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

2017年报
ANNUAL REPORT

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

目 录

主任致辞

2017 年是全面落实国家“十三五”规划的关键一年，也是全面迈入新一轮评估周期的第二年。遗传资源与进化国家重点实验室顺利通过了科技部的“评估”，在这次现场考察加综合评议的全面“检阅”中获得“良好”。在各级主管部门的领导与关怀下，实验室迎来了新一届学术委员会及领导班子，我们继续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，勠力同心、砥砺前行，在任务承担、科研成果、人才队伍建设、开放交流等各方面工作均取得了可喜进展，向成为“有重要国际影响的遗传资源与进化研究中心”的目标又迈进了一步。

在承担科研项目方面，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。新争取科研项目 57 项，包括国家自然科学基金创新研究群体延续项目 1 项、国家自然科学基金重大研究计划 1 项、国际 (地区) 合作与交流项目 1 项、优秀青年科学基金 1 项、科技部重点专项子课题 2 项、中科院前沿科学重点研究项目 1 项、中科院重大科技基础设施维修改造项目 1 项。目前在研省部级项目 198 项，国际合作项目 6 项，横向协作项目 14 项。年度到位科研经费 6335 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，参与组织了中国科学院第二次青藏高原综合科学考察的重要任务。此外，还将基础理论应用于技术创新与推广应用，例如依托于新建的中科院西南家猪育种基地实现本地小耳猪人工选育等。

在科研成果方面，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。2017 年发表 SCI 论文 130 篇，其中以第一作者或通讯作者 (含并列) 发表 95 篇，包括发表在 *Genome Research, Molecular Biology and Evolution*，*Nature Communication*，*PNAS*，*Cell Research, Gigascience, Theranostics* 等 IF5-year>9 的国际著名期刊论文 14 篇。2 项成果获得云南省自然科学二等奖，1 项获得云南省科技进步三等奖，1 项专利获得云南省专利奖三等奖。另申请发明专利 10 项。

在人才队伍建设方面，实验室继续实施“培养 + 引进”的人才队伍建设模式，取得可喜成绩。依托于实验室主持的中科院先导 B 项目团队而组建的中科院动物进化与遗传前沿交叉卓越创新中心在 10 月获批开始筹建。1 人 (施鹏) 入选“2017 年国家百千万人才工程”并被授予“有突出贡献中青年专家”荣誉称号，1 人 (车静) 荣获国家自然科学基金“优秀青年基金”资助，2 人 (施鹏、孔庆鹏) 入选“云岭英才”计划。此外，新引进研究员 2 名 (盛能印、张国捷)、青年博士 8 名，新培养青年研究员 2 名 (张志刚、王国栋)。研究生培养方面，为国家输送博士 18 名，硕士 24 名。此外，实验室还成功举办 2017 年“进化生物学”暑期班，吸引更多有志青年加入实验室。实验室还成功举办 10 期“遗传资源与进化青年学者论坛”，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。

开放交流方面，实验室继续遵循“交流促进合作”的原则推动国内外合作。成功承办中国动物学会两栖爬行动物分会 2017 年学术交流年会。此外，邀请 19 名国内外专家来室学术交流并做学术报告。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 15 项并将各科研平台开放共享。

岁月不居，天道酬勤！我们在新一届学术委员会指导下，阔步迈入华章初展的 2018 年。让我们立足过去，满怀希冀，共创未来，力争为我国“十三五”科技创新工作做出更大的贡献！在此，我也谨代表实验室向长期以来关心和帮助实验室的各级领导和朋友致以最诚挚的感谢和良好祝愿，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

Director's Report

The State Key Laboratory of Genetic Resources and Evolution participated in the comprehensive evaluation of the state key laboratories in the fields of biology and medicine and finally got "good" in 2017. The lab has a new academic committee and leadership and made considerable progress in 2017, with regards to grant awards, scientific research output, talent recruitment and scientific exchange.

Grant awards. –The lab was awarded 57 new grants in 2017，including one Creative Research Groups continuation fund, one Major Research project, one International (Regional) Cooperation and Exchanges Programs and one National Science Foundation for Outstanding Young Scholars from NSFC, two sub-projects of National Key Research and Development Program of China, one Frontier Key Program and one Major technological infrastructure maintenance projects of CAS. Currently the lab holds 198 ministerial and provincial projects, 6 international cooperation projects and 14 horizontal collaboration projects. The grant funds to the lab was totaled 63.35 million RMB. In addition to basic research, the lab also actively participated in the second comprehensive scientific investigation of the Tibetan Plateau organized by CAS, and promoted applied researches including molecular breeding and industrialization research of the southern Yunnan small-ear pig.

Publications and Awards. – The lab made systematic progress in revealing the formation and evolution of biological diversity and the genetic mechanism to provide a theoretical basis for the conservation and sustainable use of genetic resources in 2017. The lab published in total 130 papers in SCI journals, including 14 papers in top journals(IF5-year>9) such as *Genome Research, Molecular Biology and Evolution*, *Nature Communication*, *PNAS*, *Cell Research, Gigascience, Theranostics* etc as first or corresponding authors (including equal contributed ones). The lab has also won two second prizes for Natural Science, one third prize of scientific and technological progress in Yunnan Province and one third prize of Yunnan Patent Award. Ten invention patents were applicated.

Talent recruitment. –In 2017, the Center for Excellence in Animal Evolution and Genetic of CAS was approved in October based on the Strategic Priority Research Programs (B) of CAS host by the lab. Prof. Peng Shi was selected as "the National key Talent Project in 2017" and was awarded the honorary title of " Young Experts with Outstanding Contributions". Prof. Jing Che was awarded a grant from the National Science Foundation for Outstanding Young Scholars of China. And the Innovative Research Groups headed by Prof. Wen Wang was renewed by NSFC. Prof. Peng Shi and Qingpeng Kong were selected into the "Yunling Excellence" program of Yunnan Province. Prof. Nengying Sheng and Prof. Guojie Zhang joined the key lab. Eight young doctors were recruited. Dr. Zhigang Zhang and Dr. Guodong Wang became young investigator of KIZ. Eighteen Ph.D. and 24 M.Sc. students graduated from the lab in 2017. The "Evolutionary Biology" Summer School was successfully held in July, attracting many young people to join the lab. The lab also successfully held 10 "Forum by Young Scholars on Genetic Resources and Evolution", intending to improve the ability of academic expression of young scholars and promote scientific exchange and cooperation.

Scientific exchange. – In 2017, the lab continues to follow the principle of "promoting communication for cooperation" to promote academic exchanges and cooperation at home and abroad. The 2017 Symposium of Chinese Herpetological Society hosted by the key lab was successfully held in Kunming. Nineteen scholars were invited to visit the lab and to give lectures this year for scientific exchange and co-operation. In 2017, the lab has also funded 15 "open projects" and share the platforms outside to promote cooperation with scholars in related fields.

In 2018, the lab will continue to contribute to China's Thirteenth Five-year Plan on the basis of previous work. Finally, I would like to thank all organizations and friends who have provided supports and assistance to our lab and hope to have your continued help in the future!

Peng Shi

实验室概况 Laboratory Overview

一、第三届学术委员会 (The Third Academic Committee)

主任 (Director):

张亚平 院士，中国科学院
Academician Yaping Zhang, Chinese Academy of Sciences

副主任 (Deputy director):

宿 兵 研究员，中国科学院昆明动物研究所
Prof. Bing Su, Kunming Institute of Zoology, Chinese Academy of Sciences

委 员 (Members，按姓氏笔画排序):

王 文 研究员，中国科学院昆明动物研究所
Prof. Wen Wang，Kunming Institute of Zoology, Chinese Academy of Sciences
吴仲义 院士，中山大学
Academician Chung-I Wu, Sun Yat-Sen University
李德铢 研究员，中国科学院昆明植物研究所
Prof. Dezhu Li, Kunming Institute of Botany, Chinese Academy of Sciences
张克勤 教授，云南大学
Prof. Keqin Zhang, Yunnan University
汪小全 研究员，中国科学院植物研究所
Prof. Xiaoquan Wang, Institute of Botany, Chinese Academy of Sciences
金 力 院士，复旦大学
Academician Li Jin, Fudan University
杨 光 教授，南京师范大学
Prof. Guang Yang, Nanjing Normal University
施 鹏 研究员，中国科学院昆明动物研究所
Prof. Peng Shi, Kunming Institute of Zoology, Chinese Academy of Sciences
桂建芳 院士，中国科学院水生生物学研究所
Academician Jianfang Gui, Institute of Hydrobiology, Chinese Academy of Sciences
焦保卫 研究员，中国科学院昆明动物研究所
Prof. Baowei Jiao, Kunming Institute of Zoology, Chinese Academy of Sciences
魏辅文 院士，中国科学院动物研究所
Academician Fuwen Wei, Institute of Zoology, Chinese Academy of Sciences

二、现任实验室领导（Leader of the Lab.）

主任 (Director)：

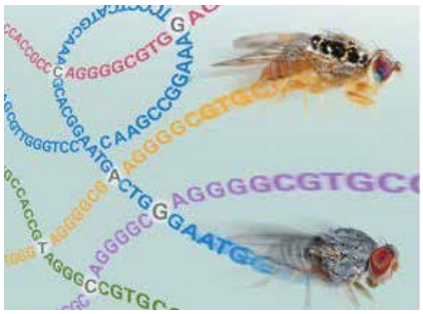
施 鹏 研究员 Prof. Peng Shi

副主任 (Deputy director)**:**

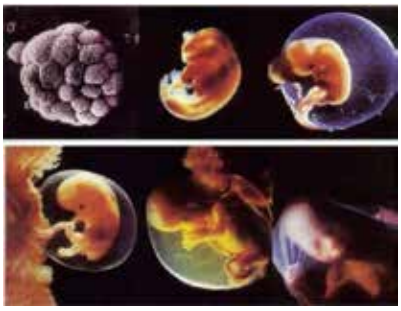
文建凡 研究员 Prof. Jianfan Wen
毛炳宇 研究员 Prof. Bingyu Mao
焦保卫 研究员 Prof. Baowei Jiao

三、研究方向 (Research Direction)

