨

核仁是真核细胞间期细胞核中最明显的结构，其基本功能是核糖体的生物合成，后来又报道了核仁的其他几种功能。目前，高等真核生物的核仁以及其蛋白质组已经被广泛研究，但低等的单细胞真核生物 — 原生生物的核仁的研究却鲜有报道。这也导致人们对核仁的结构和功能的进化知之甚少。

有趣的是原生生物贾第虫并不像其他真核生物一样具有明显的核仁结构，且其进化地位一直存在争议：它究竟是极端原始的真核生物还是高度退化的寄生虫？众所周知原核细胞不具有核仁结构，而典型真核细胞则具有很明显的核仁结构，那么贾第虫这种不具有典型的核仁结构的情形是代表了原核细胞到真核细胞进化的过渡状态还是因寄生退化所致？我们选取蓝氏贾第虫作为研究对象，重建其核仁蛋白质组，并试图从核仁蛋白质组的角度来对上述问题进行探讨。

首先，基于人的核仁蛋白质组，拟南芥和酵母的蛋白质组以及贾第虫的基因组，我们通过同源搜索和贾第虫特异核仁蛋白的鉴定重建了贾第虫核仁蛋白质组（GiNuP）。同时还构建了高等真核生物基本核仁蛋白质组（HEBNuP），即三种高等真核生物（人，拟南芥和酵母）的共有核仁蛋白质组。然后对这两种核仁蛋白质组进行蛋白组分和功能（包括六种核仁功能）的全面比较，结果发现：1）GiNuP 的蛋白数量明显比 HEBNuP 的少，但前者 78.4% 的蛋白在后者中都有直系同源物；2）GiNuP 中大部分蛋白（68%）参与核糖体合成相关的功能，其他的蛋白（约 31%）则参与了核仁的其他五种功能，这两大类蛋白的比例比 HEBNuP 中的相应两大类的蛋白占比分别高很多和少很多；3）GiNuP 特异性的蛋白占比 21.6%，且只参与 3 种功能，而 HEBNuP 的特异蛋白占比却高达 75%，且参与全部 6 种功能。

本工作首次重构了一种原生生物 — 贾第虫的核仁蛋白质组（GiNuP）。GiNuP的蛋白质数量少且大部分蛋白参与核仁的基本功能 — 核糖体的生物合成，这应该体现了贾第虫的原始性。从组成成分和功能上与高等真核生物基本核仁蛋白质组的比较分析，揭示了核仁进化的一些十分有趣的现象：1）在核仁的进化过程中，核糖体生物合成功能比其他功能出现的早。在真核细胞进化过程中，这种基本功能通过增加蛋白质的种类和数量逐渐得到完善；2）核仁的其他功能在真核细胞的早期已出现，从原始的单细胞原生生物到高等的多细胞真核生物进化的过程中，这些功能也通过增加蛋白的种类和数量得到完善；3）在物种分化和谱系分化的过程中，物种特异性和谱系特异性的蛋白被进化出来以参与核仁的各种功能，这提示这些特异性的成分对特定物种或谱系的细胞结构或功能的完善很重要。

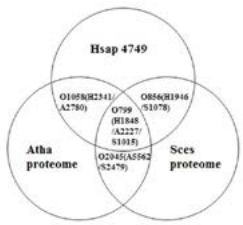


图 1. 人、拟南芥和酵母核仁蛋白质组的直系同源关系

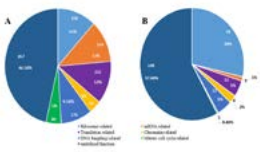


图 2. HEBNuP (A) 和 GiNuP (B) 核仁蛋白质的功能分类

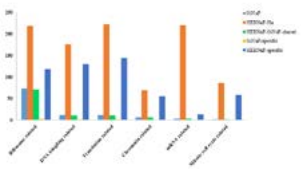


图 3. 5 个数据集中核仁蛋白质的分类及数目

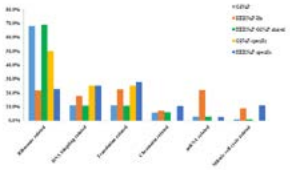


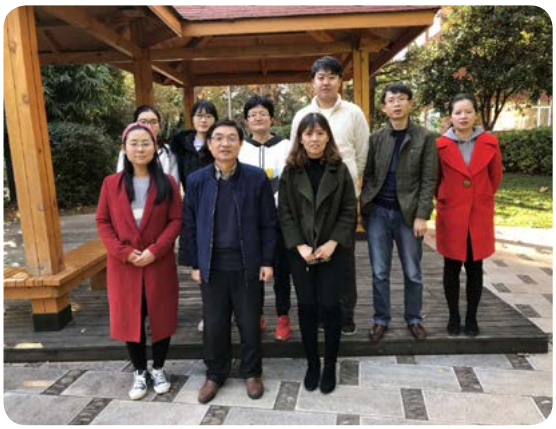
图 4. 各种核仁功能分类蛋白在 5 个蛋白数据集中的比例

2. 光合真核生物叶绿体中两种 FBPase 普遍共存的发现及其进化与功能探讨

果糖 -1,6- 二磷酸酶（FBPase）催化果糖 -1,6- 二磷酸不可逆地水解为果糖 6- 磷酸，同时释放出无机磷酸，是卡尔文循环和糖异生途径中的关键限速酶之一。光合真核生物中存在两个研究得比较清楚的果糖 -1,6- 二磷酸酶：参与糖异生途径的、对氧化还原不敏感的胞质型 FBPase（cyFBPase），以及作为卡尔文循环关键酶的、对氧化还原敏感的叶绿体型 FBPase（cpFBPase1）。在陆地植物（和极个别微藻）的叶绿体中最近有报道还存在另一种新的对氧化还原不敏感的 cpFBPase2。然而，该酶的在整个光合真核生物中的分布情况，其进化起源和生理功能均不清楚。我们通过系统全面地调查已测序的光合真核生物中 FBPase 的分布情况，发现 cpFBPase2 广泛存在于几乎所有光合真核生物中。我们进一步的系统发生分析表明，来自不同光合真核生物谱系的所有 cpFBPase2 都形成一个共同的单系，这否定了前人的“cpFBPase2 仅存在于陆地植物、较晚时期才进化出来的”观点，而表明该酶在光合真核生物进化的早期就已出现，并且很可能是在光合真核生物的共同祖先中就已经进化出来的。整个 FBPase 的进化历程应该是：cyFBPase 首先被复制产生了 cpFBPase2，然后后者再被复制而产生了 cpFBPase1。我们的分析认为这两个对氧化还原敏感性不同的 cpFBPase 在叶绿体中之所以普遍同时存在，很可能是为了确保光合作用在不同氧化还原条件（特别是那些由光照条件的不断变化而导致的）下都能顺利进行。

Evolutionary Genomics of Eukaryotic Cells

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



1. Identification and Evolutionary Analysis of the Nucleolar Proteome of the First Protist, Giardia lamblia

Nucleolus is the most prominent sub-nuclear compartment in the interphase nucleus of a eukaryotic cell. Its essential function is ribosomal biogenesis, and several other functions of it were also found later. To date, the nucleoli of the three so-called higher eukaryotes (animals, plants, and fungi) have been extensively studied, and the nucleolar proteomes of their representative species have already been reported, while there were few studies about the nucleoli of the lower eukaryotes -- protists, much less their nucleolar proteomes. Therefore, the evolution of the structure and function of the nucleolus is rarely understood. *Giardia lamblia*, a protist with the controversy of whether it is an extreme primitive eukaryote or just a highly evolved parasite, is reported to be lack of typical nucleoli, therefore it might be an interesting object to carry out the nucleolar proteome study and thus further to examine the controversy over it.

Based on the human nucleolar proteome, the proteomes of *Arabidopsis* and budding yeast, and the genome data of *Giardia lamblia*, we identified and characterized the first protist nucleolar proteome, *Gi*NuP, which contains 255 orthologous groups (and the same number of individual nucleolar proteins), and also reconstructed the Higher Eukaryote Basic Nucleolar Proteome (HEBNuP)which consists of 799 orthologous groups of the common nucleolar proteins of the three higher eukaryotes (containing 1848 human individual nucleolar proteins). Compositional and functional comparisons of the proteins in the *Gi*NuP with those in the HEBNuP revealed that: 1) *Gi*NuP is much smaller than HEBNuP, but the majority (78.4%) of its proteins have orthologs in the latter; 2) The majority (more than 68%) of the proteins in *Gi*NuP are involved in the “Ribosome related” function, and the others (about 31%) are involved in the other five functions, and these two groups of proteins are much larger and much smaller than those in HEBNuP, respectively; 3) *Gi*NuP has its specific proteins (21.6%), which participate in the “Ribosome related” and two other nucleolar functions, while in HEBNuP, there are a large number (75.0%) of specific orthologous protein groups (containing 67.8% human individual nucleolar proteins), which participate in all the six nucleolar functions.

The first protist nucleolar proteome, *G. lamblia* nucleolar proteome (*Gi*NuP), has been identified and characterized. The small *Gi*NuP with most of its proteins participating in the basic function of nucleolus -- ribosome biogenesis should reflect the primitiveness not the parasitic reduction of *Giardia*. The basic ribosome biogenesis function of the nucleolus must have arisen earlier than the other functions, and this basic function became more and more consummate in the evolution of eukaryotes by increasing protein components substantially; Besides the basic function, the other nucleolar functions have also arisen in the protist *Giardia*, and they became more and more complicated in the evolutionary process from primitive unicellular protists to higher multicellular eukaryotes also by increasing protein components greatly; Species- and linage-specific protein components are also necessary to evolve to participate the performance of all the functions of nucleolus, which might imply that in the evolution of eukaryotes, probably mainly in the divergence of species and lineages, the evolution of such specific components is also necessary for a cellular structure or a function to became more efficient and consummate in a certain species and lineage.

2. The ubiquity and coexistence of two FBPases in chloroplasts of photosynthetic eukaryotes and its evolutionary and functional implications

Fructose-1,6-bisphosphatase (FBPase), one of the key rate-limiting enzymes in the Calvin cycle and gluconeogenesis, catalyzes irreversible hydrolysis of fructose-1,6-bisphosphate into fructose-6-phosphate with the concomitant liberation of inorganic phosphate. In photosynthetic eukaryotes, there are two well-characterized FBPases: the redox-insensitive cytosolic FBPase (cyFBPase), which participates in gluconeogenesis, and the redox-sensitive chloroplastic FBPase (cpFBPase1), which is a critical enzyme in the Calvin cycle. A new redox-insensitive cpFBPase2 has recently been reported in the chloroplasts of terrestrial plants (and very few microalgae). However, the distribution of this enzyme in photosynthetic eukaryotes, its evolutionary origin and physiological functions are unclear. In this study, we comprehensively investigated the distribution of FBPase in sequenced photosynthetic eukaryotes and found that cpFBPase2 is widely present in almost all photosynthetic eukaryotes. Our further phylogenetic analysis shows that all cpFBPase2 from diverse photosynthetic eukaryotic lineages form a monophyly, which negates the previous view that cpFBPase2 is a recently evolved enzyme and only exists in land plants. Our results suggest that the enzyme evolved early in the evolution of photosynthetic organisms, and most likely, in the common ancestor of photosynthetic eukaryotes. cyFBPase was probably first duplicated to produce cpFBPase2, and then the latter duplicated to produce cpFBPase1. The ubiquitous coexistence of these two cpFBPases (redox-sensitive cpFBPase1 and redox-insensitive cpFBPase2) in chloroplasts is most likely the consequence of adaptation to different redox conditions of photosynthesis, especially those caused by recurrent changes in light conditions.

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计算生物与医学生态学科组

马占山，研究员，博导，计算生物与医学生态学学科负责人。2011 年入选“云南省高端科技人才”和“云南省高层次人才引进”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九十余篇论文。

重要成果（论文、专利）

Publications & Patents

1. Ma ZS, & Li W (2019) How and Why Men and Women Differ in Their Microbiomes: Medical Ecology and Network Analyses of the Microgenderome. *Advanced Science*. DOI: 10.1002/advs.201902054.
2. Ma ZS & Ellison AM (2019) Dominance network analysis provides a new framework for studying the diversity-stability relationship. *Ecological Monographs*. DOI: 10.1002/ecm.1358.
3. Ma ZS, Li L, Gotelli NJ (2019) Diversity-disease relationships and shared species analyses for human microbiome-associated diseases. *The ISME Journal*. https://www.nature.com/articles/s41396-019-0395-y
4. Li L & Ma ZS (2019) Comparative power law analysis for the spatial heterogeneity scaling of the hot-spring and human microbiomes. *Molecular Ecology*. 28(11)
5. Ma ZS (2019) A new DTAR (diversity–time–area relationship) model demonstrated with the indoor microbiome. *Journal of Biogeography*. DOI: 10.1111/jbi.
6. Ma ZS, Li L, Ye C, Peng M, Zhang YP (2019) Hybrid assembly of ultra-long Nanopore reads augmented with 10×-genomics contigs: Demonstrated with a human genome. *Genomics*. 111(6):1896-1901.
7. Ma ZS & Li L (2019) Semen microbiome biogeography: an analysis based on a Chinese population study. *Frontiers in Microbiology*. 9:3333.
8. Li L & Ma ZS (2019) Global microbiome diversity scaling in hot springs with DAR (diversity-area relationship) profiles. Frontiers in Microbiology. 10:118.
9. Li W, Ma ZS (2019) Diversity scaling of human vaginal microbial communities. *Zoological Research*. 40(6)
10. Sun Y, *et al* (2019) The gut microbiota heterogeneity and assembly changes associated with the IBD. *Scientific Reports*. 9(1):440.
11. Li W & Ma ZS (2019) FBA Ecological Guild: Trio of Firmicutes-Bacteroidetes Alliance against Actinobacteria in Human Oral Microbiome. *Scientific Reports*
12. Ma ZS, Li L, Zhang YP (2019) Individual-Level Genetic Diversity and Similarity Profiles. *Scientific Reports*

发明专利授权：

名称：用于组装基因组序列的方法、系统及装置 (专利号 : 201510084489.X)

申请发明专利：

(1) 一种度量个体水平遗传及突变多样性、相似性的概念和方法

(2) 一类用于细菌性阴道炎风险预测、诊断、个性化治疗及愈后监测的细菌优势度网络三角基序

(3) 挖掘微生物功能团的分析技术及其从健康口腔菌群所获得的 FBA 功能团

解析男女存在七个方面差异及其机制

“菌群性别组学”的概念，简单的讲就是人体菌群也有性别之分，或者叫“性二型”。该概念是 MB Flak 在评述 JG Markle 于 2013 年发表于 Science 的论文时新造出来的一个英文单词，即 Microgenderome。对于这一概念的科学研究则应该是揭示菌群性别差异与免疫系统、内分泌系统、“肠 — 脑轴心”等重要系统相互作用的现象和机理。这些研究的直接应用领域包括对于男女在对某些疾病易感性方面差异做出机制性解释， 并基于这些差异优化诊治和预防措施。在该研究之前，“菌群性二型”只是一个定性的概念，新的研究则对其进行了详尽的定量。该研究探究了人体四大主要部位（口腔、肠道、呼吸道和皮肤）15 个位点的菌群在男女间存在的性别差异及生态学理论机制。发现男女在菌群多样性、共有物种、异质性、核心 / 边缘物种、基本网络属性、网络骨架等 7 个方面的重要差别。

“该研究为菌群相关疾病的诊治 (研究) 奠定了一份参考标准和指南”。《Advanced Science》杂志审稿人评价说。三位审稿专家仅提出了一条修改意见（建议增加一段对研究结论的总结）， 也使得该论文从投稿到正式接收仅用了七周时间。在线发表后受到新华社、中新社、科技日报、健康报等媒体采访和报道。

Ma ZS, & Li W (2019) How and Why Men and Women Differ in Their Microbiomes: Medical Ecology and Network Analyses of the Microgenderome. *Advanced Science* (5-Year Impact Factor =15.1)

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 90 peer-refereed papers in premier platforms such as *IEEE Transactions on Reliability*, *Science Translational Medicine*, *The ISME Journal, Ecological Monographs,* and *Advanced Science*. He was a member of London-based "*Faculty 1000 of Biology and Medicine*".