遗传资源多样性的演化与保护
Evolution and conservation of the diverse genetic resources



基因与基因组进化
Evolution of genes and genomes

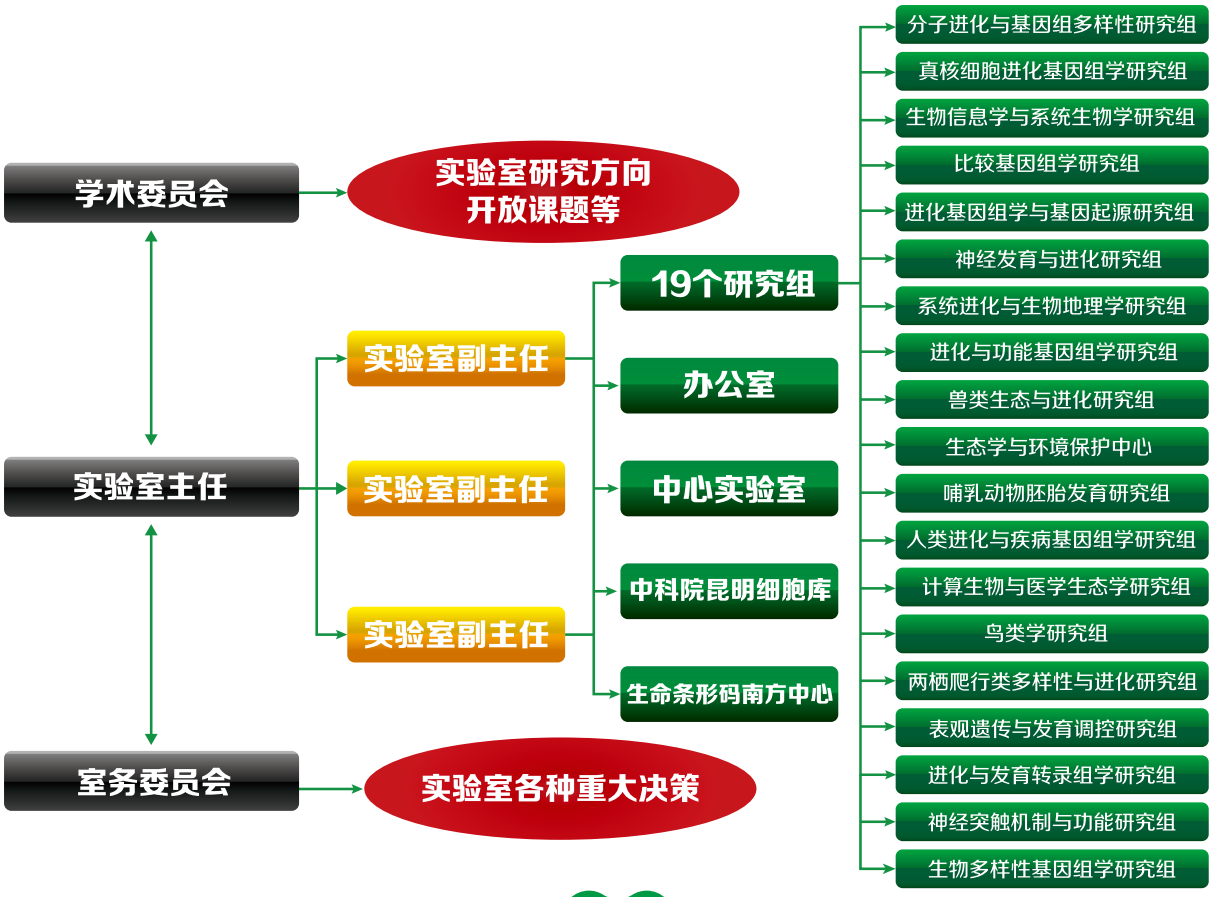


遗传发育与进化
Genetics, development and evolution

四、研究团队与组织结构 (Groups and Organization Structure)

实验室有固定研究组 18 个，客座研究组 1 个，支撑部门 3 个，现有科研工作人员 133 人，其中博士 69 人。拥有国家基金委创新群体 1 个，中科院院士 1 人，国家杰出青年基金获得者 6 人，科技创新领军人才（万人计划）3 人，青年千人计划 1 人，中科院“百人计划”8 人，云南省“高端人才”5 人。

There are 18 research groups, 1 guest research group and 3 facility centers in the key lab. Among the 133 staff members, 69 of them hold Ph.D. degrees. The research team includes one “Innovation Team Grant”from NSFC，1 academician of CAS, 6 winners of the “National Science Fund for Distinguished Young Scholars”, 3 holders of “National High-Level Talent Special Support Plan” of MOST, 1 holder of “National Youth Thousand Talents Program”, 8 holders of the “Hundred Talents Program”of CAS and 5 holders of “Top talent” project of Yunnan Province.



研究方向一：遗传资源多样性的演化与保护

代表性成果一

提出大尺度生物多样性监测方法

nature ecology & evolution
PERSPECTIVE
PUBLISHED: 22 JUNE 2017 | VOLUME: 1 | ARTICLE NUMBER: 0176

Connecting Earth observation to high-throughput biodiversity data

Alex Bush[1,2,3], Rahel Sollmann[4], Andreas Wilting[5], Kristine Bohmann[6,7], Beth Cole[8], Heiko Balzter[8,9], Christopher Martius[10], András Zlinszky[11], Sébastien Calvignac-Spencer[12], Christina A. Cobbold[13], Terence P. Dawson[14], Brent C. Emerson[15,7], Simon Ferrier[3], M. Thomas P. Gilbert[6,16], Martin Herold[17], Laurence Jones[18], Fabian H. Leendertz[12], Louise Matthews[13], James D. A. Millington[14], John R. Olson[19], Otso Ovaskainen[20,21], Dave Raffaelli[22], Richard Reeve[13], Mark-Oliver Rödel[23], Torrey W. Rodgers[24], Stewart Snape[25], Ingrid Visseren-Hamakers[26], Alfried P. Vogler[27,28], Piran C. L. White[22], Martin J. Wooster[14,29] and Douglas W. Yu[1,7]*

Understandably, given the fast pace of biodiversity loss, there is much interest in using Earth observation technology to track biodiversity, ecosystem functions and ecosystem services. However, because most biodiversity is invisible to Earth observation, indicators based on Earth observation could be misleading and reduce the effectiveness of nature conservation and even unintentionally decrease conservation effort. We describe an approach that combines automated recording devices, high-throughput DNA sequencing and modern ecological modelling to extract much more of the information available in Earth observation data. This approach is achievable now, offering efficient and near-real-time monitoring of management impacts on biodiversity and its functions and services.

Nature Ecology and Evolution. 2017,22;1(7):176.

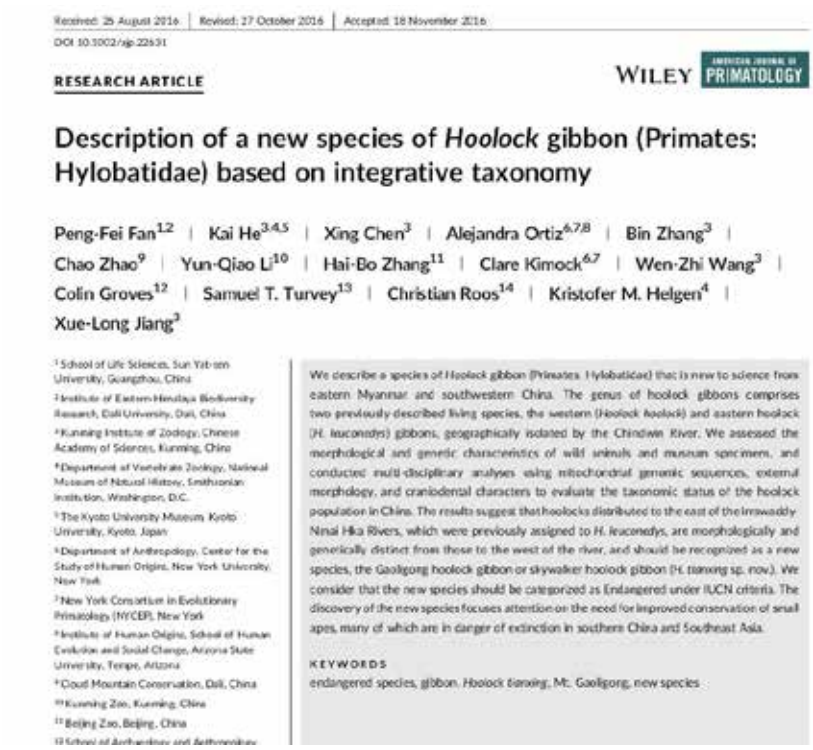
大尺度实时生物多样性管理监测，对精细研究生物多样性格局动态和物种适应策略、预测生物兴衰和分布格局态势有重要意义。《中科院十三五规划纲要》将“大尺度区域生物多样性格局与生命策略”作为 60 个有望实现创新跨越的重大突破之一进行部署，旨在通过环境 DNA 条形码、大样地野外试验观测和遥感可视化技术来实现生态学和进化生物学领域的重大突破。如今生物多样性正逐渐丧失，因此利用地球观测技术来监测生物多样性、生态系统功能和生态系统服务具有重要意义。但是生物多样性不能完全通过遥感技术观测到，并且单一的观测结果可能会产生误导，以致降低自然保护的效率，影响保护成效，因此需要改进。

为此，Douglas W. Yu 组提出通过将自动记录装置、高通量 DNA 测序技术、先进的生态模型和遥感技术结合起来，实现有效、实时、大尺度的生物多样性管理监测的构想。 并在 *Nature Ecology & Evolution* 杂志上发表了封面文章，该文对实现大尺度生物多样性监测方法进行展望，为环境保护政策的制定提供了全面的科学依据。

研究方向一：遗传资源多样性的演化与保护

代表性成果二

发现并命名长臂猿新物种——“天行者”



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DOI: 10.1002/ajp.22631

RESEARCH ARTICLE

WILEY AMERICAN JOURNAL OF PRIMATOLOGY

Description of a new species of *Hoolock* gibbon (Primates: Hylobatidae) based on integrative taxonomy