人体菌群多样性与疾病关系的"1/3 猜想"

人体菌群主要分布在肠道、口腔、皮肤、呼吸道和生殖道五大部位，菌群与宿主间通过复杂的生理生化过程与免疫、代谢、神经中枢等相互作用，因而菌群对宿主健康和疾病有着非常深刻的影响。比较疾病与健康个体间菌群多样性的差异几乎是目前所有菌群相关疾病研究的基础分析之一，菌群相关疾病的研究往往需要生态学理论的引导。为探究多样性与疾病关系的生态格局，该研究对 27 组涉及菌群相关疾病的 16S-rRNA 宏基因组数据进行了分析。检验结果显示，在 27 组数据中析发现有 18 组（67%），健康与疾病个体间多样性指数没有显著差异。此外，该研究还通过共有物种分在绝大多数的比对中疾病与健康个体间菌群的物种组成是有差异的。严格统计分析表明只有在大约 1/3 情形，" 菌群多样性 " 才与 " 菌群相关疾病 " 的发生之间具有显著相关关系。

该研究提出的菌群疾病关系的 "1/3 猜想 " 揭示了只有大约 1/3 的 " 菌群多样性 " 与 " 菌群相关疾病 " 的关系能够经得住严格的统计检验，该猜想很可能也适用于其他生态指标或模型，提醒我们进行 " 多样性 - 疾病关系 — 生态机制 — 疾病病因 " 三步曲研究的重要性。 论文发表后受到新华社、科技日报、国家自然科学基金委、美国 NBC， ABC， CBS 等媒体采访和报道。论文在线发表半年多时间已有 7 次引用。

Ma ZS, Li L, Gotelli NJ (2019) Diversity-disease relationships and shared species analyses for human microbiome-associated diseases. *The ISME Journal*. https://www.nature.com/articles/s41396-019-0395-y (5-Year Impact Factor =10.9)

经典多样性—稳定性关系理论研究取得重要突破

马占山研究员与美国哈佛大学 Aaron Ellison 教授于 2019 年 3 月在美生态学会旗舰期刊《Ecological Monographs》 发表论文 "Dominance network analysis provides a new framework for studying the diversity-stability relationship"， 在经典多样性 — 稳定性关系领域提出系列新概念和方法。" 多样性 — 稳定性关系 "（也称之为 " 复杂性 — 稳定性关系 "）被认为是生态学中最重要的核心理论课题之一，并具有极其重要的实际意义。例如：生物多样性保护的最大实际收益其实就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。复杂性 — 稳定性关系的研究不仅具有有趣的起源，而且也是跨学科研究的重要理论难题之一。

Ecological Monographs 是学界为数不多对于稿件长度有下限要求的杂志之一，每年仅发表大约 30-40 篇论文。此次发表的论文也是 Ecological Monographs 创刊近一个世纪以来首篇涉及人类疾病的论文。论文发表后受到科技日报、新华网、美国 NBC，ABC，CBS 等媒体采访和报道。论文从年初在线发表大约一年时间已有 7 次引用。

Ma ZS & Ellison AM (2019) Dominance network analysis provides a new framework for studying the diversity-stability relationship. *Ecological Monographs*. DOI: 10.1002/ecm.1358. (5-Year Impact Factor =10.9)

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人类进化与疾病基因组学

孔庆鹏，中科院昆明动物所，研究员、博导。迄今在 *Am J Hum Genet*、*Genome Res*、*Mol Biol Evol*、*Natil Sci Rev*、*PNAS*、*Theranostics* 及 *Hum Mol Genet* 等国际重要 SCI 期刊上发表论文 101 篇，论文被各类 SCI 刊物累计引用 4294 次，H 指数 31。主持有国家重点研发计划专项（任首席科学家）、国家基金委重点国际合作及优秀青年基金等项目；2013 年入选科技部科技创新中青年领军人才计划，2016 年入选国家“万人计划”领军人才；现任 SCI 期刊 *Scientific Reports* 编委。研究组目前的主要研究方向：人群起源演化及健康长寿分子机制。

重要成果及产出：

1. **Li YC**#, Ye WJ#, Jiang CG#, Zeng Z, **Tian JY**, **Yang LQ**, Liu KJ, **Kong QP***. River valleys shaped the maternal genetic landscape of Han Chinese. ***Mol Biol Evol***. 2019, 36, 1643-1652. IF=14.797
2. **Li YC**#, **Tian JY**#, Liu FW, **Yang BY**, **Gu KSY**, **Zia Ur Rahman**, **Yang LQ**, Chen FH, Dong GH* and **Kong QP***. Neolithic millet farmers contributed to the permanent settlement of the Tibetan Plateau by adopting barley agriculture. ***Natil Sci Rev***, 2019, In Press, doi: 10.1093/nsr/nwz080, IF=13.222
3. Zeng Z, **Tian JY**, Jiang CG, Ye WJ, Liu KJ, **Li YC***, Inferring the history of surname Ye based on Y chromosome high-resolution genotyping and sequencing data. ***J Hum Genet***, 2019, 64, 703–709, IF=3.545
4. **Xiao FH**, **Wang HT**, **Kong QP***, Dynamic DNA Methylation During Aging: A “Prophet” of Age-Related Outcomes. ***Front Genet***, 2019, 2019, 10, 107, IF=3.517
5. **Xia WX**, **Yu Q**, **Li GH**, **Liu YW**, **Xiao FH**, **Yang LQ**, **Zia Ur Rahman**, **Wang HT**, **Kong QP***, Identification of four hub genes associated with adrenocortical carcinoma progression by WGCNA. ***PeerJ***, 2019, 7, e6555, IF=2.353
6. **Yu Q, Pu SY, Wu H, Chen XQ, Jiang JJ, Gu KS, He YH*, Kong QP*.** TICRR Contributes to Tumorigenesis Through Accelerating DNA Replication in Cancers. ***Front Oncol***, 2019, 9, 1-14, IF=4.137

1. 新石器时期粟黍农业人群的迁徙介导了大麦农业向高原的传播

基于现代藏族（8277 份）及周边人群（58514 份）线粒体 DNA（mtDNA）数据，深入解析了藏族的遗传结构。结合不同海拔农作物遗存的碳十四测年等数据，发现藏族人群中存在大量的源于中国北方粟黍农业人群的遗传组分（占 ~20%），并且在耐寒作物大麦传播至青藏高原高海拔地区时（3600 BP），高原人群可能以粟黍农业人群组分为主（达 ~50%）。这说明粟黍农业人群可能在到达青藏高原低海拔地区后，采用了耐寒的大麦农业并进一步向高海拔迁徙，最终大规模永久定居青藏高原（图 1）。工作发表后，Natil Sci Rev 杂志同步刊发了两篇评论文章，专门对我们的成果进行了评述和介绍（图 2）。

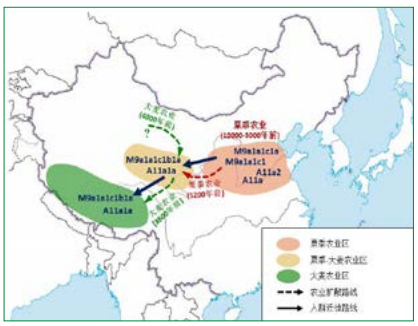

图 1. 中国北方粟黍农业人群向青藏高原的迁徙模式

图 2. Natil Sci Rev 对成果进行了评述和介绍

【Li YC et al. 2019 ***National Science Review***， IF=13.222】

2. 大规模 mtDNA 数据揭示汉族人群母系遗传结构的形成机制

通过分析中国 33 个省级行政区 21668 例汉族样本的 mtDNA 突变数据，发现不同水系的汉族人群间的遗传差异较南北差异更为显著，且该差异主要表现为三大水系（黄河、长江和珠江）之间的分化（图 3）。巧合的是，三大水系也是三大史前农业——粟黍农业（黄河流域）、水稻农业（长江流域）和热带农业（珠江流域）的起源或扩散中心，而不同水系人群在该时期均出现了人口数量急剧增长。因此，汉族人群的母系遗传结构更多地保留了新石器时期早期的遗传印记，不同流域史前农业的起源和扩散则是促进汉族人群母系遗传分化的重要原因。工作发表后，Mol Biol Evol 杂志以“news”形式对我们的工作专门进行了宣传报道。

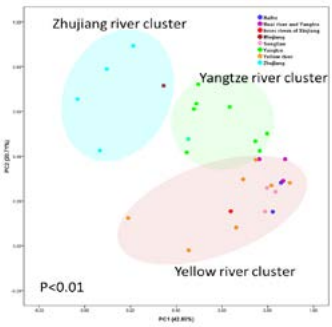

图 3. 汉族人群母系遗传结构呈现出水系分化

【Li YC et al. 2019 ***Molecular Biology and Evolution***， IF=14.797】

Human Evolution and Disease Genomics

Dr. 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 100 papers on the international peer-reviewed journals such as *Am J Hum Genet, PNAS, Genome Res, Mol Biol Evol*, *Natil Sci Rev*, *Theranostics* with total citations over 4,000 times.

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1. Neolithic millet farmers contributed to the permanent settlement of the Tibetan Plateau by adopting barley agriculture

By combining genetic and archaeological evidences, we identified haplogroups M9a1a1c1b1a and A11a1a, which are common in contemporary Tibetans (20.9%) and were probably even more common (40–50%) in early Tibetans (Fig 1), as the genetic legacy of the Neolithic millet farmers. By showing that substantial genetic components in contemporary Tibetans can trace their ancestry back to the Neolithic millet farmers, our study reveals that millet farmers adopted and brought barley agriculture to the TP ~3.6-3.3 ka, and made an important contribution to the Tibetan gene pool. **(Li YC et al. 2019 Natil Sci Rev)**

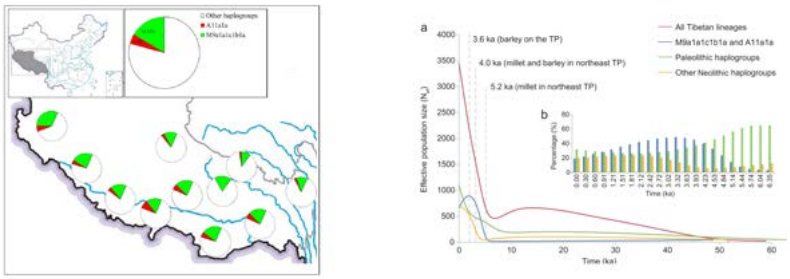

Fig 1. M9a1a1c1b1a and A11a1a are common in contemporary Tibetans and reached 48.8% at about 3.3 ka, when barley agriculture had already dispersed onto the high altitude.

2. River valleys shaped the maternal genetic landscape of Han Chinese

Our study revealed a significant genetic divergence among Han Chinese from the three main river systems (viz., the Yangtze, the Yellow, and the Zhujiang rivers), which was already established during the early Holocene and may have resulted from population expansion facilitated by ancient agricultures along these rivers. These results imply that the maternal gene pools of the contemporary Han populations have retained the genetic imprint of early Neolithic farmers from different river basins, thus highlighting the importance of the three ancient agricultures in shaping the genetic landscape of the Han Chinese. **(Li YC et al. 2019 Mol Biol Evol)**


NEWS

Scientists Explore Diversity of Han Chinese

Fig 2. This study was reported as News by Mol Biol Evol.

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郭丽云 Liyun Guo 2018

韩一鸣 Yiming Han 2018

赵 龙 Long Zhao 2019

翁崇俊 Congjun Weng 2019

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）。过去一年，课题组利用大规模全基因组测序构建反刍动物系统发育树并揭示了反刍动物演化的遗传机制，通过古今样品对比揭示朱鹮群体演化历程，解析了草莓箭毒蛙基因组，发布了所有现存企鹅物种的基因组数据并构建了企鹅的系统发育树。在 *Science* (1), *Current Biology* (1), *Molecular Biology & Evolution* (2)，GigaScience (3) 等国际刊物发表 SCI 文章 16 篇。

实验室主页：http://zhanggjlab.cn/en/index.html

重要成果及产出：

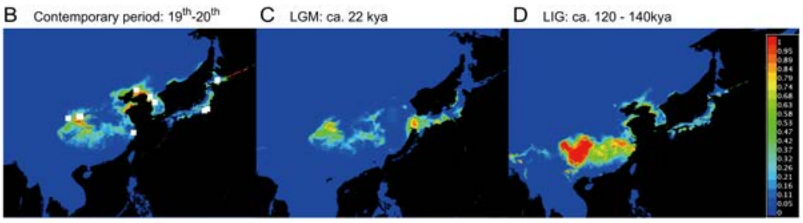
1. L. Chen[1], Q. Qiu[1], Y. Jiang[1], K. Wang[1], Z. Lin[1], Z. Li[1], F. Bibi, Y. Yang, J. Wang, W. Nie, W. Su, **G. Liu**, Q. Li, W. Fu, X. Pan, C. Liu, J. Yang, C. Zhang, Y. Yin, Y. Wang, Y. Zhao, C. Zhang, Z. Wang, Y. Qin, **W. Liu**, **B. Wang**, **Y. Ren**, R. Zhang, **Y. Zeng**, R. R. da Fonseca, B. Wei, R. Li, **W. Wan**, **R. Zhao**, W. Zhu, Y. Wang, S. Duan, Y. Gao, Y. E. Zhang, C. Chen, C. Hvilsom, C. W. Epps, L. G. Chemnick, Y. Dong, S. Mirarab, H. R. Siegismund, O. A. Ryder, M. T. P. Gilbert, H. A. Lewin, **G. Zhang***, R. Heller*, **W. Wang***, Large-scale ruminant genome sequencing provides insights into their evolution and distinct traits. ***Science***, 2019, 364(6446).
2. **S. Feng**[1], Q. Fang, R. Barnett, C. Li, S. Han, M. Kuhlwilm, L. Zhou, H. Pan, Y. Deng, G. Chen, A. Gamauf, F. Woog, R. Prys-Jones, T. Marques-Bonet, M. T. P. Gilbert, **G. Zhang***. The genomic footprints of the fall and recovery of the crested ibis. ***Current biology***, 2019, 29(2): 340-349.
3. R. Rogers[1], **L. Zhou**[1], C. Chu, R. Marquez, A. Corl, T. Linderoth, L. Freeborn, M. MacManes, **Z. Xiong**, **J. Zheng**, **C. Guo**, **X. Xun**, M. Kronforst, K. Summers, Y. Wu, **H. Yang**, C. Richards-Zawacki*, **G. Zhang***, R. Nielsen*. Genomic takeover by transposable elements in the strawberry poison frog. ***Molecular Biology and Evolution***, 2018, 35(12): 2913-2927.
4. **H. Pan**[1], T. L. Cole[1], X. Bi, M. Fang, C. Zhou, Z. Yang, D. T. Ksepka, T. Hart, J. L. Bouzat, L. S. Argilla, M. F. Bertelsen, P. D. Boersma, C. A. Bost, Y. Cherel, P. Dann, S. R. Fiddaman, P. Howard, K. Labuschagne, T. Mattern, G. Miller, P. Parker, R. A. Phillips, P. Quillfeldt, P. G. Ryan, H. Taylor, D. R. Thompson, M. J. Young, M. R. Ellegaard, M. T. P. Gilbert, M. S. Sinding, G. Pacheco, L. D. Shepherd, A. J. D. Tennyson, S. Grosser, E. Kay, L. J. Nupen, U. Ellenberg, D. M. Houston, A. H. Reeve, K. Johnson, J. F. Masello, T. Stracke, B. McKinlay, P. G. Borboroglu, D. X. Zhang and **G. Zhang***. High-coverage genomes to elucidate the evolution of penguins. ***Gigascience***, 2019, 8(9).
5. J. Stiller1*, **G. Zhang***, Comparative phylogenomics, a stepping stone for bird biodiversity studies. ***Diversity***, 2019, 11, 115.