Peng-Fei Fan[1,2] | Kai He[3,4,5] | Xing Chen[3] | Alejandra Ortiz[6,7,8] | Bin Zhang[3] | Chao Zhao[9] | Yun-Qiao Li[10] | Hai-Bo Zhang[11] | Clare Kimock[6,7] | Wen-Zhi Wang[3] | Colin Groves[12] | Samuel T. Turvey[13] | Christian Roos[14] | Kristofer M. Helgen[4] | Xue-Long Jiang[3]

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[2] Institute of Eastern-Himalaya Biodiversity Research, Dali University, Dali, China
[3] Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, China
[4] Department of Vertebrate Zoology, National Museum of Natural History, Smithsonian Institution, Washington, D.C.
[5] The Kyoto University Museum, Kyoto University, Kyoto, Japan
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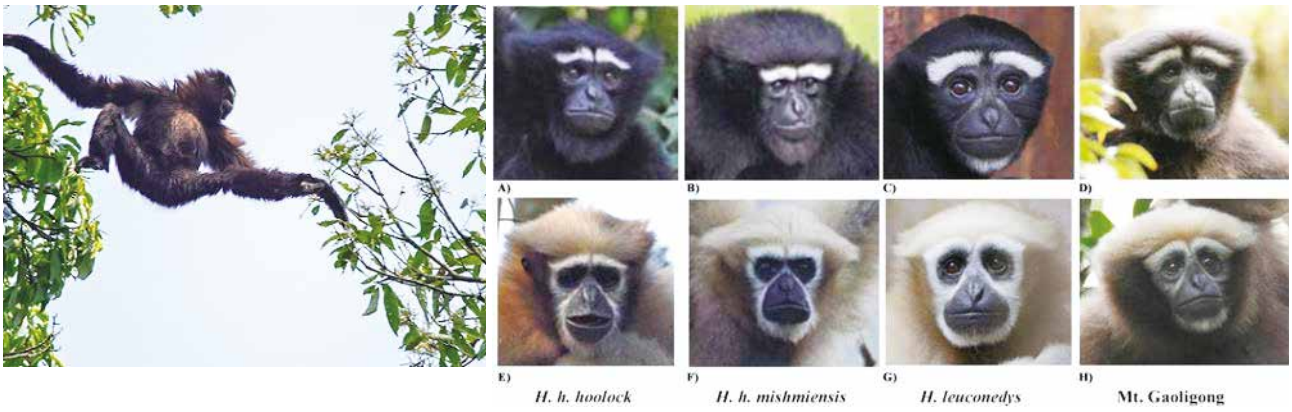
[7] New York Consortium in Evolutionary Primatology (NYCEP), New York
[8] Institute of Human Origins, School of Human Evolution and Social Change, Arizona State University, Tempe, Arizona
[9] Cloud Mountain Conservation, Dali, China
[10] Kunming Zoo, Kunming, China
[11] Beijing Zoo, Beijing, China

We describe a species of *Hoolock* gibbon (Primates: Hylobatidae) that is new to science from eastern Myanmar and southwestern China. The genus of hoolock gibbons comprises two previously described living species, the western (*Hoolock hoolock*) and eastern hoolock (*H. leuconedys*) gibbons, geographically isolated by the Chindwin River. We assessed the morphological and genetic characteristics of wild animals and museum specimens, and conducted multidisciplinary analyses using mitochondrial genomic sequences, external morphology, and craniodental characters to evaluate the taxonomic status of the hoolock population in China. The results suggest that hoolocks distributed to the east of the Irrawaddy-Nmai Hka Rivers, which were previously assigned to *H. leuconedys*, are morphologically and genetically distinct from those to the west of the river, and should be recognized as a new species, the Gaoligong hoolock gibbon or skywalker hoolock gibbon (*H. tianxing* sp. nov.). We consider that the new species should be categorized as Endangered under IUCN criteria. The discovery of the new species focuses attention on the need for improved conservation of small apes, many of which are in danger of extinction in southern China and Southeast Asia.

KEYWORDS
endangered species, gibbon, *Hoolock tianxing*, Mt. Gaoligong, new species

American Journal of Primatology 2017;79:e22631.



以中山大学和重点实验室蒋学龙研究组牵头，联合美、英、澳、德等国专家的国际团队经过多年的联合攻关，在灵长类分类学研究中获得重大进展，发现并命名了一种新的长臂猿 Hoolock tianxing，中文名为“天行长臂猿”（Skywalker hoolock gibbon）或“高黎贡白眉长臂猿”，简称“天行者”。该物种是白眉长臂猿属的第三个物种，也是长臂猿科的第二十个现生物种。 该文章在 American Journal of Primatology 杂志发表，文章发表后受到了 BBC、CNN、Discovery、National Geographic、CCTV、Daily Mail 等媒体的高度关注。

研究方向一：遗传资源多样性的演化与保护

代表性成果三

在鼹类系统发育与演化研究中取得重要进展

Talpid Mole Phylogeny Unites Shrew Moles and Illuminates Overlooked Cryptic Species Diversity

Kai He,[‡,†,1,2] Akio Shinohara,[†,3] Kristofer M. Helgen,[4] Mark S. Springer,[5] Xue-Long Jiang,[*,1] and Kevin L. Campbell[*,2]

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[2]Department of Biological Sciences, University of Manitoba, Winnipeg, MN , Canada

[3]Department of Bio-resources, Division of Biotechnology, Frontier Science Research Center, University of Miyazaki, Miyazaki, Japan

[4]National Museum of Natural History Smithsonian Institution, Washington, DC

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[†]These authors contributed equally to this work.

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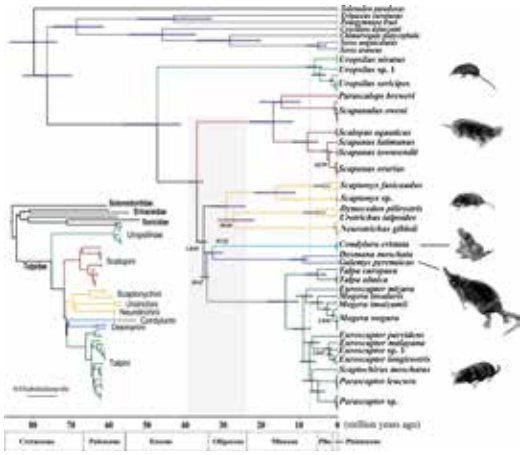
Associate editor: Emma Teeling

Abstract

The mammalian family Talpidae (moles, shrew moles, desmans) is characterized by diverse ecomorphologies associated with terrestrial, semi-aquatic, semi-fossorial, fossorial, and aquatic-fossorial lifestyles. Prominent specializations involved with these different lifestyles, and the transitions between them, pose outstanding questions regarding the evolutionary history within the family, not only for living but also for fossil taxa. Here, we investigate the phylogenetic relationships, divergence times, and biogeographic history of the family using 19 nuclear and 2 mitochondrial genes (~16 kb) from ~60% of described species representing all 17 genera. Our phylogenetic analyses help settle classical questions in the evolution of moles, identify an ancient (mid-Miocene) split within the monotypic genus *Scaptonyx*, and indicate that talpid species richness may be nearly 30% higher than previously recognized. Our results also uniformly support the monophyly of long-tailed moles with the two shrew mole tribes and confirm that the Gansu mole is the sole living Asian member of an otherwise North American radiation. Finally, we provide evidence that aquatic specializations within the tribes Condylurini and Desmanini evolved along different morphological trajectories, though we were unable to statistically reject monophyly of the strictly fossorial tribes Talpini and Scalopini.

Key words: **Talpidae, tree of life, cryptic species, aquatic, fossorial.**

Molecular Biology and Evolution,2017, 34 (1): 78-87



为了探讨鼹类适应性特征的起源、构建一棵强壮的鼹类“生命之树”、摸清我国鼹类物种多样性的家底，蒋学龙研究员团队从上世纪 90 年代开始便开始系统收集鼹类标本，并与国内外机构广泛合作，带领学科组成员开展这一研究，2017 年在鼹类系统发育与演化研究中取得重要进展。本研究解决了鼹科几个长久争论的重要问题：首次发现鼩鼹类的是一个单系群；首次强有力的证明了中国特有物种甘肃鼹是美洲鼹族中的一员；支持以美洲鼹为代表的美洲鼹族（Scalopini）和以欧洲鼹为代表的鼹族（Talpini）对地下生活的适应是独立起源的。此外，该研究发现鼹科至少包括 12 个未知物种，其中有 11 种生活在中国西南及周边区域；而针尾鼹属（Scaptonyx）的进化历史惊人的漫长，其中可能包含未知的属。研究成果发表于 *Molecular Biology and Evolution*。

研究方向一：遗传资源多样性的演化与保护

代表性成果四

揭示褐家鼠的东亚南部起源

Out of Southern East Asia of the Brown Rat Revealed by Large-Scale Genome Sequencing

Lin Zeng,[†,1,2] Chen Ming,[†,3,4] Yan Li,[1,5] Ling-Yan Su,[2,6] Yan-Hua Su,[7] Newton O. Otecko,[1,2,8] Ambroise Dalecky,[9,10] Stephen Donnellan,[11] Ken Aplin,[12] Xiao-Hui Liu,[13] Ying Song,[13] Zhi-Bin Zhang,[14] Ali Esmailizadeh,[15] Saeed S. Sohrabi,[15] Hojjat Asadollahpour Nanaei,[15] He-Qun Liu,[1,2] Ming-Shan Wang,[1,2] Solimane Ag Atteynine,[16,17] Gérard Rocamora,[18] Fabrice Brescia,[19] Serge Morand,[20] David M. Irwin,[1,21] Ming-Sheng Peng,[1,2,8] Yong-Gang Yao,[2,6] Hai-Peng Li,[*,3] Dong-Dong Wu,[*,1,2,8] and Ya-Ping Zhang[*,1,2,5]