1. 大规模基因组测序揭示反刍动物演化机制

对 44 个反刍动物基因组进行从头测序、组装及注释，同时对 7 个已发布的反刍动物基因组进行分析，通过与 12 个已公布的哺乳动物基因组作为外群比对分析鉴定到了 221,166 反刍动物特异性保守非外显子元件（RSCNEs），继而利用全基因组比对获取的 373Mbp 基因组直系同源共线序列，以虎鲸为外群构建了 51 个反刍动物的基因组系统发育树（nDNAtree）。这是迄今覆盖度最大、分支最清晰、质量最高的反刍动物系统发育树。利用 51 种反刍动物以及 12 种非反刍动物（作为外群）的编码基因，构建了高质量的直系同源基因集，并基于该基因集，找到了反刍动物正选择基因（PSGs），快速进化基因（REGs）以及新演化的基因。从基因组结构变异，编码基因及非编码调控元件进化角度，利用基因组及转录组数据建立了反刍动物表型变化与遗传差异之间的联系，为将来反刍动物基因功能研究提供了系统发育框架。【Chen et al, 2019 *Science*】

2. 古今样品对比揭示朱鹮群体演化历程，促进濒危鸟类保育

国家一级保护动物朱　是世界濒危鸟类保护的旗舰物种，也是人工保育最为成功的物种之一。本研究基于九家博物馆 57 份朱　历史样品的全基因组重测序数据，结合保育区现生朱　群体数据，进行古今朱　样品基因组比较，研究发现朱　的群体下降早在约一万年前就开始了。朱　种群的生存受到人类活动的影响远比曾以为的近几十年要发生的更早更严重。现代朱　群体失去了将近一半的历史群体遗传多样性，同时，现生群体由于长期的近交积攒了较高的有害突变积累，展现出明显的近交效应。该研究不仅为朱　的遗传恢复工作提供了一个遗传信息背景，更为其他濒危物种的保育工作提供了一个新的利用博物馆样品的遗传研究范例。【Feng et al. 2019 *Current Biology*】



3. 转座子对草莓箭毒蛙基因组的影响

对生活在尼加拉瓜到巴拿马，中美洲加勒比海沿岸的低地森林中的一种色彩绚丽、具有特殊毒性的小型陆地蛙草莓箭毒蛙进行了基因组测序，发现其基因组的大部分是由高度重复序列的转座子组成。重复元件在鱼和蛙类之间存在大量的水平转移，且在转移过后还在继续扩增。大型两栖动物基因组的大小至少在一定程度上可以解释为一个新的转座因子不断入侵的过程，且这些转座子尚未在生殖系中被抑制。除此以外，还通过基因组信息鉴定出了该毒蛙的一个特别离子通道，并讨论了其与皮肤对隔离毒素的自耐受进化的关系。【Rogers et al. 2018 *Molecular Biology & Evolution*】

4、发布所有企鹅物种基因组草图

从头测序组装了 19 种企鹅的全基因组序列，加上已经发布的 2 个企鹅物种的全基因组序列，现存所有企鹅物种的全基因组序列均完成测序及基因组拼装。通过蛋白编码基因构建了企鹅的系统发生树，发现 Aptenodytes 属是所有其他企鹅的姐妹群，为企鹅极地适应特征的研究提供了基因组信息。【Pan et al. 2019 *GigaSience*】

Biodiversity Genomics Lab

Dr. Guojie Zhang, Adjunct 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***, ***Cell***, and several grant-giving agencies in many countries. He has more than 100 publications, including ***Science***, ***Nature***, ***Cell***, ***Nature Genetics***, ***Nature Communication***, ***PNAS***, ***Current Biology***. In this year, our group reported results from a large-scale ruminant genome sequencing project, which produced a well-supported ruminant phylogenetic tree and provided insights into evolution and distinct traits of ruminants. We reported a study involved 57 genomes of historic and modern samples of crested ibis, reported the interrogated genomic characteristics of strawberry poison frog, and a phylogenetic study with genomes of 19 penguin species. Together. we published 16 high profile SCI papers, including ***Science*** (1), ***Current Biology*** (1), ***Molecular Biology & Evolution*** (2), ***GigaScience*** (3).

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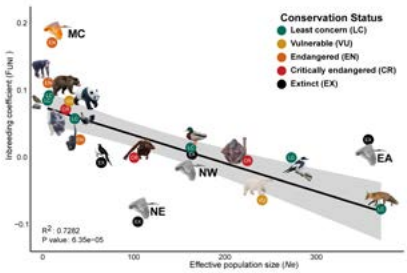
1. Large-scale ruminant genome sequencing provides insights into their evolution and distinct traits

Using whole-genome orthologous sequences obtained from 51 ruminants, we have produced a new well-supported ruminant phylogenetic tree. The new tree resolves previous controversies over the deep branches of ruminant families, as well as the highly radiated Bovidae family. We estimated the emergence of crown Ruminantia to the late Oligocene (39.1million to 32.3 million years ago) and that of Pecora to the Neocene (23.3 million to 20.8 million years ago). Investigations of demographic history revealed massive population decline events that occurred in most ruminant species, starting from ~100,000 to 50,000 years ago, which was temporally and spatially concurrent with the increased human activities on different continents during this period. We further identified many genomic changes that associate with important evolutionary innovations, such as the multichambered stomach, headgear, body size variation, cursorial locomotion, and dentition.

2. The genomic footprints of the fall and recovery of the crested ibis



To evaluate consequence of genetic restoration requires knowledge of temporal changes to genetic diversity before and after the advent of management programs. A growing number of studies have included small numbers of genomic loci extracted from historic specimens. We extend this approach to its natural conclusion, by characterizing the complete genomic sequences of modern and historic population samples of the crested ibis (*Nipponia nippon*), an endangered bird that is perhaps the most successful example of how conservation effort has brought a species back from the brink of extinction. The recovery of population size was accompanied loss of ancestral genetic variation and high deleterious mutation load. We furthermore show how genetic drift coupled to inbreeding following the population bottleneck has largely purged the ancient polymorphisms from the current population. In conclusion, we demonstrate the unique promise of exploiting genomic information held within museum samples for conservation and ecological research.

3. Genomic takeover by transposable elements in the strawberry poison frog

The strawberry poison frog, *Oophaga pumilio* is unusual because of its life history, toxicity, and variable coloration. We sequenced the genome of the strawberry poison frog. The majority of the genome are high copy number repetitive elements with low differentiation across copies. We observed phylogenetic evidence for horizontal transfer (HT) of Mariner elements, possibly between fish and frogs and evidence for ongoing proliferation after HT. We identified the complement of ion channels in the first genomic sequenced poison frog and discussed its relation to the evolution of auto-resistance to toxins sequestered in the skin.

4. High-coverage genomes to elucidate the evolution of penguins

We reported 19 high-coverage genomes that, together with 2 previously published genomes, encompass all extant penguin species. We produced a well-supported phylogenetic tree of penguins with genome data. We demonstrated that the genus *Aptenodytes* is basal and sister to all other extant penguin genera, providing intriguing new insights into the adaptation of penguins to Antarctica.

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李　冀 Ji Li, 2018
宁冬冬 Dongdong Ning, 2018

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适应性进化与进化医学

吕雪梅，博士，研究员，博士生导师，适应性进化与进化医学学科组负责人。主要从事适应性进化的群体基因组学研究。以物种和细胞群体水平的变异和进化为核心，探讨中性进化和自然选择等进化驱动力的对群体动态演化相对作用，从而揭示从遗传和表观变异的累积、到适应性改变的形成和进化一系列过程的基本规律，成果发表在 *Genome Res*、*MBE*、*PNAS* 等著名期刊上。近年来关注肿瘤形成研究，其突变规律、群体动态、多样性形成和演变、适应性改变等进化规律仍有大量悬而未决的问题。学科组从新的起点开始，经过几年的努力，在“体细胞变异和进化”方面取得了一系列原创性进展；正在将工作重点从基础理论研究转向新理论框架指导下的临床应用研发，利用新材料、新技术，研究肿瘤治疗的“老药新用”策略。

重要成果及产出：

1. Yuezheng Zhang[1],Yawei Li[1],Tao Li[1],Xu Shen[1],Tianqi Zhu,Yong Tao,Xueying Li,Di Wang,Qin Ma,1,3 Zheng Hu,-Jialin Liu,Jue Ruan,Jun Cai, Hurng-Yi Wang*,**Xuemei Lu***. Genetic Load and Potential Mutational Meltdown in Cancer Cell Populations [J]. Molecular biology and evolution, 2019, 36(3): 541-52.IF13.944
2. Ying Xiang, Kai Yan, Qian Zheng, Hai-qiang Ke, Jie Cheng,Wenjun Xiong, Xin Shi, Lei Wei, Min Zhao, Fei Yang, Ping Wang, Xing Lu,LiFu, **Xuemei Lu***, and Feng Li*. Histone Demethylase KDM4B Promotes DNA Damage by Activating Long Interspersed Nuclear Element-1 [J]. Cancer Research, 2019, 79(1): 86.IF9.602
3. YIN L, LUO Y, XU X, et al. 2019. Virtual methylome dissection facilitated by single-cell analyses. Epigenetics Chromatin [J], 12: 66.IF5.145
4. Juan Li1, Lan Jiang[1], Chung-I Wu,**Xuemei Lu***, Shu Fang*, and Chau-Ti Ting*. Small Segmental Duplications in Drosophila-High Rate of Emergence and Elimination [J]. Genome Biol Evol, 2019, 11(2): 486-96.IF4.019
5. Xue Bai[1], Zhenzhen Liu[1], Xiaojian Shao, Di Wang, Encheng Dong, Yan Wang, Chung-I Wu, Yunfei Yuan, **Xuemei Lu***, Chunyan Li*. The heterogeneity of plasma miRNA profiles in hepatocellular carcinoma patients and the exploration of diagnostic circulating miRNAs for hepatocellular carcinoma [J]. PloS one, 2019, 14(2): e0211581.IF3.337
6. Furong Qi, Airong Yang, Sadaf Ambreen, Xue Bai, Yali Hou, **Xuemei Lu***. Birth and death of Mx genes and the presence/absence of genes regulating Mx transcription are correlated with the diversity of anti-pathogenicity in vertebrate species [J]. Mol Genet Genomics, 2019, 294(1): 121-33.IF2.685

1. 肺癌细胞群的遗传负荷和突变消亡

具有高突变率的大型基因组易于积累有害突变，其速度快于自然选择所能清除的速度（穆勒棘轮）。因此，它可能导致小种群的灭绝。与大多数单细胞生物相比，基因组庞大且不能重组、突变率高的癌细胞特别容易受到这种“突变消亡”的影响。我们通过监测 HeLa 细胞系的单细胞克隆，描述了延缓细胞增殖速度的有害突变。主要的突变事件是拷贝数变异(CNVs)，从适应度数据估计，平均每个细胞分裂发生 0.29 个拷贝数变异。平均适应度降低非常高，估计每个突变达到 18%。因此 Hela 细胞系有非常大的遗传负荷，在这个水平上，自然群体可能面临突变消亡。我们推测 Hela 细胞种群只有在种群规模足够大时才有可能避免灭绝。由于 CNVs 在大多数细胞系和肿瘤组织中很常见，这提示了癌细胞的脆弱性，该发现可以在肿瘤治疗中加以利用。【Yuezheng Zhang et al., Molecular Biology and Evolution. 2019, IF=13.944】

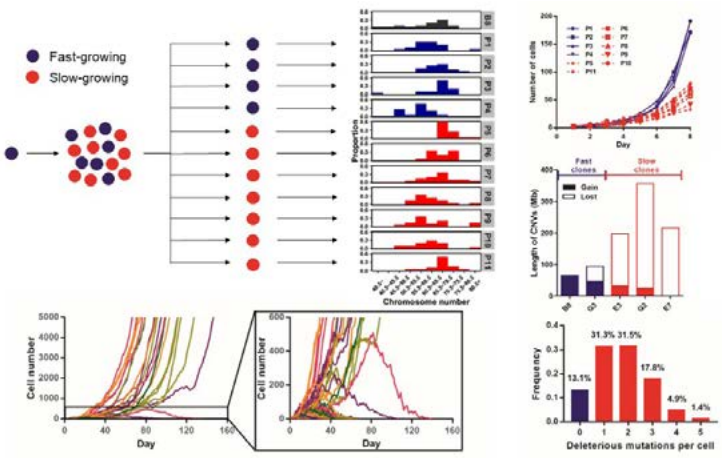

图 1. 有害突变的积累降低肿瘤细胞生长速率

2.KDM4B 通过激活 LINE-1 促进 DNA 损伤

蛋白去甲基化酶 KDM4B 能催化 H3K9me3 的去甲基化反应，通过系统分析癌细胞中 H3K9me3 的全基因组分布，我们发现 H3K9me3 在长散在元件 (LINE-1) 中大量富集（如图 2）。值得注意的是，依赖于 KDM4B 的 H3K9me3 中有相当大一部分位于进化上较年轻的的 LINE-1 元件中（如图 3），这些元件保留了反转录转座活性。进一步研究发现，过表达 KDM4B 通过对 H3K9me3 的去甲基化会导致 LINE-1 拷贝数、转座活性和 DNA 损伤程度增加。有趣的是，KDM4B 抑制剂的使用抑制了 LINE-1 介导的 DNA 损伤。我们的研究不仅发现 KDM4B 是一种新型的 LINE-1 调控因子，更多的调控进化上较年轻的 LINE-1 元件，而且提示 KDM4B 过表达在肿瘤发生过程中具有意想不到的致癌作用，为开发新的癌症预防策略和治疗方法提供了线索。【Xiang, Yan et al. 2019., Cancer Research， IF=9.602】

Adaptive Evolution and Evolutionary Medicine

Dr. Xuemei Lu, Professor, Principle Investigator. Adaptive evolution can happen at various levels, population, organism, or cellular. Both organ exhaustion and cell abnormal proliferation are involved in accumulation of somatic mutation and adaptation evolution. An obvious manifestation of such short-term evolution is cancer. The evolution theory is applicable at organism and cell population levels. Carrying out the approaches in population genetics, evolutionary biology and genomics, we study the genetic and epigenetic basis of species adaptation, and the dynamic accumulation process and features of somatic as well. Based on this framework, we are depicting the pattern of mutation accumulation and selection, as well as identifying crucial mutations driving fitness changes in animal organisms and tumor cells.

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1. Genetic load and mutation meltdown of Cancer cells

Large genomes with elevated mutation rates are prone to accumulating deleterious mutations more rapidly than natural selection can purge (Muller's ratchet). As a consequence, it may lead to the extinction of small populations. Relative to most unicellular organisms, cancer cells, with large and nonrecombining genome and high mutation rate, could be particularly susceptible to such "mutational meltdown." However, the most common type of mutation in organismal evolution, namely, deleterious mutation, has received relatively little attention in the cancer biology literature. Here, by monitoring single-cell clones from HeLa cell lines, we characterize deleterious mutations that retard the rate of cell proliferation. We suspect that HeLa cell populations may avoid extinction only after the population size becomes large enough. Because CNVs are common in most cell lines and tumor tissues, the observations hint at cancer cells' vulnerability, which could be exploited by therapeutic strategies.

2.KDM4B promotes DNA damage by activating LINE-1

Here, we assess whole-genome H3K9me3 distribution in cancer cells and find that H3K9me3 is largely enriched in long interspersed nuclear element-1 (LINE-1). Asignificant proportion of KDM4B-dependent H3K9me3 was located in evolutionarily young LINE-1 elements, which likely retain retrotransposition activity. Furthermore, KDM4B overexpression enhanced LINE-1 retrotransposition efficacy, copy number, and associated DNA damage. Interestingly, Pharmacologic inhibition of KDM4B significantly reduced LINE-1 expression and DNA damage in breast cancer cells with excessive KDM4B. Our study not only identifies KDM4B as novel regulator of LINE-1, but it also suggests an unexpected oncogenic role for KDM4B overexpression in tumorigenesis.

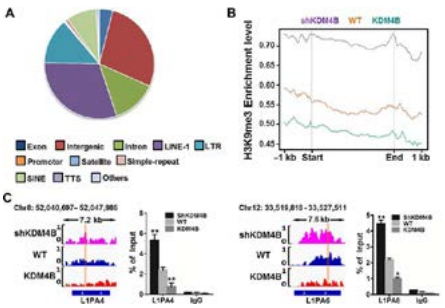

Fig2. KDM4B preferentially regulates H3K9me3 signal on evolutionarily young LINE–1 elements

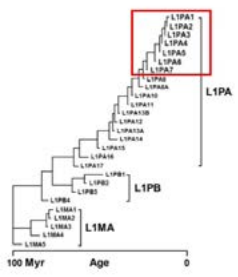

Fig3. LINE–1 phylogenetic tree

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客座学生（Visiting Students）

李梓锋 Li, ZF 李丰邑 Li, FY

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。

重要成果及产出：

1. **Pengcheng Ma**[1], Ning-Ning Song[1], **Yongxin Li**[1], Qiong Zhang, Lei Zhang, **Longlong Zhang, Qinghua Kong,Li Ma, Xiangcai Yang, Biyu Ren, Chaocui Li, Xudong Zhao,** Yan Li, Ying Xu,Xiang Gao*, Yu-Qiang Ding*,and **Bingyu Mao*.** Fine-Tuning of Shh/Gli Signaling Gradient by Non-proteolytic Ubiquitination during Neural Patterning. ***Cell Reports***, 2019，28, 541–553
2. **Pengcheng Ma**[1], Ning-Ning Song[1], Xiaoning Cheng[1], **Liang Zhu**, Qiong Zhang , **Longlong Zhang**, **Xiangcai Yang**, **Huishan Wang , Qinghua Kong**, Deli Shi*, Yu-Qiang Ding*, **Bingyu Mao** *. ZC4H2 stabilizes RNF220 to pattern ventral spinal cord through modulating Shh/Gli signaling. ***J Mol Cell Biol***, 2019，mjz087
3. Lei Zhang[1], Ning-Ning Song, Qiong Zhang,Wan-Ying Mei, Chun-Hui He, **Pengcheng Ma**, Ying Huang,Jia-Yin Chen, **Bingyu Mao**, Bing Lang, Yu-Qiang Ding*. Satb2 is required for the regionalization of retrosplenial cortex. ***Cell Death & Differentiation***, 2019, doi.org/10.1038/s41418-019-0443-1

1. 泛素连接酶 RNF220 调控 Shh 信号与神经系统图式形成

Shh 信号在脊椎动物腹侧神经管的图式形成中起着关键作用。Shh 信号在腹侧神经管形成一个由腹侧到背侧递减的浓度梯度，调节转录因子 Gli 的激活形式（GliA）与抑制形式（GliR）的比例，最终决定不同区域神经细胞的分化命运。RNF220 在小鼠胚胎腹侧神经管特异性表达，在 RNF220 敲除小鼠胚胎中，背侧神经管发育正常，而腹侧神经管的图式形成发生紊乱，提示 RNF220 可能参与了 Shh 信号的调控。在分子机制上，通过体内体外实验，证实 RNF220 与 Gli 相互作用并可以促进其 K-63 连接的泛素化，并诱导 Gli 的出核转运，并鉴定了参与这一调控过程的 Gli 出核转运信号序列。RNF220 对 Gli 的这种调控效应对于 GliA 和 GliR 都是成立的，从而降低细胞核内有效的 Gli 水平，维持适当的 GliA 和 GliR 的活性梯度，参与神经细胞分化的调控。本研究揭示了早期脊椎动物神经系统发育过程中形态发生素活性梯度调控的一种新的分子机制，阐明了非降解性泛素化修饰介导的 Shh/Gli 信号通路调控的新机制。 【Ma P et al. 2019， ***Cell Reports***】

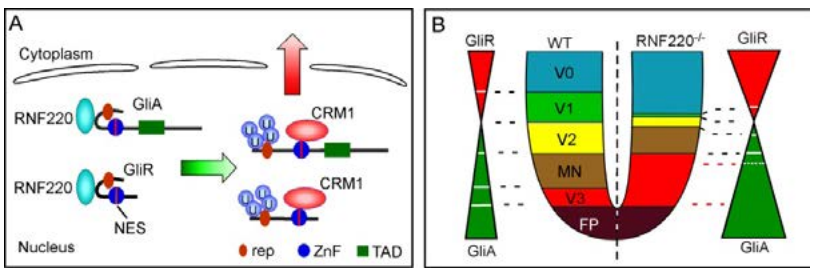

图 1.RNF220 通过 Shh/Gli 信号通路调控脊椎动物腹侧神经管的图式形成。
Fig.1. RNF220 regulates Shh/Gli signaling and ventral neural patterning.