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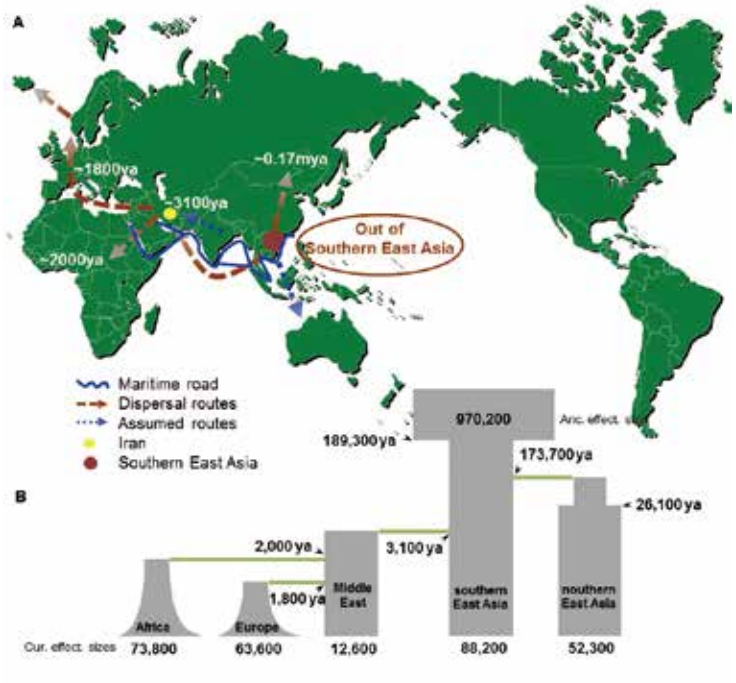
Abstract

The geographic origin and migration of the brown rat (*Rattus norvegicus*) remain subjects of considerable debate. In study, we sequenced whole genomes of 110 wild brown rats with a diverse world-wide representation. We reveal brown rats migrated out of southern East Asia, rather than northern Asia as formerly suggested, into the Middle East then to Europe and Africa, thousands of years ago. Comparison of genomes from different geographical populat reveals that many genes involved in the immune system experienced positive selection in the wild brown rat.

***Key words:* *Rattus norvegicus*, origin, demographic history, natural selection.**

Molecular Biology and Evolution,2017, 35(1):149–158



褐家鼠是重要的伴人鼠类之一，除两级冰盖之外，几乎遍布全球，在人类活动区域非常常见。褐家鼠也是最主要的害鼠之一，携带多种病毒，传染类似鼠疫等的传染性疾病。关于褐家鼠的起源及扩散问题，学术界目前仍存在争议。大量的历史及研究基本确定褐家鼠是起源于亚洲，但是具体起源区域及迁徙路线尚无定论。

张亚平研究组、吴东东研究组与上海生科院李海鹏课题组，利用高通量大规模测序平台对全球多地区 110 个褐家鼠样本进行测序，解析和阐明了褐家鼠的东亚南部起源及迁移问题，并描绘了其从起源地往东亚北部以及欧洲 / 非洲 / 中东的两条主要扩散路线。同时，在褐家鼠的迁徙过程中，很多与免疫系统相关的基因受到了快速进化。相关工作发表于 Molecular Biology and Evolution 上。

研究方向二：基因与基因组的进化 ▶ 代表性成果一

在家鸡矮小化研究中获得系列进展

An Evolutionary Genomic Perspective on the Breeding of Dwarf Chickens

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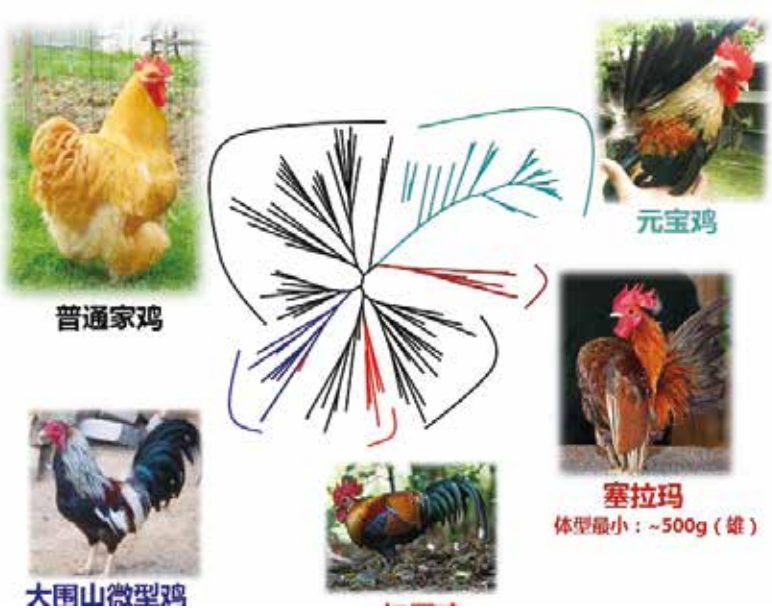
Associate editor: Rasmus Nielsen

Abstract

The evolutionary history for dwarfism in chickens remains an enigma. Herein, we explore the evolution of the Serama, the smallest breed of chicken. Leveraging comparative population genomics, analyses identify several genes that are potentially associated with the growth and development of bones and muscles. These genes, and in particular both *POU1F1* and *IGF1*, are under strong positive selection. Three allopatric dwarf bantams (Serama, Yuanbao, and Daweishan) with different breeding-histories, form distinct clusters and exhibit unique population structures. Parallel genetic mechanisms underlay their variation in body size. These findings provide insights into the multiple and complex pathways, depending on genomic variation, that chicken can take in response to aviculture selection for dwarfism.

Key words: **chicken, Serama, genome, body size, dwarf, selection.**

Molecular Biology and Evolution, 2017,1;34(12):3081-3088.



作为重要的经济性状，家鸡的体型一直受到育种工作者的长期关注。其中，家鸡的矮小化（dwarfism）在蛋鸡和观赏鸡选育中至关重要。针对家鸡的矮小化现象，为揭示不同品系矮小化家鸡的遗传机制，张亚平院士研究团队在前期研究基础上，进一步选取了世界上体型最小的鸡——塞拉玛（Serama）和我国云南著名的小型鸡——大围山微型鸡开展了群体基因组学研究。群体遗传结构分析揭示元宝鸡、塞拉玛和大围山微型鸡有着独立的遗传组分。对三个矮小化鸡种的比较分析它们矮小化的遗传机制并不相同，很可能是多次独立选育的结果。相关结果也为今后的家鸡育种工作提供重要的靶点和参考。研究成果发表在 Molecular Biology and Evolution。

研究方向二：基因与基因组的进化

代表性成果二

揭示实验大鼠被成功驯化的遗传机制

Rapid Evolution of Genes Involved in Learning and Energy Metabolism for Domestication of the Laboratory Rat

Lin Zeng,[1,2] Chen Ming,[2,3] Yan Li,[1,4] Ling-Yan Su,[2,5] Yan-Hua Su,[6] Newton O. Otecko,[1,2] He-Qun Liu,[1] Ming-Shan Wang,[1] Yong-Gang Yao,[5] Hai-Peng Li,[3] Dong-Dong Wu,*[,1] and Ya-Ping Zhang*[,1]

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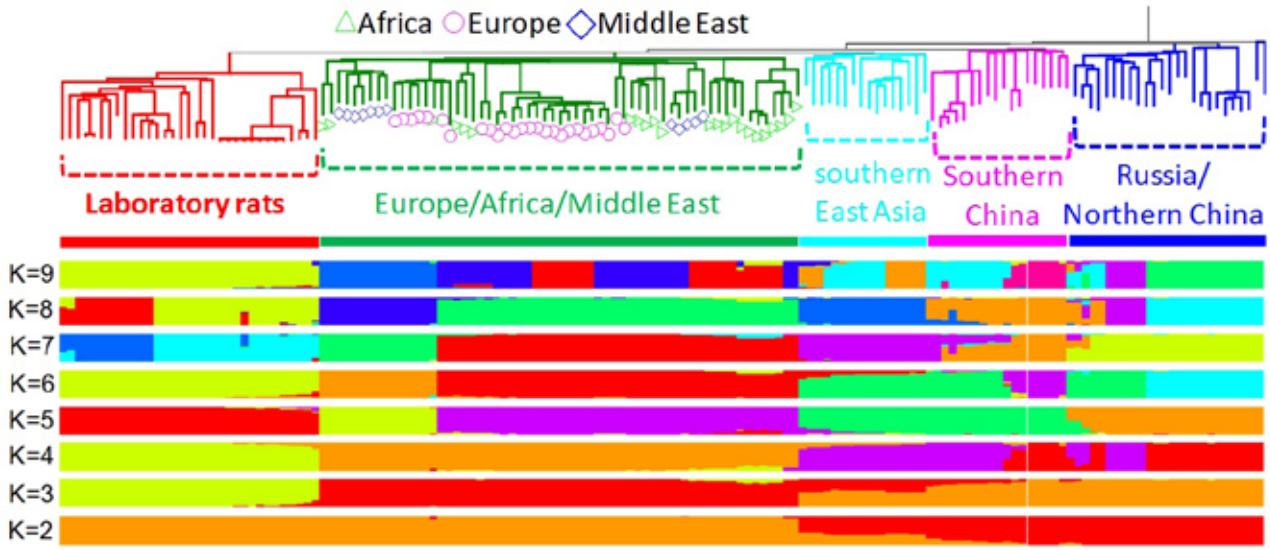
Associate editor: Gregory Wray

Abstract

The laboratory rat, widely used in biomedical research, is domesticated from wild brown rat. The origin and genetic mechanism underlying domestication of the laboratory rat remain largely elusive. In the present study, large scale genomes supported a single origin for the laboratory rat, possibly from a sister group to wild rats from Europe/Africa/Middle East. Genomic and transcriptomic analyses uncovered many artificially selected genes (e.g., *FOXP2*, *B3GAT1*, and *CLOCK*) involved in the nervous system. These genes associate with learning ability and regulation of circadian rhythm, which likely enabled the successful domestication of the laboratory rat. Particularly, many genes, including mitochondrial genes responsible for energy metabolism, displayed a substantially increased expression in the brain of laboratory rats compared with wild rats. Our findings demystify the origin and evolution of this model animal, and provide insight into the process of its domestication.

Molecular Biology and Evolution, 2017, 34(12):3148-3153.



实验大鼠作为一种广泛使用的模式动物，由野生褐家鼠驯化而来，也是一种家养动物。与其野生祖先褐家鼠相比，实验大鼠在形态、行为及生理方面发生了很大的变化，然而实验大鼠的起源以及导致其被驯化成功的机制尚不清楚。张亚平研究组与吴东东研究组，通过比较野生褐家鼠和实验大鼠的基因组和转录组数据，解析了实验大鼠的起源和驯化遗传机制。

研究方向二：基因与基因组的进化 ▶ 代表性成果三

开发出适用于高通量异质性数据算法并成功揭示泛肿瘤存在基因表达紊乱共有模式

IVYSPRING INTERNATIONAL PUBLISHER

Theranostics

2017; 7(11): 2888-2899. doi: 10.7150/thno.19425

Research Paper

A Normalization-Free and Nonparametric Method Sharpens Large-Scale Transcriptome Analysis and Reveals Common Gene Alteration Patterns in Cancers

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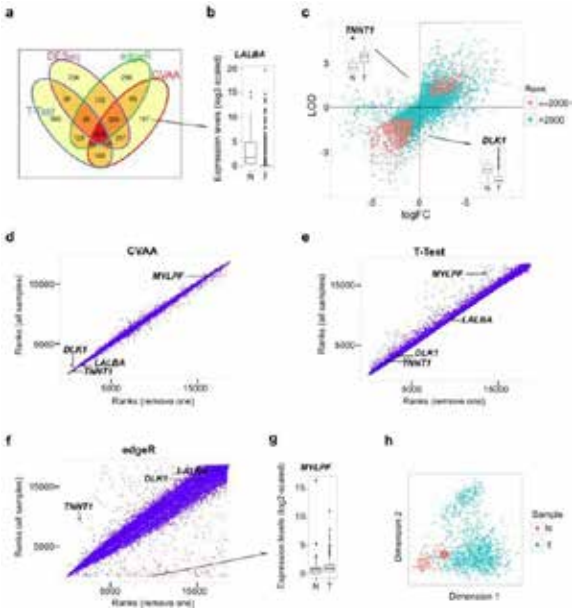
Abstract

Heterogeneity in transcriptional data hampers the identification of differentially expressed genes (DEGs) and understanding of cancer, essentially because current methods rely on cross-sample normalization and/or distribution assumption—both sensitive to heterogeneous values. Here, we developed a new method, Cross-Value Association Analysis (CVAA), which overcomes the limitation and is more robust to heterogeneous data than the other methods. Applying CVAA to a more complex pan-cancer dataset containing 5,540 transcriptomes discovered numerous new DEGs and many previously rarely explored pathways/processes; some of them were validated, both *in vitro* and *in vivo*, to be crucial in tumorigenesis, e.g., alcohol metabolism (*ADH1B*), chromosome remodeling (*NCAPH*) and complement system (*Adipsin*). Together, we present a sharper tool to navigate large-scale expression data and gain new mechanistic insights into tumorigenesis.

Theranostics. 2017,8;7(11):2888-2899.



挖掘肿瘤大数据有助于识别和总结肿瘤发生、发展过程的分子变化规律。然而，肿瘤组织高度异质性、批次效应等因素是肿瘤数据分析的重要难题，而目前常用的转录组数据分析方法对于肿瘤离群值极度敏感，容易产生假阴性结果。针对此，孔庆鹏研究团队联合所内陈勇彬研究组开发了一种新的不依赖均一化、非参的高维大数据分析算法（Cross-Value Association Analysis，CVAA）。该项工作不但成功鉴定出大量新的肿瘤相关基因和通路，为深入理解肿瘤发生发展提供研究靶标，同时也表明 CVAA 算法在大批量、异质性数据分析中具有重要的应用价值。研究成果发表于 Theranostics。

研究方向二：基因与基因组的进化

代表性成果四

发现导致表型趋同进化的新机制

Functional Effects of a Retained Ancestral Polymorphism in *Prestin*

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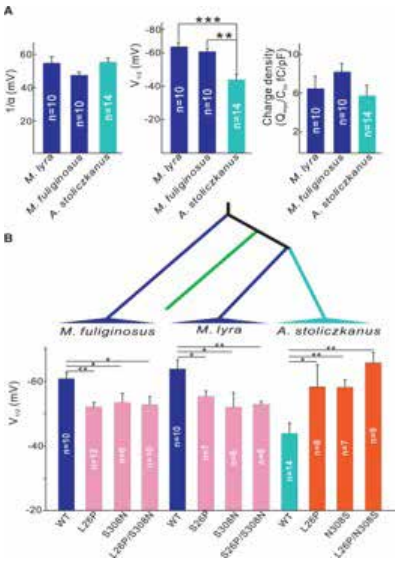
Associate editor: Jianzhi Zhang

Abstract

Molecular basis for mammalian echolocation has been receiving much concerns. Recent findings on the parallel evolution of *prestin* sequences among echolocating bats and toothed whales suggest that adaptations for high-frequency hearing have occurred during the evolution of echolocation. Here, we report that although the species tree for echolocating bats emitting echolocation calls with frequency modulated (FM) sweeps is paraphyletic, *prestin* exhibits similar functional changes between FM bats. Site-directed mutagenesis shows that the amino acid 308S in FM bats is responsible for the similar functional changes of *prestin*. We strongly support that the occurrence of serine at position 308 is a case of hemiplasy, caused by incomplete lineage sorting of an ancestral polymorphism. Our study not only reveals sophisticated molecular basis of echolocation in bats, but also calls for caution in the inference of molecular convergence in species experiencing rapid radiation.

Molecular Biology and Evolution. 2017, 34(1):88-92.

趋同进化是进化生物学领域的研究热点，通常表现为，不同物种为了应对相似的生境而发展出的相同的生存策略。因此，人们普遍认为，表型的趋同变化是适应性进化的结果。对趋同表型分子机制的阐释不仅能够提供一种将基因型和适应性表型相联系的新的思路，而且能够探究基因在演化过程中在多大程度上是可预测的和可重复的。



施鹏研究组一直以来将哺乳动物回声定位作为研究模型，利用分子进化理论和分析方法，探索驱动这种复杂趋同表型发生和发展的内在分子机制。在前期研究基础上，通过进一步研究，发现具有不同回声定位发声特征的蝙蝠其 prestin 的功能也不尽相同，特别是，在物种系统发育树中处于并系的调频蝙蝠。与其近缘的恒频蝙蝠相比，调频蝙蝠 prestin 的功能呈现出了相同的变化趋势。值得注意的是，该研究结果强力支持了，导致这种功能上的相同变化趋势的位点并不是受到趋同或平行进化的位点；起决定作用的是分别固定于调频蝙蝠祖先支系上的源自蝙蝠共同祖先的多态位点，并且该多态位点的固定很有可能是受到了自然选择的影响。该结果提示着，并非所有的趋同表型都是由受到趋同或平行进化的基因及其趋同或平行位点所导致，一些受到自然选择而特异固定下来的祖先多态位点也有可能是其产生的分子机制；同时，提醒研究人员注意，在不同物种中，特别是在那些经历适应性辐射的物种中，进行基因的趋同或平行进化推断和分析时，一定要注意区分不同的形成机制。 研究结果发表于 Molecular Biology and Evolution 杂志。

研究方向三： 遗传、发育与进化

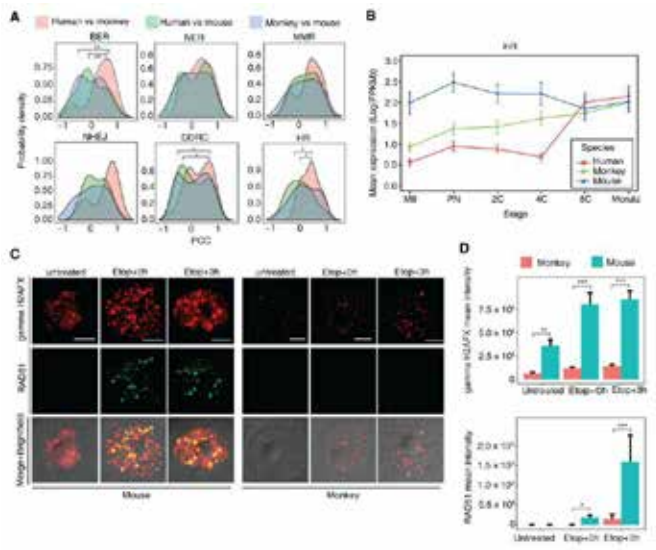
代表性成果一

在猕猴早期胚胎发育研究中取得重要进展

Transcriptome analyses of rhesus monkey preimplantation embryos reveal a reduced capacity for DNA double-strand break repair in primate oocytes and early embryos

Abstract: Preimplantation embryogenesis encompasses several critical events including genome reprogramming, zygotic genome activation (ZGA), and cell-fate commitment. The molecular basis of these processes remains obscure in primates in which there is a high rate of embryo wastage. Thus, understanding the factors involved in genome reprogramming and ZGA might help reproductive success during this susceptible period of early development and generate induced pluripotent stem cells with greater efficiency. Moreover, explaining the molecular basis responsible for embryo wastage in primates will greatly expand our knowledge of species evolution. By using RNA-seq in single and pooled oocytes and embryos, we defined the transcriptome throughout preimplantation development in rhesus monkey. In comparison to archival human and mouse data, we found that the transcriptome dynamics of monkey oocytes and embryos were very similar to those of human but very different from those of mouse. We identified several classes of maternal and zygotic genes, whose expression peaks were highly correlated with the time frames of genome reprogramming, ZGA, and cell-fate commitment, respectively. Importantly, comparison of the ZGA-related network modules among the three species revealed less robust surveillance of genomic instability in primate oocytes and embryos than in rodents, particularly in the pathways of DNA damage signaling and homology-directed DNA double-strand break repair. This study highlights the utility of monkey models to better understand the molecular basis for genome reprogramming, ZGA, and genomic stability surveillance in human early embryogenesis and may provide insights for improved homologous recombination-mediated gene editing in monkey.

Genome Research,2017,27: 567–579.