2. ZC4H2 通过稳定 RNF220 调控 Gli 信号与神经系统图式形成

ZC4H2 基因编码一种锌指蛋白，其突变与多种人类疾病相关，包括发育迟滞、智力障碍、肌张力障碍等，但其致病机制尚不清楚。本研究发现，ZC4H2 在小鼠神经管腹侧中高表达，在小鼠和斑马鱼模型中，ZC4H2 突变都会引起腹侧神经管神经分化异常，与 RNF220 突变表型完全一致。进一步的分析表明，ZC4H2 可结合并稳定 RNF220。在 ZC4H2 突变小鼠中，RNF220 蛋白水平严重下调，进而引起 Gli 泛素化修饰与信号活性的异常，最终造成神经细胞分化的异常。本研究为揭示 ZC4H2 突变导致神经发育缺陷的分子机制提供了重要线索。 【Ma P et al. 2019， ***J Mol Cell Biol***】

Mechanisms of Neural Patterning and Evolution

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

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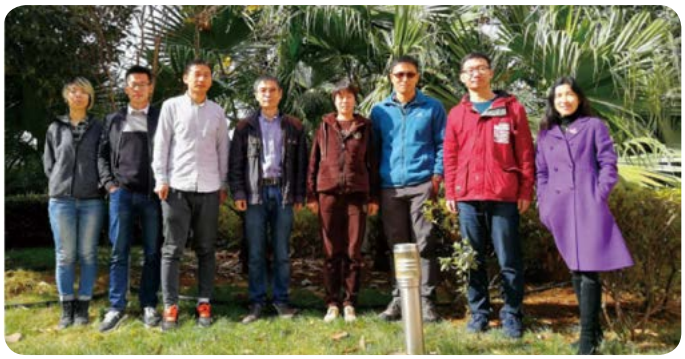

1. Fine tuning of Shh/Gli signaling gradient by non-proteolytic ubiquitination during neural patterning

Sonic Hedgehog (Shh) signaling plays crucial roles in patterning the ventral neural tube, which is transformed into opposing gradients of repressor and activator forms of Glis. Here we show that the fine tuning of the shape of the Gli gradients through non-proteolytic ubiquitination-mediated nuclear exportation plays an important role in the control of local neural cell fate. Loss of RNF220, a ventral neural specific ubiquitin E3 ligase, leads to expansion of both the intermediate V0 and ventral V3 neurons, at the expenses of motor neurons, V1 and V2 neurons in between. We show that RNF220 interacts with all Glis, either in their activator or repressor forms, induces their K63-linked ubiquitination and promotes their nuclear export, likely through unmasking of a newly identified nuclear export signal. We propose that RNF220 works to refine the Gli gradients during neural patterning through limiting the effective Gli levels in the nucleus. Our work provides another level of the regulation of Shh signaling and gradient formation.

2. ZC4H2 stabilizes RNF220 to pattern ventral spinal cord through modulating Shh/Gli signaling

ZC4H2 encodes a C4H2 type zinc-finger nuclear factor, the mutation of which has been associated with disorders with various clinical phenotypes in human, including developmental delay, intellectual disability and dystonia. ZC4H2 has been suggested to regulate spinal cord patterning in zebrafish as a co-factor for RNF220, an ubiquitin E3 ligase involved in Gli signaling. Here we showed that ZC4H2 and RNF220 knockout animals phenocopies each other in spinal patterning in both mouse and zebrafish, with mispatterned progenitor and neuronal domains in the ventral spinal cord. We showed evidence that ZC4H2 is required for the stability of RNF220 and also proper Gli ubiquitination and signaling *in vivo*. Our data provides new insights into the possible etiology of the neurodevelopmental impairments observed in ZC4H2 associated syndromes.

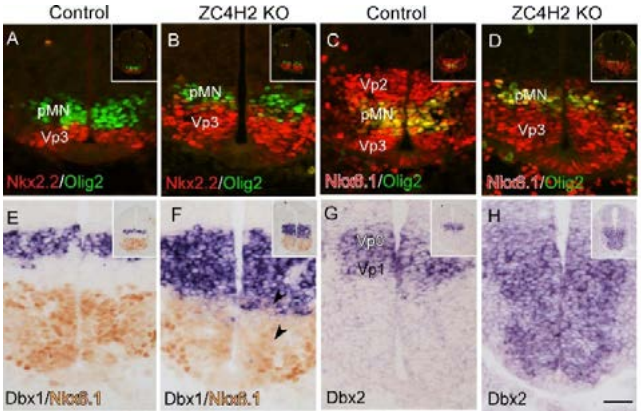

图 2. ZC4H2 突变引起小鼠胚胎神经管腹侧神经分化异常。
Fig.2. Mutation of ZC4H2 leads to ventral neural patterning defects in mouse embryos.

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哺乳动物胚胎发育

郑　萍，博士，研究员，课题组长。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. **Zhang WD** [1], **Chen ZL** [1], Zhang DF, **Zhao B**, Liu L, Xie ZY, Yao YG, **Zheng P***. KHDC3L mutation causes recurrent pregnancy loss by inducing genomic instability of human early embryonic cells. ***PLOS Biology***, 2019 Oct 14;17(10): e3000468, 5 yr IF 9.311.
2. **Ma H** [1], Zhai J [1], Wan H [1], Jiang X [1], Wang X, **Wang L**, Xiang Y, **He X**, Zhao ZA, **Zhao B**, **Zheng P***, Li L*, Wang H*. In vitro culture of cynomolgus monkey embryos beyond early gastrulation. ***Science***, 2019 Nov 15; 366(6467), 5 yr IF 43.644.
3. **Xin Luo** [1], **Yaoxi He** [1], Chao Zhang [1], **Xiechao He** [1], Lanzhen Yan [1], **Min Li**, **Ting Hu**, **Yan Hu**, **Jin Jiang**, **Xiaoyu Meng**, Weizhi Ji, Xudong Zhao, **Ping Zheng***, Shuhua Xu*, **Bing Su***. Trio deep-sequencing does not reveal unexpected off-target and on-target mutations in Cas9-edited rhesus monkeys. ***Nature Communications,*** 2019 Dec 4;10(1):5525. 5 yr IF 13.811.

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对胚胎顺利发育至关重要。我们以人胚胎干细胞为研究模型，发现 *KHDC3L* 基因在人早期胚胎多能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 DNA 双链断裂损伤修复，并激活 PARP1 酶活性，促进其他的 DNA 损伤修复途径。上述功能受到两个重要苏氨酸位点的磷酸化调控。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）。利用人胚胎干细胞研究体系，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，发生胚胎致死和复发性流产。

【***PLOS Biology***, 2019 Oct 14;17(10): e3000468】

2. 建立了灵长类着床后早期胚胎体外培养体系，为研究灵长类早期胚胎发育提供了关键技术平台

受限于伦理和研究技术，灵长类早期胚胎发育的研究非常有限，特别是着床后的早期发育。目前，人类对灵长类胚胎内、中、外三个胚层的分化及胚胎体轴的建立等关键发育事件仍知之甚少。通过合作研究，我们建立了猴胚胎体外培养系统，可以将食蟹猴囊胚体外培养至原肠运动出现，并进一步发育至受精后 20 天。并且，从形态学、标记分子染色和单细胞转录组等多个角度提供了充分的证据，证明体外发育的食蟹猴胚胎高度重现体内胚胎发育包括原肠运动在内的多个重要事件。本研究以与人遗传与进化较为接近的食蟹猴作为模式动物，避免了人类胚胎培养 14 天的伦理限制，首次证明灵长类动物胚胎可以在没有母体支撑的情况下体外发育至原肠运动，并重现了灵长类动物早期胚胎发育的几个关键事件。为探索灵长类早期胚胎发育和原肠运动开辟了崭新研究平台，也为人类深入认识胚胎发育机制和体外孕育生命（非人）探索提供了重要数据。【***Science***, 2019 Nov 15; 366(6467】

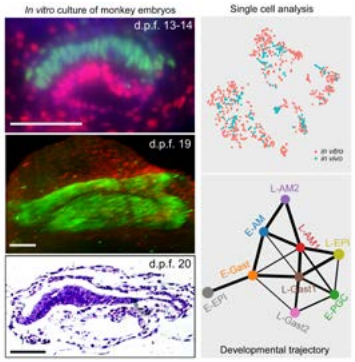

图 1. 体外培养的猴早期胚胎

Mammalian Embryonic Development

Dr. Ping Zheng, Principal Investigator, joined in Kunming Institute of Zoology, Chinese Academy of Sciences in 2009. The laboratory studies 1) how stem cells safeguard their genomic stability, 2) the biology of germ-line stem cells in male and female gonads, and 3) the early embryogenesis of non-human primates. We use mouse, monkey and tree shrew as animal models.

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1. KHDC3L mutation causes recurrent pregnancy loss by inducing genomic instability of human early embryonic cells

Recurrent pregnancy loss (RPL) is an important complication in reproductive health. ~50% of RPL cases are unexplained and understanding the genetic basis is essential for its diagnosis and prognosis. Herein we report causal KHDC3L mutations in RPL. KHDC3L is expressed in human epiblast cells and ensures their genome stability and viability. Mechanistically, KHDC3L binds to PARP1 to stimulate its activity. In response to DNA damage, KHDC3L also localizes to DNA damage sites and facilitates homologous recombination (HR)-mediated DNA repair. KHDC3L dysfunction causes PARP1 inhibition and HR repair deficiency, which is synthetically lethal. Notably, we identified two critical residues Thr145 and Thr156, whose phosphorylation by ATM is essential for KHDC3L's functions. Importantly, two deletions of KHDC3L (p.E150_V160del and p.E150_V172del) were detected in female RPL patients, both of which harbor a common loss of Thr156 and are impaired in PARP1 activation and HR repair. In summary, our study reveals KHDC3L as a new RPL risk gene and its critical function in DNA damage repair pathways.

2. In vitro culture of cynomolgus monkey embryos beyond early gastrulation

Gastrulation is a key event in embryonic development when the germ layers are specified and the basic animal body plan is established. The complexities of primate gastrulation remain a mystery due to the difficulties in accessing primate embryos at this stage. Here, we report the establishment of an in vitro culture (IVC) system which supports the continuous development of cynomolgus monkey blastocysts beyond early gastrulation and to 20 days post fertilization. The IVC embryos highly recapitulated the key events of in vivo early post-implantation development, including segregation of the epiblast and hypoblast, formation of the amniotic and yolk sac cavities, appearance of the primordial germ cells, and establishment of the anterior-posterior axis. Single-cell RNA-seq analyses of the IVC primate embryos provide information about lineage specification during primate early post-implantation development. This system provides a platform to explore the characteristics and mechanisms of early post-implantation embryogenesis in primates with possible conservation of cell movements and lineages in human embryogenesis.

团队成员 (Lab Member)

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郭　琨 (Dr. Guo, K)	助理研究员
马怀孝 (Dr. Ma, HX)	助理研究员
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姜方洁	Jiang, Fangjie	2017
宁雨琪	Ning, Yuqi	2017
龚道华	Gong, Daohua	2018
唐　敏	Tang, Min	2018
谢　恒	Xie, Heng	2018
陶慧玲	Tao, Huiling	2019

表观遗传与发育调控

焦保卫，博士，研究员，博士生导师。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。研究团队发现 TAR DNA 结合蛋白 43 (TDP-43) 在乳腺再生及发育过程中起关键作用，同时发现 TDP-43 影响乳脂分泌过程。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. **Zhao LM**[1], **Li LL**[1], **Xu HB**, **Ke H**, **Zou L**,**Yang Q**,Shen C-K J, Nie JY, **Jiao BW***. TDP-43 is required for mammary gland repopulation and proliferation of mammary epithelial cells. ***Stem Cells Dev.*** 2019 Jul 15;28(14):944-953
2. **Zhao LM**[1], **Ke H**[1], **Xu HB, Wang GD, Zhang HL, Zou L**, Xiang S, Li MY, Peng L, Zhou MF, Li LL, Ao L, **Yang Q**, Shen C-K J, Yi P*, Wang L*, **Jiao BW***. TDP-43 facilitates milk lipid secretion by post-transcriptional regulation of Btn1a1 and Xdh. ***Nature Communications.***2019(Accepted)

1. TDP-43 对乳腺再生和乳腺上皮的增殖是必须的

乳腺干细胞（MaSCs）被认为是乳腺癌的起始细胞，在调节乳腺内环境平衡和发育方面发挥重要作用。我们早期的研究发现 TAR DNA 结合蛋白 43 (TDP-43)，是一种 RNA 结合蛋白，在三阴性乳腺癌的进展过程中起关键的调节作用。然而，TDP-43 在 MaSCs 中的功能尚不清楚。基于乳腺的单细胞数据分析，TDP-43 可能参与了 MaSCs 的调控。因此，我们研究了 TDP-43 对乳腺发育的影响。我们通过体内和体外实验验证了 TDP-43 是乳腺再生所必须的，这也揭示了其在 MaSCs 调控中的潜在作用。TDP-43 敲降能抑制乳腺上皮细胞的增殖和乳腺的形态发生。RNA-seq 数据及其他实验发现，TDP-43 的缺失导致了细胞周期相关基因的上调，为 TDP-43 调控乳腺再生提供了可能的机制。因此，我们的结果揭示了 TDP-43 在乳腺上皮细胞中先前未知的角色。【Zhao LM et al. 2019 *Stem Cells and Development*, IF=3.147】

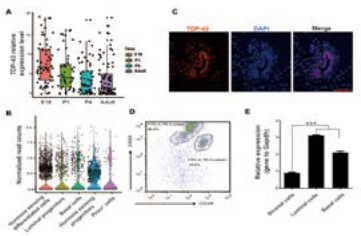

图 1. TDP−43 表达与 MaSCs 呈正相关

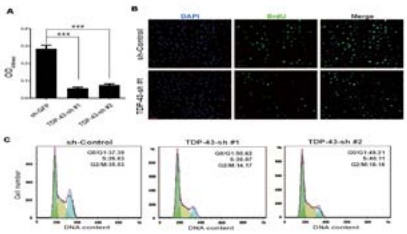

图 2. 下调 TDP43 抑制乳腺上皮细胞增殖

2. 染色体水平基因剂量重平衡有利于肿瘤进程

乳脂的分泌是将营养和能量从亲代传递给后代的关键过程。但是，潜在的分子机制尚不清楚。我们发现 RNA 结合蛋白 TDP-43 在哺乳动物进化中受到正向选择。乳腺特异性敲除小鼠模型中，发现 TDP-43 基因的缺失会导致乳脂上皮细胞中大量脂质液滴的积累，引起乳汁分泌异常，最终导致幼仔严重营养不良。在哺乳期妇女的人乳样品中，我们发现 TDP-43 的表达水平与较高的产奶量呈正相关。在分子机制上，TDP-43 通过转录后水平调控，稳定下游基因 Btn1a1 和 Xdh 的 mRNA 水平，从而影响乳脂分泌过程。我们的结果表明 TDP-43 在乳脂分泌中的关键作用，为临床泌乳不足的筛查和干预提供了潜在的策略。【Zhao LM et al. 2019 *Nature Communications*. IF=13.811】