已知灵长类的早期胚胎与小鼠比较，具更高的染色体异常发生率及胚胎发育失败率，但机制并不清楚。郑萍研究组与中科院马普计算所韩敬东研究组合作，通过绘制首个详尽的猕猴着床前不同阶段胚胎发育基因表达图谱，发现了可能调控猕猴胚胎合子基因组重编程及合子基因组激活的母源基因和调控网络。并且，通过系统比较和分析小鼠、猕猴及人卵细胞及早期胚胎发育表达谱数据，结合功能验证，揭示了灵长类（猕猴及人）卵和早期胚胎维持遗传物质稳定性的能力显著低于小鼠，差异主要表现在 DNA 损伤反应通路的激活及 DNA 同源重组介导的损伤修复途径上。这一研究结果提示，非人灵长类动物（如猕猴）较小鼠更适合于研究人类早期胚胎发育调控机制。也解释了人及非人灵长类早期胚胎存在较高的染色体不稳定性及发育成功率低下的现象。最后，论文还指出了当前在猴中利用 CRISPR/Cas9 技术及 DNA 同源重组原理，进行精准基因替换效率极其低下的内在原因，并提出在 1- 细胞合子期通过导入重组酶增强同源重组能力，有望能提高猴精准基因敲入的效率。 结果发表于 *Genome Research*。

研究方向三： 遗传、发育与进化

代表性成果二

在藏族高原适应遗传机制研究中取得重要进展

Down-Regulation of *EPAS1* Transcription and Genetic Adaptation of Tibetans to High-Altitude Hypoxia

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Abstract

Tibetans are well adapted to the hypoxic environments at high altitude, yet the molecular mechanism of this adaptation remains elusive. We reported comprehensive genetic and functional analyses of *EPAS1*, a gene encoding hypoxia inducible factor 2α (HIF-2α) with the strongest signal of selection in previous genome-wide scans of Tibetans. We showed that the Tibetan-enriched *EPAS1* variants down-regulate expression in human umbilical endothelial cells and placentas. Heterozygous *EPAS1* knockout mice display blunted physiological responses to chronic hypoxia, mirroring the situation in Tibetans. Furthermore, we found that the Tibetan version of *EPAS1* is not only associated with the relatively low hemoglobin level as a polycythemia protectant, but also is associated with a low pulmonary vasoconstriction response in Tibetans. We propose that the down-regulation of *EPAS1* contributes to the molecular basis of Tibetans' adaption to high-altitude hypoxia.

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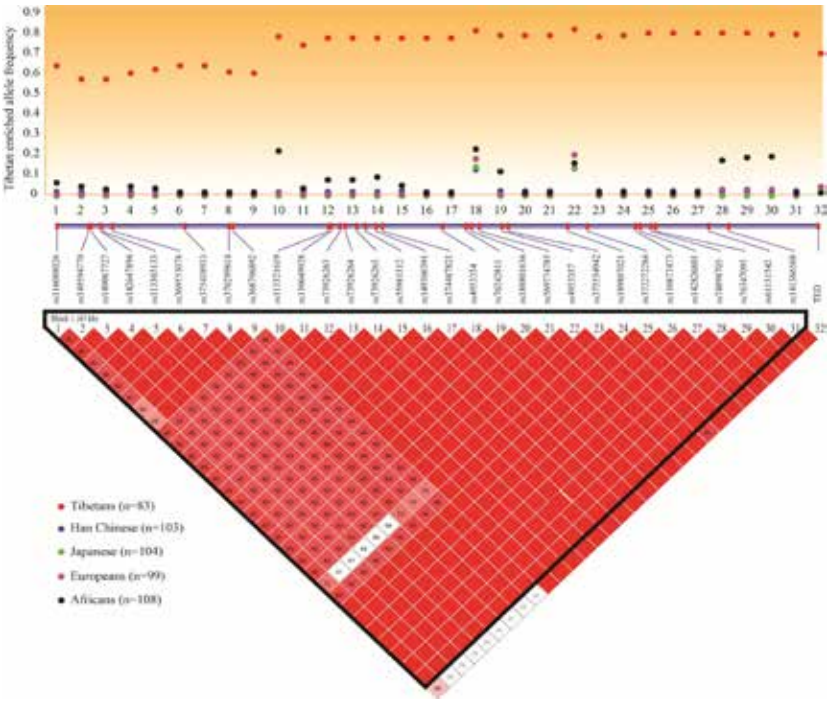

藏族人群对高原低氧极端环境表现出了较好的适应能力，这种适应能力是长期自然选择的结果。然而，藏族人群的遗传适应是如何通过分子水平的精细调控实现心、肺等氧交换和氧运输器官在高原低氧下的正常生理功能的仍是未解之谜。宿兵团队与西藏大学高原医学中心的崔超英教授、青海省高原医学科学研究院吴天一院士通过多年的紧密合作，对高原藏族与平原汉族人群间的全基因组遗传差异分析，发现了一批与藏族人群对高原低氧适应相关的候选基因。

在前期工作基础上，研究团队通过对EPAS1 基因的全长精细测序发现藏族人群中受到强烈选择的变异位点都位于非编码区，提示这些藏族富集的变异很可能在转录水平参与调控。他们进一步对藏族人群中富集的的 32 个 EPAS1 突变位点进行了大样本的遗传相关性分析、藏族胎盘组织的转录组分析、藏族新生儿脐带内皮细胞的低氧诱导实验、EPAS1 基因敲除小鼠的低氧诱导实验等综合的遗传学分析和功能验证试验，发现藏族富集的 EPAS1 变异位点下调了 EPAS1 在脐带内皮细胞和胎盘中的表达水平；杂合 EPAS1 敲除小鼠表现出与高原藏族人群相似的对慢性低氧的生理钝化反应。除此之外，他们还发现 EPAS1 基因除了下调藏族人群在高原低氧环境中的血红蛋白水平外，可能还参与下调藏族人群的肺动脉压，进而实现对高原低氧环境的长期适应。这是宿兵团队在藏族人群对高原低氧环境适应机制研究中的又一阶段性成果，首次解析了高原适应关键基因 EPAS1 基因表达调控模式，向最终阐明人类对高原低氧极端环境适应的遗传机制迈出了重要的一步。结果发表于 Molecular Biology and Evolution。

系统进化与生物地理学

杨君兴，博士，研究员，博士生导师。研究方向包括：生物多样的考察监测及评价、系统分类、系统发育与生物地理学；珍稀特有物种的生态学研究和保育；湿地生态系统的恢复研究。本年度共有在研课题 27 项，其中新申请批准的项目 9 项。发表论文 10 篇，其中 SCI 论文 6 篇，获授权国家发明专利 1 项，云南省专利三等奖 1 项。

重要成果（Highlights）

论著（Publications）

1. **Yu GH**[1], **Rao DQ**[1], Matsui M, **Yang JX***. 2017. Coalescent-based delimitation outperforms distance-based methods for delineating less divergent species: the case of Kurixalus odontotarsus species group. Scientific Reports, 7: 16124. doi: 10.1038/s41598-017-16309-1.
2. **Yu GH**[1]*, **Wang JS**[1], Hou M, **Rao DQ**, **Yang JX***. 2017. A new species of the genus Kurixalus from Yunnan, China (Anura, Rhacophoridae). Zookeys, 694: 71-93.
3. Hou M, **Yu GH**, Chen HM et al. 2017. The taxonomic status and distribution range of six Theloderma species (Anura: Rhacophoridae) with a new record in China. Russian Journal of Herpetology, 2: 99-127.
4. **Zheng LP**, **Yang JX***. 2017. Characterization of the complete mitochondrial genome of Discogobio longibarbatus (Cypriniformes, Cyprinidae), an endangered and endemic species from China. Conservation Genetic Resourse. 9: 447–449.
5. **Zhang YW**, **Pan XF**, **Wang XA**, **Jiang WS**, **Yang KF**, **Liu Q**, **Yang JX***. 2017. Selection of Reliable Reference Genes for Quantitative Real-Time PCR in Golden-Line Barbell (Sinocyclocheilus grahami) During Juvenile and Adult Stages. Journal of FisheriesSciences.com, 11(2): 074-082.
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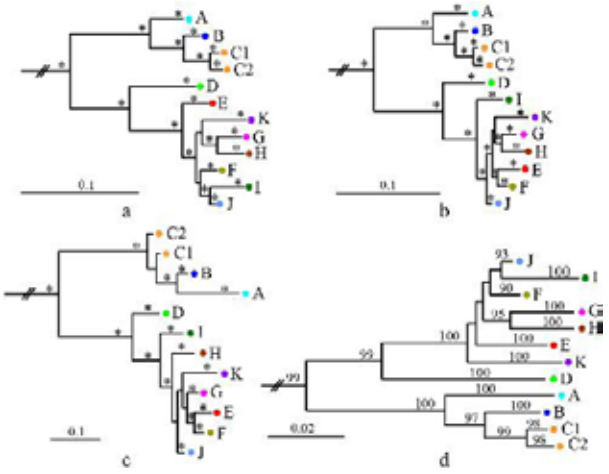
7. 滇池金线鲃的人工训养繁殖方法，云南省专利三等奖

1. 锯腿原指树蛙物种分化研究

利用锯腿原指树蛙种组探讨了基于溯祖理论的物种划分方法和基于遗传距离的 DNA 条形码技术在区分近缘种上的表现。结果表明，与基于遗传距离的条形码间隙自动发现方法（ABGD）相比，以溯祖为基础的物种划分方法对假阴性（将多个近缘种合并为同一种）更为保守。基于固定条形码间隙的方法虽然可能得到与溯祖方法相同的物种划分结果，但它严重依赖于研究者对条形码间隙的主观选择并且缺乏统计上的支持。



2. 锯腿原指树蛙、鳅属等鱼类分类取得综合进展

本年度课题组成员对原指树蛙、鳅属等鱼类进行了分类学研究，发现了 2 新种，分别是冷泉原指树蛙和高黎贡鳅。并发现了树蛙科棱皮树蛙属在中国分布的一新记录，即双色棱皮树蛙。分类学研究共发表 SCI 论文 2 篇。

3. 云南珍稀特有鱼类的人工繁殖、养殖推广和野外种群复壮

2017 年繁殖滇池金线鲃鱼苗 200 余万尾，抚仙金线鲃鱼苗 3 万余尾。突破程海白鱼、宽鳍鱲、桥街结鱼和大眼圆吻鮈的人工繁殖，繁殖程海白鱼 2 万余尾、宽鳍鱲 1000 余尾、桥街结鱼 1000 余尾、大眼圆吻鮈 1 万余尾。繁殖西畴金线鲃 2 万余尾，繁殖鳡鱼良白鱼 20 万余尾，繁殖软鳍新光唇鱼 30 万余尾（其中昆明 1 万余尾，西畴 20 万余尾）。选育滇池金线鲃 F1、F2 和 F3 代亲鱼 3 万余尾，繁殖短须裂腹鱼 20 万余尾（其中昆明 1000 余尾，会泽 30 万余尾）。申报滇池金线鲃“鲃优 1 号”养殖新品种并通过现场审查。