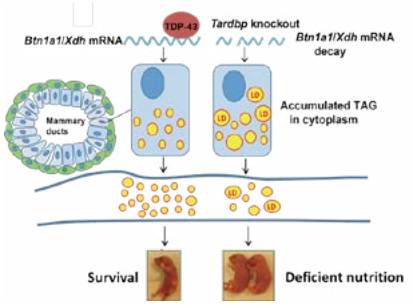

图 3.TDP−43 调控乳脂分泌的机制

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. Research team identified a crucial regulatory role of TAR DNA-binding protein 43 (TDP-43), which is important in regulating mammary gland repopulation and development. Meanwhile, our results highlights the critical role of TDP-43 in milk lipid secretion. Currently, over 20 papers have been published in international journals,such as *Cell*、*PNAS*、*Cell Death & Disease*.
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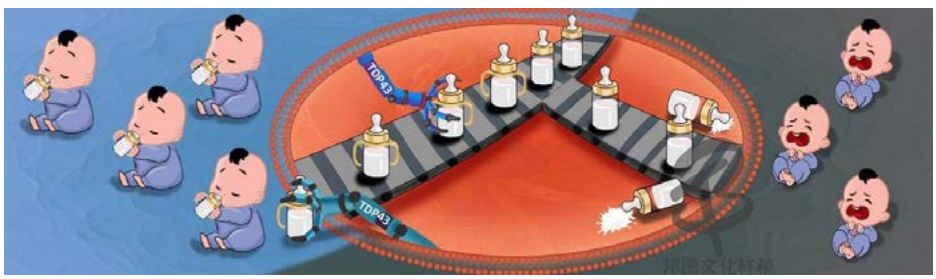
1.TDP-43 is Required for Mammary Gland Repopulation and Proliferation of Mammary Epithelial Cells

Mammary gland stem cells (MaSCs), assumed to be the original cells of breast cancer, play essential roles in regulating mammary gland homeostasis and development. Previously, we identified a crucial regulatory role of TAR DNA-binding protein 43 (TDP-43), an RNA-binding protein, in the progression of triple-negative breast cancer. However, the function of TDP-43 in MaSCs is unclear. Based on single-cell data analysis of the mammary gland, TDP-43 showed potential involvement in the regulation of MaSCs. We therefore investigated the effects of TDP-43 on the mammary gland development. Our data both in vitro and in vivo demonstrated that TDP-43 was required for the mammary gland repopulation, which suggested the potential role in the regulation of MaSCs. Knockdown of TDP-43 inhibited proliferation of mammary epithelial cells (MECs) and mammary morphogenesis. RNA-seq data and other experiments identified that loss of TDP-43 induced the upregulation of genes related to the cell cycle, providing a possible mechanism for TDP-43 in regulating mammary gland repopulation. Thus, our findings indicate a previously unknown role of TDP-43 in MECs.

2. TDP-4 3 facilitates milk lipid secretion by post-transcriptional regulation of Btn1a1 and Xdh

Milk lipid secretion is a critical process for the delivery of nutrition and energy from parent to offspring. However, the underlying molecular mechanism is less clear. Here we report that TDP-43, an RNA-binding protein, underwent positive selection in the mammalian lineage. Furthermore, TDP-43 gene (Tardbp) loss induces accumulation of large lipid droplets and severe lipid secretion deficiency in mammary epithelial cells to outside alveolar lumens, eventually resulting in pup starvation within three weeks postpartum. In human milk samples from lactating women, the expression levels of TDP-43 is positively correlated with higher milk output. Mechanistically, TDP-43 exerts post-transcriptional regulation of Btn1a1 and Xdh mRNA stability, which are required for the secretion of lipid droplets from epithelial cells to the lumen. Taken together, our results highlights the critical role of TDP-43 in milk lipid secretion, providing a potential strategy for the screening and intervention of clinical lactation insufficiency.



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灵长类进化遗传与发育

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

重要成果及产出：

1. Ming-Li Li#, Shi-Hao Wu#, Jin-Jin Zhang, Hang-Yu Tian, Yong Shao, Zheng-Bo Wang, David M. Irwin,Jia-Li Li, Xin-Tian Hu* and **Dong-Dong Wu***, 547 transcriptomes from 44 brain areas reveal features of the aging brain in non-human primates. ***Genome Biology***, 2019, 20:258
2. Yong Shao#, Hang-Yu Tian#,Jing-Jing Zhang#,Hamed Kharrati-Koopaee#,Xing Guo,Xiao-Lin Zhuang, Ming-Li Li, Hojat Asadollahpour Nanaie, Elahe Dehghani Tafti, Bahador Shojaei,Mohammad Reza Namavar, Narges Sotoudeh, Adeola Oluwakemi Ayoola, Jia-Li Li, Bin Liang,*Ali Esmailizadeh,* Shu Wang,* and **Dong-Dong Wu***, Genomic and Phenotypic Analyses Reveal Mechanisms Underlying Homing Ability in Pigeon, ***Molecular Biology and Evolution***, doi:10.1093/molbev/msz208
3. Lin Zeng#, Xiao-Long Tu#, He Dai#, Feng-Ming Han#, Bing-She Lu#, Ming-Shan Wang,Hojjat Asadollahpour Nanaei, Ali Tajabadipour, Mehdi Mansouri, Xiao-Long Li, Li-Li Ji, David M. Irwin,Hong Zhou, Min Liu, Hong-Kun Zheng, Ali Esmailizadeh* and Dong-Dong Wu*, Whole genomes and transcriptomes reveal adaptation and domestication of pistachio, ***Genome Biology***, 2019,20:79
4. Shi Y, Fan S, Wu M, Zuo Z, Li X, Jiang L, Shen Q, Xu P, Zeng L, Zhou Y, Huang Y, Yang Z, Zhou J, Gao J, Zhou H, Xu S, Ji H, Shi P, **Wu DD*,** Yang C*, Chen Y*. ***Nature Communications***. 2019 10(1):4892.4.
5. **Wu DD**#, Yang CP#, Wang MS#, Dong KZ#, Yan DW#, Hao ZQ, Fan SQ, Chu SZ, Shen QS, Jiang LP, et al: Convergent genomic signatures of high altitude adaptation among domestic mammals. ***National Science Review*** 2019.

1. 揭示非人灵长类大脑衰老的遗传机制

随着老龄化社会的发展，大脑衰老成为大家日益关系的话题。大脑衰老会带来记忆力减退，认知能力下降，并且与很多神经退行性疾病密切相关。大脑衰老是一个复杂的过程，它依赖于多个脑区的精确调控，而以往的研究通常集中于少数脑区。我们缺乏一个涵盖多个脑区的转录图谱来解析大脑衰老背后的分子机制。

基于大规模转录组数据分析发现，随着年龄的增长，皮质内脑区之间的表达连接性以及皮质内左右脑半球之间的表达连接性都发生了明显的下降。在各个脑区中，基因表达和选择性剪接通过不同的机制来调控大脑衰老，而不同脑区之间老化的分子机制大同小异。通过对老年狝猴的转录组数据基因共表达网络分析，研究人员发现了九个在老年猴中表现出连接性增强的模块，并解析出一个网络关键驱动基因 *PGLS*，在老年猴中表达上调，可能对大脑衰老有重要作用。通过在小鼠体内过表达 *PGLS*, 发现 *PGLS* 过表达导致小鼠出现衰老的表型，例如认知能力下降，运动能力下降和厌食等等。 进一步的生物学实验也证明 *PGLS* 过表达导致突触的丢失和细胞的凋亡。因此，研究人员推断 *PGLS* 很可能是大脑衰老的一个新的标记基因。

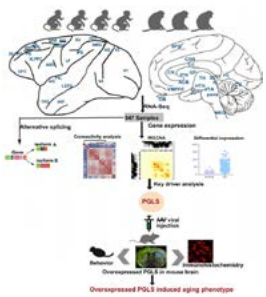

图 1. 研究路线示意图

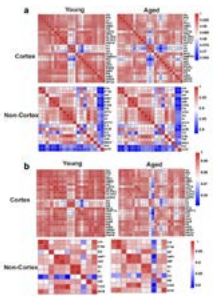

图 2. 随着年龄的增长大脑皮层对左右半球之间的表达连通性和对称性下降

2. 家鸽归巢能力的表型和遗传机制解析

信鸽的长距离归巢能力是一个令人着迷且非常复杂的性状。我们利用比较群体基因组学和表型分析揭示了家鸽归航能力的潜在分子遗传机制。神经系统相关基因 (特别是空间学习和记忆方面基因，例如 *LRP8*) 在信鸽群体中受到强烈正选择作用。进一步比较家鸽品系间转录组数据发现在海马中大量基因发生差异表达。另外，正选择作用基因 *GSR* 可能也参与到磁感应通路中影响信鸽归巢能力。

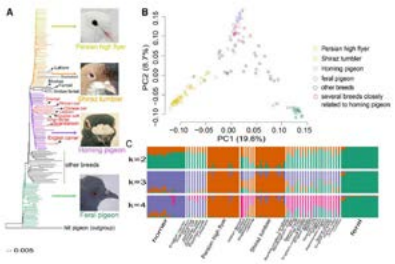

图 3. 家鸽种群遗传分析

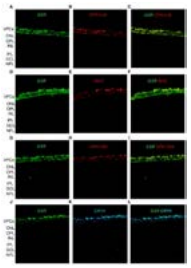

图 4. 家鸽视网膜 GSR 和视觉相关基因的表达情况。

Primate Evolutionary Genetics and Development

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

We explore non-human primate brain aging using 547 transcriptomes originating from 44 brain areas in rhesus macaques (*Macaca mulatta*). We show that expression connectivity between pairs of cerebral cortex areas as well as expression symmetry between the left and right hemispheres both decrease after aging. Although the aging mechanisms across different brain areas are largely convergent, changes in gene expression and alternative splicing vary at diverse genes, reinforcing the complex multifactorial basis of aging. Through gene co-expression network analysis, we identify nine modules that exhibit gain of connectivity in the aged brain and uncovered a hub gene, *PGLS*, underlying brain aging. We further confirm the functional significance of *PGLS* in mice at the gene transcription, molecular, and behavioral levels.

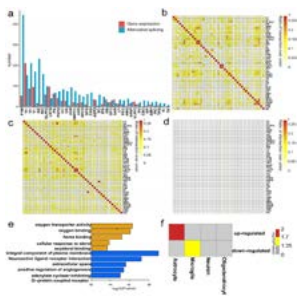

Fig 5. Aging-related transcriptional profile changes.

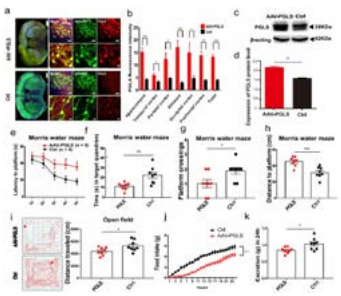

Fig 6. Overexpression of PGLS gene in mice causes aging phenotypes.

2. Mechanisms Underlying Homing Ability in Pigeon

We generate a total of 95 whole genomes from diverse pigeon breeds.Comparing the genomes fromthe homing pigeon population with those from other breeds identifies candidate positively selected genes.The hippocampus is the key organ for memory and navigation and exhibits significantly larger size in the homing pigeon.In addition,we uncover a candidate gene *GSR* (encoding glutathione-disulfide reductase) experiencing positive selection in the homing pigeon. In vitro, a magnetic field stimulates increases in calcium ion concentration in cells expressing pigeon GSR. These findings support the importance of the hippocampus (functioning in spatial memory and navigation) for homing ability,and the potential involvement of GSR in pigeon magnetoreception.

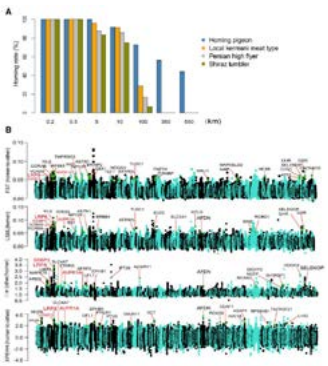

Fig 7. Comparisons of homing ability and selective sweep analyses.

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神经突触机制与功能

盛能印，博士，研究员，博士生导师。云南省“云岭高层次人才”获得者。长期从事神经科学相关研究工作，包括中枢神经系统发育形成和神经突触信息传递作用分子机制。已经在 *Cell*、*Developmental Cell*、*PNAS*、*Nature Communications* 等国际学术期刊发表论文 16 篇。目前实验室以小鼠、树 和猕猴为模型，主要研究：（1）神经突触正常生理活性的调控机制；（2）灵长类神经突触进化发育的遗传分子基础；（3）人类神经环路功能进化与神经精神疾病的内在联系及分子机制。

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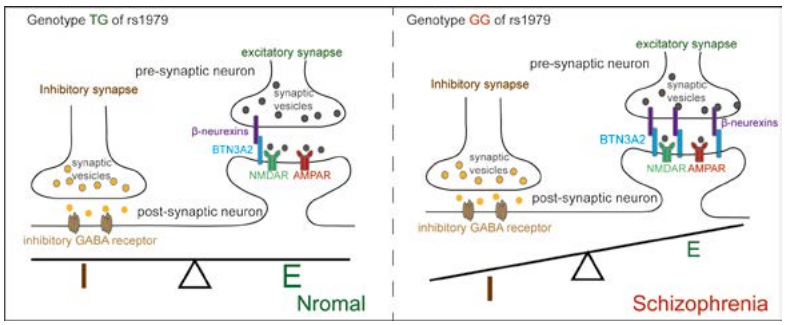
重要成果及产出：

1. Wu Y, Bi R, Zeng C, Ma C, Sun C, Li J, Xiao X, Li M, Zhang DF, Zheng P, **Sheng N***, Luo XJ*, Yao YG*. (2019) Identification of the primate-specific gene BTN3A2 as an additional schizophrenia risk gene in the MHC loci. ***EBioMedicine*** 44: 530-541.
2. Zhang DF, Fan Y, Xu M, Wang G, Wang D, Li J, Kong LL, Zhou H, Luo R, Bi R, Wu Y, Li GD, Alzheimer’s Disease Neuroimaging Initiative (ADNI), Li M, Luo XJ, Jiang HY, Tan L, Zhong C, Fang Y, Zhang C, **Sheng N**, Jiang T, Yao YG*. (2019) Complement C7 is a novel risk gene for Alzheimer’s disease in Han Chinese. ***National Science Review.*** 6: 257-274.