目前，珍稀鱼类保育基地饲养有土著鱼类 50 余种，40 万余尾，无重大鱼病出现。单位养殖水体的养殖密度逐年提高。对西畴、曲靖、会泽、芒市、保山、丽江、大理、德泽鱼类增殖放流站等养殖基地定期进行技术指导。

2017 年度在昆明晋宁古滇艺海码头放流滇池金线鲃 9 万余尾。支持西畴、会泽三个水产公司滇池金线鲃鱼苗 30 余万尾，裂腹鱼、光唇鱼等种鱼 200 余千克。3 月 29 日在墨江县三江口水电站库区放流软鳍新光唇鱼苗种 3 万尾。

Phylogenetics and Biogeography

Prof. Junxing Yang, Professor. The research team is mainly interested in biodiversity monitoring survey and evaluation, fauna taxonomic, phylogenetic and biogeographic; ecology and conservation research to rare and native species; especially focuses on the restoration of wetland ecosystem and application. In 2017, total 27 research programs have been implementing with 9 programs newly approved. A total of 10 papers have been published which 6 of them are SCI papers. One national invention patent licensing and one patent third prize of Yunnan Province .

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1. Coalescent-based delimitation outperforms distance-based methods for delineating less divergent species: the case of Kurixalus odontotarsus species group

Two coalescent-based (BFD and BPP) and two distance-based barcoding (ABGD and jMOTU) methods were used to delimit closely related species in the Kurixalus odontotarsus species group. Phylogenetic analyses revealed that the K. odontotarsus species group comprises 11 distinct maternal clades with strong support values. Based on the genetic and morphological evidences, we consider that species diversity in the K. odontotarsus species group was underestimated and the 11 clades represent 11 species, of which six are unnamed. The coalescent based delimitations decisively supported the scenario of 11-species corresponding to the 11 clades. However, the distance-based ABGD only obtained 3–6 candidate species, which is not consistent with morphological evidence. These results indicate that BFD and BPP are more conservative than ABGD to false negatives (lumping). Method of fixed threshold (jMOTU) may obtain a resolution similar to that inferred by BFD and BPP, but it severely relies on subjective choice of the threshold and lacks statistical support. We consider that coalescent-based BFD and BPP approaches outperform distance-based methods for delineation of less divergent species.

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

In this year, we described two new species (*Kurixalus lenquanensis* sp. nov. and *Exostoma gaoligongense* sp. nov.) from Yunnan province. *Kurixalus lenquanensis* sp. nov., is distinguished from other congeneric species by a combination of morphological and molecular evidence. The molecular results indicated that the ancestor of this new species might have come from Taiwan Island or the ancestor of this new species may have been widespread in southern China and the descendent species in between Taiwan and Yunnan has become extinct. *Exostoma gaoligongense* sp. nov. is the 10th species of the genus and is most similar to *E. vinciguerrae* in morphology but can be distinguished from it by morphological characters. In addition, a new record of Thelodema species (Anura: Rhacophoridae) in China was discovered.

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

We keep moving in the way of conservation and utilization of the endemic and endangered fishes. In this year, we cultivated and produced more than 2 million fish fry of these fishes, including *Sinocyclocheilus grahami*, *Anabarilius liui chenghaiensis*, *Zaccoplatypus*, *Anabarilius grahami*, *Torqiaojiensis* and *Distoechodon macrophthalmus*. More than 2 million individuals were expanded to cultivated in other fish farms which in Huize County and Xichou County, and more than 0.3 million individuals were released in wild to rebuilt and restore the wild population of these fishes.

FOR THE WAY HOME
——releasing *S. grahami* into Dianchi Lake

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研究生（Graduate Students）

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张源伟　Yuanwei Zhang 2013
Marco Endruweit 2014
牛诚祎　Chengyi Niu 2015
杜丽娜　Lina Du 2016
孙　超　Chao Sun 2017
殷艳慧　Yanhui Yin 2017
吴安丽　Anli Wu 2017

兽类生态与进化

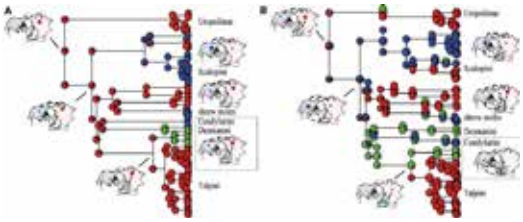
蒋学龙，博士，研究员。长期从事哺乳动物分类、系统演化与生物地理，灵长类动物种群生态与保护，兽类资源考察、监测与保护研究。研究区域主要包括横断山区、青藏高原和东非。从宏观和微观两个方面，揭示横断山地区哺乳动物多样性的形成机制及在特殊生态条件下的适应性进化与保护。近年来，主要以东喜马拉雅－横断山地区特有与常见小型哺乳动物、灵长类及地栖大中型兽类为研究对象，重点研究横断山区哺乳动物分布格局及其演化机制、西黑冠长臂猿的生态行为与适应性，并全面布局横断山区兽类资源监测网络与数据库建设，开展亚洲象生态学研究，为人象冲突防范与亚洲象保护提供科学对策。

重要成果（Highlights）
论著（Publications）

1. **He K**[1], Akio S[1], Kristofer MH, Mark SS, **Jiang XL***, Kevin L C*. Talpid mole phylogeny unites shrew moles and illuminates overlooked cryptic species diversity. **Molecular Biology and Evolution.**2017,34(1):78-87.
2. **Chen ZZ**[1], **He K**[1]*, **Huang C**, **Wan T**, Lin LK, Liu SY, **Jiang XL** *. Integrative systematic analyses of the genus *Chodsigoa*(Mammalia: Eulipotyphla: Soricidae), with descriptions of new species. **Zoological Journal of the Linnean Society**.2017, 180(3): 694-713.
3. **Cheng F**[1], **He K**[1] *,**Chen ZZ** ,**Zhang B**, **Wan T**, Li JT, Zhang BW*, **Jiang XL** *. Phylogeny and systematic revision of the genus *Typhlomys* (Rodentia, Platacanthomyidae), with description of a new species . **Journal of Mammalogy.2017**, 98(3):731-743.
4. **Koju NP**, **He K***, Chalise MK, Ray C, **Chen ZZ**, **Zhang B**, **Wan T**, **Chen S** , **Jiang XL***. Multilocus approaches reveal underestimated species diversity and inter-specific gene flow in pikas (*Ochotona*) from southwestern China. **Molecular Phylogenetics and Evolution**. 2017,107, 239-245.
5. **Chen ZZ**, **He K**, **Cheng F**, **Khanal L**, **Jiang XL***. Patterns and underlying mechanisms of non-volant small mammal richness along two contrasting mountain slopes in southwestern China. **Scientific Reports** .2017,7(1).13277 .
6. Buzzard PJ*, **Li XY**, Bleisch, WV. The status of snow leopards *Panthera uncia* and high altitude use by common leopards *P. pardus* in northwest Yunnan, China. **Oryx** .2017, 51: 587-589.
7. 肖志术 *, 李学友，向左甫，李明，蒋学龙，张礼标．中国兽类多样性监测网络的建设规划与进展．生物多样性 .2017,25（3）:237-245.
8. 程峰，万韬，陈中正，**Koju NP**, 何锴 *, 蒋学龙 *. 云南兽类鼩鼱科一新记录 -- 台湾灰麝鼩．动物学杂志 ,2017,52(5):865-869

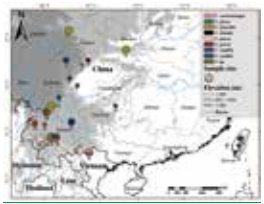
1. 鼹科系统发育与分类

鼹科是哺乳动物中生态型最丰富、适应性进化特征最显著的类群，除了保留原始陆栖习性的鼩形鼹（Uropsilinae），还有适应半地下生活的鼩鼹 Scaptonychini, Neurotrichini 和 Urotrichini）、严格适应地下环境的真鼹（Talpini, Scalopini）、适应水下生活的水鼹（Desmanini）和同时适应水下和地下的星鼻鼹（Condylurini）。兽类生态与进化课题组通过与多个国际团队合作，测定了全世界鼹科的大部分物种的数十个核基因，第一次较为系统地阐明了鼹科的系统演化关系。研究首次解决了关于鼹科起源与进化中几个长久争论的问题：证明了亚洲和欧洲的鼩鼹类是一个单系群；首次证明了中国特有物种甘肃鼹是美洲鼹族中的一员；有趣的是，该研究第一次显著支持美洲鼹族（Scalopini）和鼹族（Talpini）两个类群对地下生活的适应是独立起源的。此外，该研究发现鼹科物种多样性被低估约 30%，其中大部分生活在采样缺乏的中国西南山地。



2. 缺齿鼩属系统发育和分类

缺齿鼩属（Chodsigoa）隶属于哺乳纲鼩形目鼩鼱科，主要分布中国南方及东南亚地区。为了厘清缺齿鼩属物种的分类地位与系统发育关系，研究人员检视了馆藏于中国科学院昆明动物研究所、四川省林业科学研究院、美国自然历史博物馆和哈佛大学比较动物学博物馆的 150 号馆藏标本，并首次使用分子系统学方法对近年来采集到的标本进行分析。结果显示澜沧江东、西两岸的云南缺齿鼩（*Chodsigoa parca*）存在显著分化，研究人员将澜沧江以东的种群描记为一个新物种，为纪念美国国家自然历史博物馆已故教授 Robert Hoffmann 在亚洲国家特别是中国哺乳动物分类学研究中做出的卓越贡献，研究人员将新种命名为霍氏缺齿鼩（*Chodsigoa hoffmanni* sp. nov.）。此外，通过分子系统学分析以及与美国自然历史博物馆馆藏模式标本的比对，确认此前被归为云南缺齿鼩亚种的烟黑缺齿鼩（*Chodsigoa furva*）为独立种，恢复其有效种的地位。