1. 灵长类特有分子 BTN3A2 在神经突触进化和功能调控中的作用机制

在哺乳类动物的演化过程中，最显著的改变则是由大脑所决定的高级认知功能，大脑结构和功能调控的复杂性被认为是人类区别于其他物种的重要原因。人类大脑神经突触环路在出生后依然持续发育，在青春期乃至成年的特定脑区，仍发生突触成熟、修剪以及轴突髓鞘化等重要事件。伴随着大脑神经突触连接的复杂性和发育时程的长期性，人类在进化过程中也增加了罹患相关脑病的风险，特别是神经精神疾病，在青春期前后表现出明显症状，而这些疾病通常也被认为是人类所特有。我们的合作者通过疾病遗传整合分析鉴定出一个精神分裂症新的风险基因 BTN3A2，并发现其为灵长类所特有。当我们以海马脑片为研究系统，在 CA1 锥体神经元中异位表达该基因，发现 BTN3A2 可以特异性抑制 AMPA 受体和 NMDA 受体所介导的谷氨酸兴奋性突触传递活性，但不影响突触后兴奋性电流（EPSC）的比值。进一步的分析发现，BTN3A2 可以显著性增强 AMPA 受体 EPSC 双脉冲比值 PPR，表明其是通过抑制突触前神经递质释放活性以发挥作用。BTN3A2 为免疫球蛋白超家族成员之一，因此我们提出如下工作模型和假说：BTN3A2 作为新型突触黏附分子特异定位于兴奋性神经突触，通过与突触前关键调控分子如 neurexin 等相互作用形成跨突触复合物以调节突触前神经递质的释放，从而实现兴奋性和抑制性突触传递活性的平衡；其基因位点突变所导致的表达水平的异常提高则使得该平衡被破坏，从而引起精神分裂症疾病发生。相关工作发表于 **Wu Y et al. 2019 *EBioMedicine***。为了进一步研究上述科学假说，我们正在筛选鉴定由 BTN3A2 形成的跨突触黏附分子复合物，以深入研究其调控神经递质释放的分子机制，同时我们构建了条件性 BTN3A2 基因敲入小鼠，并与 Nestin-Cre 等工具鼠杂交，以使在大脑或特定脑区中异位表达 BTN3A2 分子，结合神经电生理、光遗传、动物行为学等研究手段，深入研究突触环路进化和功能调控，与大脑生理和病理功能的内在联系。



2. 红藻氨酸受体（KAR）突触转运机制

谷氨酸受体是大脑中兴奋性突触传递的重要接收器，在前期工作中，我们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，揭示了同质性 GluK1 和 GluK2 受体所依赖的不同的分子基础（**Sheng N et al. 2015 *Elife***，**Sheng N et al. 2017 *PNAS***，**Duan GF et al. 2018 *Nature Communications***）。但是在大脑中，主要表达的是 GluK2/GluK4 和 GluK2/GluK5 等异质性 KAR 受体，而它们的突触转运的调控分子基础，以及高亲和力亚基 GluK4 和 GluK5 在其中的功能机制，相关研究仍是空白。针对该科学问题，我们构建了特异性表达系统，使得在神经细胞中表达异质性 KAR 受体 GluK2/GluK4 和 GluK2/GluK5。初步研究发现，GluK2/GluK4 受体能够定位于 Mossy Fiber-CA3 神经突触，但是不能定位于 Schaffer collateral-CA1 突触；而 GluK2/GluK5 受体均能定位于该两种海马神经突触，并且该两种受体均有效的转运至 CA1 神经细胞膜表面，提示此两种 KAR 受体的突触转运和定位依赖于不同的调控机制。进一步研究发现，KAR 受体辅基 Neto 蛋白并不参与该调控过程，而是由 GluK4 和 GluK5 亚基的胞外结构域所决定。因此，我们提出如下科学假说：高亲和力亚基 GluK4 和 GluK5 与突触前未知分子形成跨突触调控复合物，以决定异质性 KAR 受体突触转运和定位的特异性。目前我们正在展开该跨突触调控复合物的筛选鉴定相关研究工作。

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. The role and mechanism of primate specific molecule BTN3A2 for the evolution and regulation of neural synapse

During the mammalian evolution, the most striking change is the acquirement of high cognitive ability determined by the brain. And the complication of brain's structure, as well as its functional regulation, is regarded as the most significant character to distinguish homo sapiens from other species. The neural synapse and circuit in human brain continues for development after birth, and many important developmental procedures, including synaptic maturation, pruning and axon myelination, are still happened in adolescence's brain and even in adult's specific brain regions. Accompanied by the complication of the synaptic connections and its developmental chronicity, the risk is increased for human to suffer from the brain-related diseases during evolution, especially neuropsychiatric disorders which manifest obvious symptoms around adolescence period and are regarded as specific for human beings. Our collaborators have identified the primate-specific gene *BTN3A2* as a novel risk gene for schizophrenia through the integrative analyses of disease genetics study. Then we used hippocampal slice as the study system and ectopically overexpressed this gene in CA1 pyramidal neurons. It was found that BTN3A2 specifically represses the glutamatergic excitatory synaptic transmission mediated by AMPA and NMDA receptors, but has no effect on the ratio of AMPA and NMDA EPSCs. Furthermore, we found that BTN3A2 significantly increases the paired-pulse ratio of AMPA EPSCs, suggesting that it regulates this process through repressing the release process of presynaptic neurotransmitter vesicles. As BTN3A2 is a member of IgG super family, we therefore propose such a working model and hypothesis: BTN3A2 is a novel synaptic cell adhesion molecule (CAM) and specifically localizes at excitatory synapse; it regulates presynaptic neurotransmitter release through a trans-synaptic CAMs complex by interacting presynaptic critical CAMs such as neurexins, thereby playing a critical role for the balance of excitatory and inhibitory synaptic activity; the mutation of regulatory SNPs of BTN3A2 causes the abnormal increase of its expression and then the impairment of such synaptic balance, therefore finally leads to schizophrenia condition. The results of this study has been published as ***Wu Y et al. 2019 EBioMedicine***. To further examine such working hypothesis, we are continuing to screen and identify the specific trans-synaptic CAMs complex of BTN3A2, in order to study its functional mechanism of regulating presynaptic neurotransmitter release. Moreover, we have constructed a conditional knock-in mice model of *BTN3A2*, and are trying to cross it with Nestin-Cre or other mice lines to ectopically express BTN3A2 in mice brain or specific brain region. Combining with the techniques such as electrophysiology, optogenetics, animal behavior analyses etc., we wish to reveal the internal relationship between the evolution and functional regulation of synaptic circuit and the brain's physiological or pathological conditions.

2. The regulatory mechanisms for KAR synaptic trafficking

Glutamate receptors are most important mediators for excitatory synaptic transmission in the brain. In our previous work, we have focused on a subfamily of kainate receptors (KARs) and systematically studied the regulatory mechanisms for their synaptic trafficking and physiological properties, and reveal the distinct molecular machinery for homomeric GluK1 and GluK2 receptors (**Sheng N et al. 2015 *Elife***, **Sheng N et al. 2017 *PNAS***, **Duan GF et al. 2018 *Nature Communications***). However, it is the heteromeric KARs including GluK2/GluK4 and GluK2/GluK5 that are major receptors expressed in the brain. Currently it remains elusive about the molecular bases for their synaptic trafficking and the functional roles of high-affinity subunits GluK4 andGluK5. To answer these questions, we have constructed a specific expression system to express the heteromeric KARs in neuronal cells. Our preliminary studies have found that GluK2/GluK4 receptors successfully traffic to Mossy fiber-CA3 synapses but not Schaffer collateral-CA1 synapses, while GluK2/GluK5 receptors can localize at both hippocampal synapses. Moreover, these two receptors traffic to cell membrane efficiently, suggesting that the synaptic trafficking and localization of these two KARs are determined by distinct mechanisms. Moreover, it was found that the KAR auxiliary subunits Neto proteins are not involved in such process and the different trafficking abilities are determined by the extracelluar amino-terminal domains of GluK4 and GluK5. Therefore, we propose such a working hypothesis: it is the trans-synaptic complex, formed by high-affinity subunits GluK4 and GluK5 and presynaptic unknown molecules, that determine the specificity of heteromeric KARs synaptic trafficking and localization. We are currently trying to identify the specific trans-synaptic complex of GluK4 and GluK5.

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万 梨	Wan Li	2018 硕士
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卜宇飞	Bu Yufei	2018 硕士
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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 349 种动物的细胞系 2236 株 20000 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. Chen L, Qiu Q, Jiang Y, Wang K, Lin Z, Li Z, Bibi F, Yang Y, **Wang J**, **Nie W**, **Su W**, Liu G, Li Q, Fu W, Pan X, Liu C, Yang J, Zhang C, Yin Y, Wang Y, Zhao Y, Zhang C, Wang Z, Qin Y, Liu W, Wang B, Ren Y, Zhang R, Zeng Y, da Fonseca RR, Wei B, Li R, Wan W, Zhao R, Zhu W, Wang Y, Duan S, Gao Y, Zhang Y, Chen C, Hvilsom C, Epps CW, Chemnick LG, Dong Y, Mirarab S, Siegismund HR, Ryder OA, Gilbert MTP, Lewin HA, Zhang G, Heller R, Wang W. 2019. Large-scale ruminant genome sequencing provides insights into their evolution and distinct traits. Science 364, eaav6202.

1. 细胞资源的收集和保藏

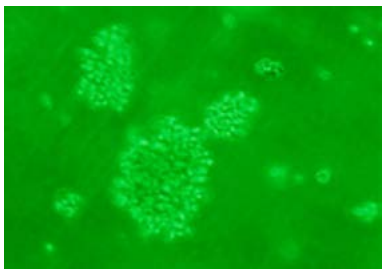
2019 年度，昆明细胞库利用从野外采集以及从其他途径获得的动物材料，共新建各类动物细胞系 52 株，其中包括黑冠长臂猿、长吻鼹鼹、牙獐、白腹巨鼠、斯氏鼹鼩等 6 种野生动物的细胞系 21 株，建立家养动物、人和实验动物的正常细胞系和肿瘤细胞系 41 株。复苏和扩增各类动物细胞系 619 株次。

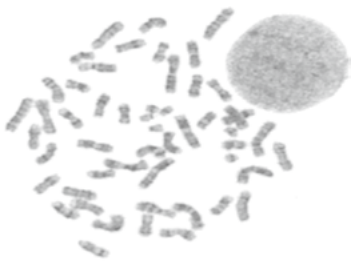
2. 对外服务

在 2019 年度，昆明细胞库为全国各地的 443 家单位，其中高等院校 199 家，科研院所 84 家，企业 160 家的研究人员提供各类野生和家养动物细胞系、人及常见实验动物的各类正常组织来源的细胞系、肿瘤细胞系及培养液共计 853 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 92 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. 黑冠长臂猿永生化淋巴细胞系的建立

黑冠长臂猿是中型长臂猿，被 IUCN 红色名录列为极度濒危级，是国家一级保护动物。利用 EB 病毒转化的方法和获得的少量外周血，我们成功建立并冻存了西黑冠长臂猿的永生化淋巴细胞系株，为后续开展相关研究储备了细胞材料。





4. 牙獐不同组织来源细胞系的建立

牙獐，是偶蹄鹿科动物，也是一种很有开发前途的经济动物。2019 年，利用课题组提供的四个牙獐个体的组织材料，我们成功建立并冻存了包括牙獐的肺、肾、脾、肌肉和皮肤等不同组织来源的体细胞系 13 株，满足了课题组的研究需求。

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 2236 cell lines from 349 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 2019, 52 cell lines from various wild animals, domestic animals and humans had been established and frozen. Among these cell lines, 21 cell lines were derived from 6 species of wild animals such as West Black-crested Gibbon, Gracile Shrew Mole, Chinese Water Deer, White-bellied Rat etc; 31 cell lines were established from domestic animals, experimental animals and humans. Six hundred and nineteen of frozen-stored cell lines were also resuscitated and subcultured.

2. Cell lines service and technical service

In this year, 853 cell lines and culture medium, 92 times of karyotype analysis and STR test had been provided for the researchers not only at State key laboratory of genetic resources and evolution, but also at other 199 Chinese universities, 160 enterprises, and 84 scientific research institutions. 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 line from the Black-crested gibbon

The Black-crested gibbon is a medium-sized gibbon listed as critically endangered on the IUCN red list. It is also a national first-class protected animal. By using of the method of Epstein barr virus transformation and the small amount of peripheral blood obtained, we succeeded in establishing and freezing the immortalized lymphocyte cell line of the Black-crested gibbon. The preservation of this cell line will provide cell materials for the follow-up research.

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

The Chinese water deer, belonging to the order Artiodactyla and the family Cervidae, is a very promising economic animal. To meet the research needs of the research group, we successfully established and frozen 13 cell lines by using tissue materials provided by the research group. The tissue materials were obtained from four Chinese water deer individuals, including the lungs, kidneys, spleens, muscles and skins.

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生命条形码南方中心

South China DNA Barcoding Center

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。中国是国际生命条形码计划（iBOL）的核心成员，中国科学院昆明动物研究所顺应形势于 2011 年成立生命条形码南方中心，负责我国和东南亚地区野生动物 DNA 条形码数据的产出和管理，拥有完全访问国际生命条形码数据库 BOLD 系统的权限。生命条形码南方中心专门从事 DNA 条形码技术的标准化、信息化和规模化，高通量条码实验平台的建立，利用 DNA 条形码技术进行生物多样性评价和保护、濒危野生动物的物种识别。是国内首家面向 DNA 条形码研究和利用的综合性平台。

重要成果及产出：

1. **张浩淼**. 中国蜻蜓大图鉴 Dragonflies and Damselflies of China. 重庆：重庆大学出版社，2019. ISBN 978-7-5689-8.
2. **张浩淼**. 新昆虫记—神秘航线. 武汉：湖北科技出版社，2019. ISBN 978-7-5352-9682-5.
3. **张浩淼。**《从水中诞生的空中芭蕾—蜻蜓》. 海峡书局出版集团. 计划于 2020 年 3 月出版

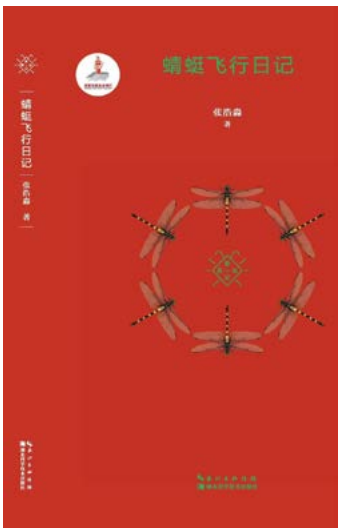
1. 蓟马的 DNA 条形码研究

蓟马科（Thripidae）昆虫，体型微小、隐匿性强，极易对化学农药产生抗药性，已逐渐成为世界上最重要的农业害虫类群之一。蓟马的研究和防控较为困难，主要原因是该类昆虫体型微小，有雌雄二型和多型现象，准确鉴定极为困难；而在农业生产上，由于其体型微小、危害隐蔽，难以发现，一旦爆发成灾，便很难有效控制。蓟马种类的快速准确鉴定是开展蓟马生物学研究和科学有效防控的前提和基础，也是目前蓟马防治中的瓶颈问题。快速准确的进行物种鉴定是害虫防治、益虫利用和昆虫生物学和防治研究的前提和基础。传统的蓟马分类必须依赖专业的分类学家才能开展，存在明显的局限性，分子生物学技术可以从分子水平上快速而准确地为基于形态的分类系统提供信息。生命条形码南方中心结合云南农业大学张宏瑞团队开展蓟马 DNA 条形码研究，提供高通量 DNA 条形码实验平台，在构建中国蓟马科的 DNA 条形码数据库中起到巨大作用。

2.《中国蜻蜓大图鉴》、《新昆虫记 — 蜻蜓飞行日记》云南发布

生命条形码南方中心张浩淼博士，原创著作《中国蜻蜓大图鉴》分为上下两册，共 1460 页，以中英双语的文字编排。内容包括“蜻蜓概述”和“中国蜻蜓图鉴”两大部分，覆盖了蜻蜓的形态学、生物学和分类学等多方面知识，每个物种配有简洁而精准的概括性描述。该书收录了中国蜻蜓 3 亚目 23 科 175 属 820 种，占中国已知蜻蜓总数的 83.42%。其中束翅亚目 13 科 65 属 293 种，间翅亚目 1 科 1 属 3 种，差翅亚目 8 科 106 属 524 种。2019 年 5 月 22 日，正值国际生物多样性日，中科院昆明动物研究所、重庆大学出版社在昆明联合发布《中国蜻蜓大图鉴》。该书是世界最大蜻蜓专著，同时也是全球蜻蜓目文献收录物种最多的一本彩色图鉴。

同年 4 月，张浩淼博士所著另一本图书 —《新昆虫记 — 蜻蜓飞行日记》也入选中国好书，受到央视《读书》栏目推荐。



South China DNA Barcoding Center

China is a core member of the international Barcode of (IBOL). Kunming Institute of zoology, Chinese Academy of Sciences established the South China DNA Barcoding Center (SCDBC) in 2011, which is responsible for the production and management of DNA barcoding data of wild animals in China and Southeast Asia, and has full access to the international life barcoding database--BOLD SYSTEMS. SCDBC focus on establishing experimental platform which is high-throughput, standardized and informationalized. SCDBC also use DNA barcoding technology for biodiversity evaluation and protection, species identification of endangered wildlife. It is the first comprehensive platform for DNA barcoding research and utilization in China.

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1. Study on DNA barcoding of Thripidae

Thripidae insects are small in size and strong in concealment, which are easily resistant to chemical pesticides. They have gradually become one of the most important agricultural pest groups in the world. It is difficult to study and control thrips, mainly due to the small size of the insects, the phenomenon of male and female dimorphism and pleomorphism, so it is very difficult to accurately identify. Rapid and accurate species identification is the premise and basis of pest control. Rapid and accurate species identification is the premise and basis of pest control. The rapid and accurate identification of thrips species is not only the premise and basis for carrying out biological research and scientific and effective control of thrips, but also the bottleneck problem in the current control of thrips. The traditional classification of thrips must rely on professional taxonomists, which has obvious limitations. Molecular biology technology can provide information for morphological classification system quickly and accurately at the molecular level. The SCDBC, cooperation with Zhang Hongrui's team from Yunnan Agricultural University, carried out the research of thrips DNA barcoding. SCDBC provided a high-throughput DNA barcode experimental platform, which played a big role in the construction of DNA barcode database of thrips in China.

2.Dragonflies and Damselflies of China

Dr. Zhang Haomiao, who from SCDBC, the original writer of "Dragonflies and Damselflies of China". 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.

On May 22 of 2019, the International Biodiversity Day, Kunming Institute of zoology, Chinese Academy of Sciences and Chongqing University Press jointly released "China Dragonfly atlas" in Kunming. The book is the world's largest book on dragonflies, and also a color atlas with the largest number of species in the world's dragonflies. In April of the same year, another book written by Dr. Zhang Haomiao, "the new insect diary of dragonfly flight", was also selected as a good book in China and recommended by the reading column of CCTV.

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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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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，能够快速可靠地分离单个细胞并进行基因组分析。

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。Fluidigm 的微流控 qPCR 芯片融合了芯片的高通量和 qPCR 的准确性。

5. 新一代实时定量 PCR 仪

QuantStudio 12K Flex 实时荧光定量 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

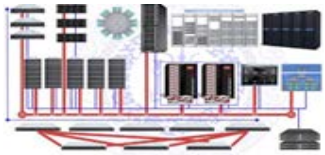
BD LSRFortessa™ 流式细胞分析仪兼顾了分析性能和可拓展性，可提供强大的扩展空间以满足不断发展的多色流式细胞仪实验的需求。

二、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。

三、高性能计算平台

设计目标融合高性能计算和大数据分析于同一机群；系统双精度理论峰值计算能力 157.65 万亿次；4PB 容量读写带宽高达 20GB 每秒，单点带宽 >4GB 每秒；采用 cc-numa 架构 superdome flex 配置 16 路处理器 12TB 内存作为胖节点；3 台 4 路服务器厚节点配置 3TB 内存，50 台 2 路服务器计算节点配置 384GB 内存；4 块 volta 架构 Tesla v100 卡的 GPU 服务器。

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, Micro-imaging Analysis Platform , and High Performance Computing Platform. Each platform is supported by professional technicians, from the experimental design, instrument operation, to data analysis.

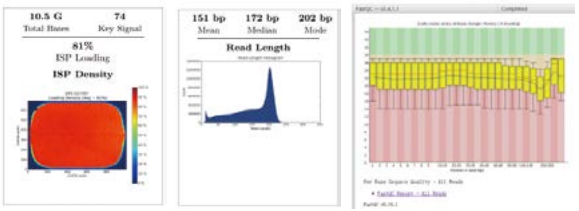
http://www.kiz.cas.cn/gre/gre6/gre61/

The Three Technical Platforms

I. Genomic Analysis Platform

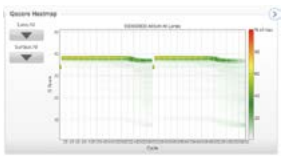
1. Ion Torrent Sequencers

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.



3. Single-Cell Preparation System

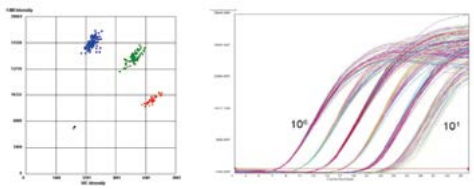
The C1 system enables cell capture, lysis, and preparation of individual cells for genomic applications. The system is an electrically and pneumatically operated desktop instrument. It has a built-in vacuum pump to hold the IFC in position. The embedded PC inside the system regulates all the functions and monitors the performance of the instrument. 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.

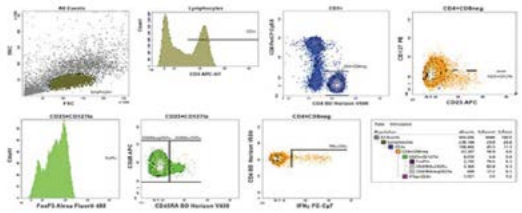
5. QuantStudio 12K Flex Real-Time PCR System

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.



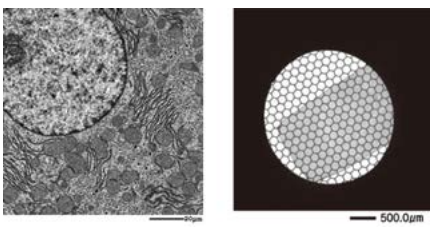
6.Miseq Sequencer

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. 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.



III. High Performance Computing Platform

It is a scalable linux platform with convergence of HPC and big data. The peak performance of the new Linux cluster is 157Tflops. One superfome flex from HPE with 16 way cpus and 12TB RAM serves as the fat node. The cluster consists of 50 inspur two-way servers with 384GB RAM as computing node and 3 four-way servers with 3TB RAM each as thick node. It is connected with 100Gbps infiniband communications link as computing network and Gbps LAN as administration network. DDN Inc supplies the 4PB file system storage volume with read/write aggregate throughput as high as 20GB/sec and over 4GB/sec single client throughput. We also have GPU platform with Nvidia Tesla v100 GPU for GPGPU computing applications.

重要在研项目

序号	项目名称	项目来源	项目类别	负责人	执行期	总经费（万元）	参与类型
1	第二次青藏高原综合科学考察研究任务五——生物多样性保护与可持续利用	科技部	科技基础资源调查项目	施　鹏	2019-2024	18993	主持
2	中国健康长寿人群多队列的系统研究	科技部	国家重点研发计划	孔庆鹏	2018-2022	2820	主持
3	中国长寿家系人群健康老龄调控因子甄别研究	科技部	国家重点研发计划	李功华	2019-2022	530	主持
4	利用多组学技术解析社交与情感的遗传基础和调控网络	科技部	国家重点研发计划	王国栋	2019-2024	438	主持
5	动物多样性起源与地理格局形成机制及其进化动力	科技部	国家重点研发计划	孙　航	2017-2020	340	参与
6	自噬和 DNA 损伤修复维持 PSC 稳态的机制研究	科技部	国家重点研发计划	秦宝明	2016-2020	239.5	参与
7	企鹅物种进化树、进化格局以及对地质环境变迁的响应	科技部	国家重点研发计划	张国捷	2018-2021	228	参与
8	基于多模态分子影像的移植后细胞生物行为的在体研究	科技部	国家重点研发计划	焦保卫	2016-2021	175	参与
9	国家万人计划领军人才项目（车静）	中组部	国家万人计划人才项目	车　静	2019-2022	80	主持
10	国家万人计划青年拔尖人才项目（王国栋）	中组部	国家万人计划人才项目	王国栋	2019-2022	177	主持
11	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	农业部	国家转基因重大专项	高　云	2016-2020	658.91	参与
12	基因组中新遗传结构的起源与动物的适应进化（延续）	基金委	创新研究群体项目	王　文	2017-2019	525	主持
13	多组学视角下家犬行为微进化的基因相互作用机制	基金委	重大研究计划	吴东东	2017-2019	883	主持
14	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	基金委	重大研究计划	宿　兵	2017-2019	289	主持
15	灵长类大脑进化分子机制的转基因猕猴研究	基金委	重点项目	宿　兵	2018-2022	340	主持
16	多能干细胞高效调控 DNA 复制压力反应的关键 lncRNA 鉴定与功能分析	基金委	重点项目	郑　萍	2020-2024	312	主持
17	回声定位蝙蝠高频听力适应性进化的遗传发育机制	基金委	重点项目	施　鹏	2020-2024	303	主持

序号	项目名称	项目来源	项目类别	负责人	执行期	总经费（万元）	参与类型
18	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	基金委	国际合作	孔庆鹏	2017-2021	235	主持
19	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	基金委	国际合作	Douglas W Yu	2016-2019	161	主持
20	全球视角下全基因组数据解析家鸡的起源和扩散	基金委	联合基金	吴东东	2020-2023	230	主持
21	剪接因子 SFPQ 对三阴性乳腺癌中 Erα 的转录调控研究	基金委	联合基金	焦保卫	2019-2022	220	主持
22	阿尔茨海默症（AD）转基因树鼩模型的创建及有效性评价	基金委	联合基金	郑　萍	2018-2021	204	主持
23	鲤科鱼类肌间刺系统演化及其在滇池金线鲃遗传机制	基金委	联合基金	杨君兴	2018-2021	200	主持
24	动物复杂性状的进化解析与调控	中科院	B 类先导专项	施　鹏	2014-2019	21583.5	主持
25	鸟类趋同演化及病毒协同演化机制	中科院	B 类先导专项	张国捷	2018-2023	300	主持
26	人类早期活动及其对高寒环境的适应策略	中科院	A 类先导专项	孔庆鹏	2018-2022	3242.1	主持
27	驯化动植物对高寒环境的适应及基因资源利用	中科院	A 类先导专项	彭旻晟	2018-2022	1160	主持
28	高原湿地垫脚石式廊道生态修复技术与示范	中科院	A 类先导专项	杨君兴	2019-2023	1145	主持
29	猪育种示范基地建设与完善	中科院	A 类先导专项	张亚平	2019-2024	1130	主持
30	关键区域的高通量、连续覆盖生物多样性监测与评估	中科院	A 类先导专项	Douglas W Yu	2018-2023	1094.23	主持
31	气候环境变化对典型动物及种群的影响	中科院	A 类先导专项	车　静	2018-2023	1060.29	主持
32	高原人群适应高寒环境的遗传资源发掘	中科院	A 类先导专项	孔庆鹏	2018-2022	686.31	主持
33	西南山地旗舰动物生态廊道设计技术与示范	中科院	A 类先导专项	蒋学龙	2019-2023	621.54	主持
34	东非脊椎动物多样性格局及形成机制	中科院	国际合作项目	蒋学龙	2016-2020	500	主持
35	东非重要动物类群系统发育与进化	中科院	国际合作项目	彭旻晟	2016-2020	400	主持

序号	项目名称	项目来源	项目类别	负责人	执行期	总经费（万元）	参与类型
36	现生鸟类多样性演化历史及机制研究	中科院	国际合作项目	张国捷	2019-2022	270	主持
37	健康长寿人群基因组表观修饰模式及功能利用研究	中科院	国际合作项目	孔庆鹏	2016-2020	250	主持
38	利用线粒体宏基因组方法研究气候变化对整个生态群落的影响	中科院	国际合作项目	Douglas W Yu	2017-2019	229.2	主持
39	过去 2500 年新疆民族融合遗传机制和模式研究	中科院	院级项目	张亚平	2019-2020	900	主持
40	家养动物肠道微生物组功能解析与调控	中科院	重点部署项目	施　鹏	2017-2021	625	主持
41	建立哀牢山自然保护区快速生物多样性监测方法	中科院	重点项目	Douglas W Yu	2017-2020	400	主持
42	肿瘤的异质性演化理论指导下的新疗法研究	中科院	重点部署项目	吕雪梅	2018-2020	350	主持
43	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	中科院	重大科技基础设施维修改造项目	高　云	2017-2019	223	主持
44	自闭症食蟹猴模型的创建	中科院	西部之光交叉团队	郑　萍	2019-2021	200	主持
45	西部之光引进人才项目（吕雪梅）	中科院	西部之光人才引进项目	吕雪梅	2019-2021	200	主持
46	云南省高端科技人才项目（焦保卫）	云南省	云南省高端科技人才引进计划	焦保卫	2014-2019	210	主持
47	云南省高端科技人才项目（施鹏）	云南省	云南省高端科技人才引进计划	施　鹏	2013-2019	200	主持
48	云南省高端人才项目（利用树鼩精原干细胞建立树鼩基因修饰技术）	云南省	云南省高端人才项目	郑　萍	2015-2019	160	主持
49	云岭学者	云南省	云南省云岭学者人才计划	宿　兵	2015-2019	200	主持
50	昆明长水国际机场威胁性鸟类防控中心项目	企业合作	横向项目	杨晓君	2018-2021	295	主持

发表论文及专著

（蓝色标注：实验室为文章第一单位；加粗：标注实验室的人员；通讯作者 *；共同第一作者 [1]）

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6. **Bi WX*[1], He JW[1],** Chen CC, Kundrata R, **Li XY*.** Sinopyrophorinae, a new subfamily of Elateridae (Coleoptera, Elateroidea) with the first record of a luminous click beetle in Asia and evidence for multiple origins of bioluminescence in Elateridae. 2019. ***Zookeys***:79-97.

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专著

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授权专利

专利号	专利名称	类别	授权日期	完成人（固定人员）
ZL201510860377.9	一种安水金线鲃脾脏细胞系的构建方法	发明专利	2019-03-01	潘晓赋，王晓爱 杨君兴，刘　倩
ZL201510864325.9	一种犀角金线鲃心脏细胞系的构建方法	发明专利	2019-03-01	王晓爱，潘晓赋 杨君兴，刘　倩
ZL201610976570.3	一种大理裂腹鱼肾脏细胞系的构建方法	发明专利	2019-09-01	王晓爱，潘晓赋 杨君兴，刘　倩
ZL201510084489.X	用于组装基因组序列的软件、算法及装置	发明专利	2019-04-01	马占山
ZL201510353906.6	一种大样本高通量生物数据关联分析方法	发明专利	2019-01-01	孔庆鹏

获　奖

省部级奖励

序号	成果名称	成果类型	等级	完成人	排名
1	羊的进化基因组学研究	云南省自然科学奖	一等	姜　雨，董　扬，王　文，苏　蕊， 李金泉，张文广，赵若苹	1

其它获奖

姓名	获奖年度	奖项	导师
曾　琳	2019	中国科学院优秀博士学位论文	张亚平、吴东东
和耀喜	2019	中国科学院院长优秀奖	宿　兵

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）
GREKF19-01	Taal Levi	副教授	Oregon State University	Connecting Earth Observation to Biodiversity and Ecosystems	7.5
GREKF19-02	刘　芹	讲师	宜宾学院	游蛇科蛇类分子系统与进化	7.5
GREKF19-03	Chatmongkon Suwannapoom	助理教授	University of Phayao, Thailand	中国南方和东南亚地区代表两栖物种的系统发育和物种分化研究：以角蟾科和树蛙科为例	7.5
GREKF19-04	陈中正	讲师	安徽师范大学	灰刚毛鼠复合群分类、系统发育与生物地理研究	7.5
GREKF19-05	聂建云	主任医师	云南省肿瘤医院 / 昆明医科大学第三附属医院	CD146 在乳腺干细胞中的调控作用及其机制研究	7.5
GREKF19-06	杨　桦	副主任医师	云南省第三人民医院	抗肿瘤药物新靶标 HKDC1 的功能与作用研究	7.5
GREKF19-07	陈红菊	讲师	红河学院	肠道菌群多样性与疾病关系的生态机制研究	7.5
GREKF19-08	李　光	副教授	厦门大学	基于单细胞转录组水平的文昌鱼不同组织和胚胎发育过程中的细胞谱系分析	7.5
GREKF19-09	唐爱辉	教授	中国科学技术大学	黏附分子介导跨突触纳米结构耦联的分子机制	7.5
GREKF19-10	张宏瑞	教授	云南农业大学	蓟马科昆虫比较线粒体基因组学研究	7.5
GREKF19-11	陈　垒	助理研究员	西北工业大学	反刍动物基因组进化特征分析	7.5
GREKF19-12	李　艳	研究员	云南大学	基因组研究揭示中国家马的起源驯化历史	7.5
GREKF19-13	叶建平	副教授	绍兴文理学院	中国鼠兔属动物的分子细胞遗传学研究	7.5
GREKF19-14	白玛康卓	副教授	西藏大学	藏族人群中高原肺动脉高压的致病机理及其对高原低氧环境适应的遗传影响	7.5
GREKF19-15	李子璇	讲师	西藏大学	重建青藏高原藏族人群中乙肝病毒 CD 基因型的起源与流行病学动态历史	7.5

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）
GREKF19-16	谢正媛	助理研究员	云南省人口和计划生育科学技术研究所	KHDC3L 维持人胚胎干细胞遗传物质稳定的研究	7.5

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	萤火虫及其生物荧光起源与进化研究	李学燕	云南省“八学会”2019 年新春联谊会	云南昆明	2019-1
2	基因重叠对内含子保留的作用及意义	薛　敏	云南省“八学会”2018 年新春联谊会	云南昆明	2019-1
3	Genome evolution and genomics	张国捷	SERB Sponsored School in Evolutionary Biology 2019	印度班加罗尔	2019-3
4	蝴蝶基因组特征与进化 Characterization and evolution of butterfly genome	李学燕	中国昆虫学会第四届传粉昆虫学术研讨会	北京	2019-5
5	Progress on the Dog 10K genome project	王国栋	第十届家犬家猫遗传基因组国际大会	瑞士	2019-5
6	Multiple roles of the ubiquitin E3 ligase RNF220 in neural development	毛炳宇	2019 年第九届发育生物学金陵会议	江苏南京	2019-6
7	Whole-genome sequencing reveals population structure and diversity of Nigerian indigenous pigs	Adeniyi Charles Adeola	第 37 届国际动物遗传学大会	西班牙莱里达	2019-7
8	Initiative for Global Chicken Genome Project (GCGP)	彭旻晟	第 37 届国际动物遗传学大会	西班牙莱里达	2019-7
9	Long-read assembly of the Chinese rhesus macaque genome and identification of ape-specific structural variants	和耀喜	美国分子生物学与进化学会 2019 年会	英国曼彻斯特	2019-7
10	Trio deep-sequencing does not reveal unexpected off-target and on-target mutations in Cas9-edited rhesus monkeys	罗　鑫	美国分子生物学与进化学会 2019 年会	英国曼彻斯特	2019-7
11	Genomic Perspective towards the Domestication of Guinea Fowl in Africa（墙报）	彭旻晟	美国分子生物学与进化学会 2019 年会	英国曼彻斯特	2019-7
12	Chromatin accessibility landscape and regulatory network of high-altitude hypoxia adaptation	宿　兵	美国分子生物学与进化学会 2019 年会	英国曼彻斯特	2019-7
13	Phylogeny of Fireflies (and other luminous beetles) and their evolution	李学燕	第十六届全国昆虫区系分类学术讨论会和第二届昆虫系统学与进化生物学国际研讨会	浙江杭州	2019-7

序号	报告名称	报告人	会议名称	地点	会议时间
14	Genome characteristics and evolution in Butterflies (Insecta, Lepidotera, Papilionoidea)	李学燕	第四届国际昆虫基因组学大会暨第七届国际昆虫生理生化与分子生物学学术研讨会	重庆	2019-7
15	Pattern of genetic diversity & population structure in silver butter catfish Schilbe intermedius from African river system（墙报）	Adeniyi Charles Adeola	欧洲进化生物学协会 2019 年会	芬兰图尔库	2019-8
16	Human overexploitation caused rapid recent population decline for green peacock (Pavo muticus	董　锋	第 15 届全国鸟类学大会	吉林长春	2019-8
17	Systems Biology study of Entomology—butterflies as a model	李学燕	中国动物学会第十八届全国会员代表大会暨第二十四届学术年会	陕西西安	2019-8
18	Molecular mechanism of protecting cochlear hair cells in echolocating bats	刘　振	中国动物学会第十八届全国会员代表大会暨第二十四届学术年会	陕西西安	2019-8
19	人工选择和自然选择下的犬科基因组	王国栋	中国动物学会第十八届全国会员代表大会暨第二十四届学术年会	陕西西安	2019-8
20	贾第虫：极原始的真核细胞还是高度退化的寄生原虫?	文建凡	中国动物学会第十八届全国会员代表大会暨第二十四届学术年会	陕西西安	2019-8
21	寄生原虫基因组中原核类似基因的起源探讨	程姣妮	中国动物学会原生动物学分会第二十次学术讨论会	黑龙江哈尔滨	2019-9
22	绿藻混合营养和两栖营养的甄别与比较研究	邓　琪	中国动物学会原生动物学分会第二十次学术讨论会	黑龙江哈尔滨	2019-9
23	原核型 FBPase II 基因经水平转移到绿藻后其内含子获得的研究	薛　敏	中国动物学会原生动物学分会第二十次学术讨论会	黑龙江哈尔滨	2019-9
24	Biodiversity genomic sequencing reveals animal macroevolutionary process	张国捷	Genomics for biodiversity symposium-Spain-2019	西班牙巴塞罗那	2019-9
25	Human overexploitation caused rapid population decline for Pavo muticus	董　锋	第七届国际鸡形目鸟类学术研讨会	越南洞海	2019-9
26	History, selection, and genomic basis of complex traits of dogs	王国栋	第二届中国 · 磐安大健康产业 - 前沿交叉学科论坛	浙江磐安	2019-9
27	肿瘤细胞群体多样性和进化	吕雪梅	2019 种群遗传学与基因组学高级培训班暨研讨会	北京	2019-10
28	Global Chicken Genome Project (墙报)	彭旻晟	第 11 届欧洲家禽遗传研讨会	捷克布拉格	2019-10
29	RNA 结合蛋白 TDP-43 在乳腺发育中的作用研究	焦保卫	第八届国际乳腺癌干细胞高峰论坛暨乳腺癌转化医学论坛	陕西西安	2019-10
30	德宏州芒市菲氏叶猴活动时间分配及食性研究	成　市	中国动物学会灵长类学分会第十六届学术年会	贵州贵阳	2019-11

序号	报告名称	报告人	会议名称	地点	会议时间
31	Influence of food availability and climate on behavior patterns of western black crested gibbons(Nomascus concolor) at Mt. Wuliang, Yunnan, China	宁文鹤	中国动物学会灵长类学分会第十六届学术年会	贵州贵阳	2019-11
32	一夫二妻制西黑冠长臂猿鸣声功能假说的回放实验验证	牛晓炜	中国动物学会灵长类学分会第十六届学术年会	贵州贵阳	2019-11
33	家犬的警用行为和转圈行为研究	王国栋	中国动物学会动物行为学分会第三届（2019）学术年会暨第七次全国动物行为学研讨会	海南海口	2019-11
34	Niche conservatism promotes allopatric speciation of sky island Pyrrhula erythaca species complex	董　锋	第十五届全国野生动物生态与资源保护学术研讨会	海南海口	2019-11
35	墨脱县大中型兽类多样性格局与驱动因素初探	李学友	第十五届全国野生动物生态与资源保护学术研讨会	海南海口	2019-11
36	高原适应中低氧压力依赖及逐步适应的表型及遗传机制	张　涛	第十五届全国野生动物生态与资源保护学术研讨会	海南海口	2019-11
37	通过回声定位哺乳动物进化基因组学预测新的听力基因	朱　磊	第十五届全国野生动物生态与资源保护学术研讨会	海南海口	2019-11
38	Systems Biology study of Entomology—butterflies as a model	李学燕	第四届“中国生物系统学学术论坛”	北京	2019-12
39	Convergent evolution in echolocation-related phenotypes and genotypes reveals a new echolocating genus in mammals	刘　振	第四届“中国生物系统学学术论坛”	北京	2019-12
40	犬科种间的基因渐渗	王国栋	第四届“中国生物系统学学术论坛”	北京	2019-12
41	Deciphering evolutionary history and mechanism of a high taxonomic unit and its distinct traits by phylogenomics	王　文	第四届“中国生物系统学学术论坛”	北京	2019-12
42	进化系统生物学(eGPS, evolutionary genotype-phenotype systems biology)——进化研究新思路	王　文	雄安昆虫学高峰论坛	河北保定	2019-12

邀请学术报告

序号	专家姓名	单位	报告日期	报告题目
1	Antonio Torroni	意大利帕维亚大学	教　授	1月4日
2	Ornella Semino	意大利帕维亚大学	副教授	1月4日

序号	专家姓名	单位	报告日期	报告题目
3	Hans-Jürgen Bandel	德国汉堡大学	教　授	1 月 4 日
4	黄　勋	中国科学院遗传与发育生物学研究所	研究员	5 月 23 日
5	杨振业	中国科学技术大学	教　授	5 月 23 日
6	孟飞龙	中国科学院上海生化细胞所	研究员	5 月 28 日
7	周　波	中国科学院上海生化细胞所	研究员	5 月 28 日
8	Wang Hurng-Yi（王弘毅）	国立台湾大学	教　授	5 月 27 日
9	苏正昌	北卡罗来纳大学	教　授	6 月 13 日
10	陈正一	哈佛大学	副教授	9 月 9 日
11	Hehuang Xie（谢荷煌）	弗吉尼亚理工大学	副研究员	10 月 10 日
12	Oyekanmi Nashiru	尼日利亚国家生物技术发展署	教　授	11 月 4 日
13	黄开耀	中国科学院水生生物研究所	研究员	12 月 31 日

第三章　人才队伍建设

新增人才称号

序号	姓名	荣誉称号	项目来源	获得年份
1	车　静	万人计划 —— 领军人才	中组部	2019
2	王国栋	万人计划 —— 青年拔尖人才	中组部	2019

序号	姓名	荣誉称号	项目来源	获得年份
3	刘　振	国家优秀青年科学基金获得者	基金委	2019
4	潘晓赋	关键技术人才	中科院	2019
5	张国捷	海外评审专家	中科院	2019
6	潘晓赋	王宽诚率先人才计划——产研人才扶持项目	中科院	2019
7	焦保卫	西部之光——交叉创新团队	中科院	2019
8	吕雪梅	西部之光——西部引进人才	中科院	2019
9	尹婷婷	西部之光——青年学者 B 类	中科院	2019
10	余　琴	西部之光——青年学者 B 类	中科院	2019
11	张伟道	西部之光——青年学者 B 类	中科院	2019
12	薛　敏	西部之光——青年学者 B 类	中科院	2019
13	吕雪梅	高层次人才引进计划	云南省	2019
14	张国捷	高层次人才引进计划（柔性引才）	云南省	2019
15	王　慧	高层次人才引进计划——青年人才	云南省	2019
16	李春梅	高层次人才引进计划——青年人才	云南省	2019
17	刘薇薇	高层次人才引进计划——青年人才	云南省	2019

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		杨洋、李宗煦、王晓阳、蔡望、罗明洁	李沅衡
2	车　静	于中斌、余传鑫、曹如君、董文捷、卢宸祺、冯小刚	高伟、侯绍兵、张毅、吴云鹤、付婷婷、徐伟	
3	佴文惠	高简奥、吴甜甜		
4	蒋学龙	胡文强、胡哲畅、魏婉宜、李弈仙	宁文鹤、宋文宇、李权、牛晓炜、于秋鹏	陈顺德

序号	导师	硕士生	博士生	博士后
5	焦保卫	成美、刁显红、刘霈、邵海莉	徐海波、赵丽娜、杨星、郭璐、杨旭	
6	孔庆鹏	郭荣慧、郜宗亮、顾康蜀云、翁崇峻、赵龙	葛明侠、王昊天	
7	吕雪梅	陶鑫灵、魏昀旸	陈泽宇、殷利夺、冯璇、闫凯	
8	马占山	肖琬蒙、杨旭、乔玉亭	陈红菊、李连伟、夏尧、李文迪	
9	毛炳宇	李雨薇、茶靖美、杨陈成	祁飞燕、王绘山、张龙龙、朱良	
10	盛能印	吴月春、万梨、唐杰、易雅星、易琳昀	叶雅馨、刘娅敏	
11	施　鹏	雷孟龙、陶乐、华秦杨、马苑硕	周鑫、陈艳艳、朱磊、刘奇、郑智中、陈杰、张涛、郭媛婷、华绒、蔡婉芷、白婧	刘广帅
12	王　文		曾严、陈海涛、刘威、王宝	
13	文建凡	邱兰、邓琪	吕章夏、程姣妮	
14	吴东东	任小蝶、庄晓琳、陈勇璇、李彦旭	张佳进、张锦锦、田航宇、李明莉	王　胜
15	宿　兵	王永琴、曾雪芮、张凤云、吴海旭、张悦	罗鑫、姜瑾、郭永博、郑王山、袁佳妙、孟晓宇、岳天、周斌	
16	祁学斌	黄家卉		
17	杨君兴	吴安丽、殷艳慧、黄新迪	孙超、潘晓赋	
18	杨晓君	陈逸林、袁兴海、赵岩、吴青琴、姚舜禹	王继山、高建云、单鹏飞、王洁	
19	张国捷	李冀	张霞芳	高琼华
20	张亚平	刘行、王蓉、王凤娟、母昌概	马云飞、胡靖扬、耿伟航、李建波、汪轩、黄翠萍、颜晨、沈全宽、李应菊、周博闻、戴珊珊、伍胤桥	李锦秀
21	王国栋		张越东、黎武略、马成、许明敏	
22	高　云	施贤、牛文静		
23	郑　萍	谢恒、陶慧玲、唐敏	陈忠良、孙春丽、姜方洁、李竞争、龚道华、李聪、宁雨琪	

毕业研究生一览表

序号	姓名	攻读专业	学位	导师姓名	毕业日期
1	陈进民	遗传学	博士	车　静	2019 年 1 月
2	张宝林	遗传学	博士	车　静	2019 年 1 月
3	徐　凯	动物学	硕士	车静、Douglas w Yu	2019 年 7 月
4	郑俊娟	遗传学	博士	黄京飞	2019 年 1 月
5	黄　程	动物学	博士	蒋学龙	2019 年 7 月
6	赵丽敏	细胞生物学	博士	焦保卫	2019 年 7 月
7	董　蕾	遗传学	硕士	孔庆鹏	2019 年 7 月
8	江建军	遗传学	博士	孔庆鹏	2019 年 1 月
9	夏王晓	遗传学	博士	孔庆鹏	2019 年 7 月
10	余　琴	遗传学	博士	孔庆鹏	2019 年 1 月
11	SAID ISMAEL NG'ANG'A	遗传学	硕士	彭旻晟	2019 年 7 月
12	李媛媛	遗传学	博士	施　鹏	2019 年 1 月
13	罗　杰	遗传学	博士	施　鹏	2019 年 7 月
14	吴群富	生物工程	硕士	施　鹏	2019 年 1 月
15	杨丽丽	遗传学	硕士	施　鹏	2019 年 7 月
16	文晓岚	动物学	博士	王瑞武	2019 年 7 月
17	薛　敏	遗传学	博士	文建凡	2019 年 1 月
18	和耀喜	遗传学	博士	宿　兵	2019 年 7 月
19	胡　庭	遗传学	硕士	宿　兵	2019 年 7 月
20	胡　艳	遗传学	硕士	宿　兵	2019 年 7 月

序号	姓名	攻读专业	学位	导师姓名	毕业日期
21	杨晏冬	遗传学	博士	宿　兵	2019 年 1 月
22	周亚楠	生物工程	硕士	宿　兵	2019 年 7 月
23	杜丽娜	动物学	博士	杨君兴	2019 年 7 月
24	何书航	动物学	硕士	杨晓君	2019 年 7 月
25	黎思涵	动物学	硕士	杨晓君	2019 年 7 月
26	HADI CHARATI	遗传学	博士	张亚平	2019 年 7 月
27	NEWTON OTIENO OTECKO	遗传学	博士	张亚平	2019 年 1 月
28	尹婷婷	遗传学	博士	张亚平	2019 年 1 月
29	周其俊	生物工程	硕士	张亚平	2019 年 7 月
30	李秀峰	细胞生物学	硕士	郑　萍	2019 年 7 月
31	张伟道	细胞生物学	博士	郑　萍	2019 年 1 月

研究生优秀论文奖

序号	姓名	获奖等级	期刊	IF	作者排序
1	周博闻	一等奖	Cell Research	18.448	并列一作第二位
2	李明莉	一等奖	Genome Biology	18.358	第一作者
3	田宇航	一等奖	Molecular Biology and Evolution	13.944	并列一作第二位
4	张　涛	一等奖	Molecular Biology and Evolution	13.944	并列一作第二位
5	罗　鑫	一等奖	Nature Communications	13.811	第一作者
6	罗　鑫	一等奖	Nature Communications	13.811	并列一作第二位

序号	姓名	获奖等级	期刊	IF	作者排序
7	高　伟	一等奖	Proceedings of the National Academy of Sciences of the United States of America	10.6	第一作者
8	罗　鑫	二等奖	National Science Review	13.833	并列一作第二位
9	孙春丽	二等奖	Genome Research	13.796	并列一作第四位
10	祁飞燕	二等奖	Science Advances	11.511	并列一作第二位
11	陈忠良	二等奖	Plos Biology	9.311	并列一作第二位
12	李连伟	二等奖	Molecular Ecology	6.614	第一作者
13	殷利夺	三等奖	Epigenetics & Chromatin	5.145	第一作者
14	李连伟	三等奖	Frontiers in Microbiology	4.84	第一作者
15	李文迪	三等奖	Frontiers in Microbiology	4.84	第一作者
16	马云飞	三等奖	Scientific Reports	4.525	第一作者

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
吕雪梅	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

Adeniyi Charles Adeola	白慧掀	曾　琳	柴　静	常云艳	陈宏满
陈进民	陈　鹏	邓家坤	董　锋	董志巍	高建云
高　云	郭　彦	郝军军	何　锴	何水旺	何文彬
何永捍	和耀喜	侯东敏	季吟秋	金洁琼	柯　浩
李朝翠	李春梅	李功华	李梦雯	李欣然	李学燕
李学友	李玉春	李毓劲	廖爱文	刘贵春	刘鹤群
刘　倩	刘淑伟	刘薇薇	刘　振	柳延虎	罗　杰
马怀孝	马鹏程	潘晓赋	彭旻晟	彭　云	浦绍艳
祁学斌	饶定齐	邵　永	舒树森	苏伟婷	孙艳波
汤易雨立	汪嘉欣	王国栋	王洪娇	王　慧	王　洁
王金焕	王　林	王　林	王晓爱	王运宇	王　壮
吴春莹	吴　飞	吴汝念	吴世芳	伍和启	肖富辉
谢海兵	徐　沙	薛　敏	岩　道	杨春燕	杨　晖
杨利琴	杨敏敏	杨　钦	叶青青	尹婷婷	余　琴
张宝林	张栋儒	张海林	张浩淼	张洪磊	张　慧
张树润	张伟道	张晓明	张　昕	张　洋	张源伟
赵　洁	赵丽敏	赵若含	赵若苹	赵士萍	赵亚鹏
郑俊娟	周其俊	周炜帏	周　鑫	周中银	朱春玲
朱建国	朱玮璟	邹　丽			

2019年度报告

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