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 ofblack crested gibbon, as well as conservation biology of Asian elephant and other large mammals.
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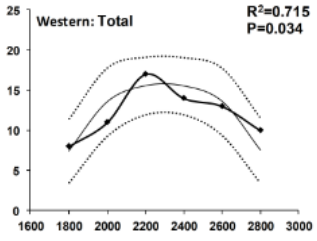
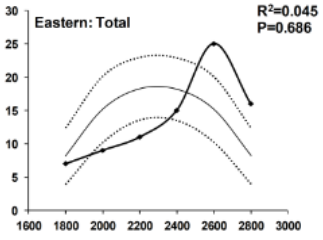
1. Multilocus approaches reveal underestimated species diversity and inter-specific gene flow in pikas (*Ochotona*) from southwestern China

The phylogeny of living pikas (Ochotonidae, *Ochotona*) remains obscure, and pika species diversity insouthwestern China has never been well explored. In this study, 96 tissue samples from 11 valid species in three classified subgenera (*Pika*, *Ochotona* and *Conothoa*) from 23 locations were characterized using multilocus sequences of 7031 bp. Two mitochondrial (*CYT B* and *COI*) and five nuclear gene segments (*RAG1, RAG2, TTN, OXAIL* and IL*1RAPL1*) were sequenced. We analysed evolutionary histories using maximum likelihood (RAxML) and Bayesian analyses (BEAST), and we also used molecular species delimitation analyses (BPP) to explore species diversity. Our study supported *O. syrinx* (*O. huangensis*) as a distinct clade from all named subgenera. Relationships among subgenera were not fully resolved, which may be due to a rapid diversification in the middle Miocene (-13.90 Ma). Conflicting gene trees implied mitochondrial introgression from *O. cansus* to *O. curzoniae*. We uncovered three cryptic species from Shaanxi, Sichuan and Yunnan with strong support, suggesting an underestimation of species diversity in the "sky-island" mountains of southwest China.

2. Patterns and underlying mechanisms of non-volant small mammal richness along two contrasting mountain slopes in southwestern China

The species richness patterns of small mammals and the processes shaping them in two gradients of a mountain with different spatial and climatic characteristics were examined using standard sampling scheme. We trapped 2,006 small mammals representing 37 species, along elevational gradients on both western and eastern slopes of the Ailao Mountains, Southwest China. Using mid-domain effect model, model selection and model averaging, we examined the effects of slope, area, mean annual temperature (MAT), mean annual humidity (MAH), productivity, plant species richness (PSR) and the mid-domain effect (MDE) on the patterns of small mammal diversity. The hump-shaped patterns were favored along the elevational gradient, but shapes of diversity curves were different on the contrasting slopes. Area and productivity were the most important factors in explaining the variation of total species richness. However, for each specific group of small mammals (i.e. insectivores vs. rodents, largeranged vs. small-ranged species, endemic vs. non-endemic species), the peaks of species richness and their primary drivers varied. The major explanatory factors for richness pattern of each small mammal group were not significantly different between the slopes, suggesting the existence of the general underlying mechanisms on two slopes of a mountain.





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鸟类学

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重要成果（Highlights）

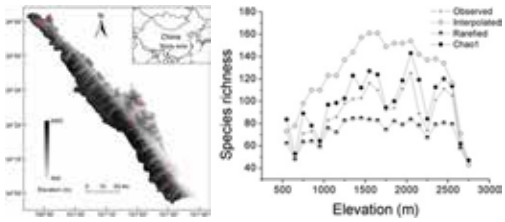
论著（Publications）

1. **Hu WZ**[1], **Wu F**[1], **Gao JY**, **Yan D**, Liu LM, **Yang XJ***. Influences of interpolation of species ranges on elevational species richness gradients. **Ecography,** 2017, 40:1231-1241.
2. **Dong F**[1], Hung ChM[1], **Li XL**, **Gao JY**, Zhang Q, **Wu F**, Lei FM*, **Li** SH*, **Yang XJ***.Ice age unfrozen: severe effect of the last interglacial, not glacial, climate change on East Asian avifauna. **BMC Evolutionary Biology**, 2017, 17:244
3. **Lu GY**, **Wang RX**, Ma LR, **Yang XJ***. Characteristics of Dry Upland Roosts of the Black-Necked Crane (Grus nigricollis) Wintering In Yongshan, China. **The Wilson Journal of Ornithology**, 2017,129(2):323-330.
4. Zhang LX*, An B, Shu ML, Zhao CM, **Yang XJ***, Suo YL, Se YJ, DaBu XLT. Incubation strategies of the Black-necked Crane (Grus nigricollis) in relation to ambient temperature and time of day. **Avian Research**, 2017, 8:19.
5. **Wu F**, Liu LM, Fang JL, Zhang RG, **Yang XJ***. Conservation value of human-modified forests for birds in mountainous regions of south-west China. **Bird Conservation International**, 2017, 27:187–203.
6. Zhang LX*, An B, Shu ML, **Yang XJ***. Nest-site selection, reproductive ecology and shifts within core-use areas of Black-necked Cranes at the northern limit of the Tibetan Plateau. **Peerj**, 2017, 2939.
7. Zhang LX, Shu ML, An B, Zhao CM, **Yang XJ***.Biparental incubation pattern of the Black-necked Craneon an alpine plateau[J]. **Journal of Ornithology**, (2017) 158:697–705
8. 孔德军，杨晓君 *. 绿孔雀及其在中国的保护现状 _ 孔德军 [J]. 生物学通报 , 2017, 52(1): 9-12.

1. 插值法对于评估物种丰富性垂直分布格局的影响

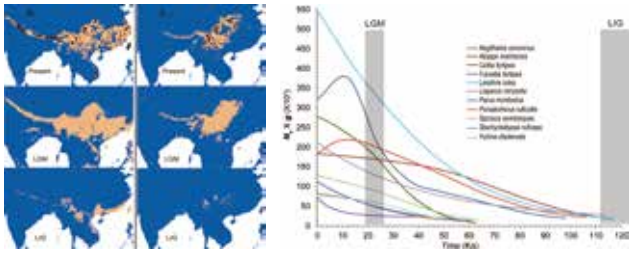
插值法是一种广泛使用的弥补物种空间分布上取样不足的方法。但对这种方法的潜在误差仍然不清楚。本研究中我们详细评估了插值法对物种丰富性垂直分布梯度的影响，并讨论了导致这些影响的可能原因和过程。我们首先对中国西南部哀牢山地区的鸟类多样性垂直梯度开展了深入的实地调查，然后使用多元线性回归法和分层分割方法比较基于实地观测法、插值法、稀疏法以及 Chao I 非参数估计法等四种方法得到的鸟类物种丰富度垂直分布格局。在分布格局的影响因素中，实际蒸散量和中域效应高度相关，分别较好的解释了该地区鸟类多样性沿海拔分布的单峰格局，两者对其它因子（如面积）的解释力具有抑制作用。结果发现，插值法会显著提高实际蒸散量和中域效应，同时降低面积和人为干扰登其它因子的解释力。这些研究结果表明，插值法在弥补取样不足的同时，也可能错误的填补实际分布范围之间的缺口，从而低估造成这些分布缺口的非单调或不连续变量的影响。研究中同时发现上述误差对于中域分布物种的影响最为强烈。

综合以上结果，我们认为，在区域尺度上，插值法在识别和解释物种丰富度分布格局中可能会带来误差，应当谨慎使用。具体研究宜结合使用其它更为可靠的估计方法以准确评估物种丰富度格局值并客观理解其潜在机制。



2. 东亚鸟类的历史种群动态学研究

欧洲和北美的研究显示 LGM 对于其当前遗传多样性的分布格局具有决定性的作用。相比之下，亚洲的相关研究却因不同证据间的相互矛盾而无法形成系统理论。基于化石 – 孢粉记录的模拟分析揭示 LGM 对于东亚种群演化具有剧烈影响，而基于现生种群的种群动态分析却揭示 LGM 期间的种群稳定甚至增长。本研究使用生态和遗传数据深入探讨 11 种东亚广泛分布鸟类对于更新世气候变迁的种群动态历史。生态位模型分析揭示所有研究鸟类的分布区均在 LIG 收缩至南部避难所，而在 LGM 期间向北扩展，以致形成近似当前的分布范围。与此相符，基于 25–30 个独立演化基因的溯祖模拟分析揭示了在 LIG 之后、LGM 之前的种群增长。这一格局与传统认定的循间冰期 – 冰期循环的扩张 – 收缩模型显著相异。基于气候数据的统计分析进一步揭示 LIG 期间显著增强的气候变异度可能造成了东亚地区不同寻常的气候变迁应对模型。本研究将增进人们对于东亚鸟类演化历史的认识。



Ornithology

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

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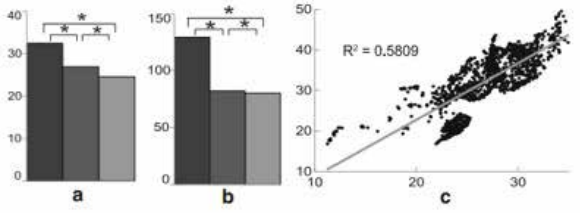
1. The influences of one-dimensional interpolation on elevational species richness gradients

Interpolation of species ranges has been a common approach to compensate for the unevenness or incompleteness in sampling effort in studies of geographic species richness gradients. However, potential biases introduced by this estimation method remain unclear. Here, we presented an explicit examination of the influences of one-dimensional interpolation on elevational species richness gradients, and discussed potential causes and processes of these influences. We conducted intensive surveys of birds along the elevational gradients of the Ailao Mountains, southwestern China, and compared richness patterns based on interpolation with raw data as well as estimated data from rarefaction and Chao1 non-parametric estimator; we also compared results of multiple linear regressions and hierarchical partitioning analyses explaining these four measures of richness. Actual evapotranspiration (AET) and the mid-domain effect (MDE) were highly correlated and separately provided a good potential explanation for the unimodal richness pattern in the Ailao Mountains, with modifying and suppressive effects of other variables such as area. Interpolation consistently and significantly increased the effects of AET/MDE, while it reduced contributions of area and human disturbance. Our results demonstrated that while compensating for biases in sampling effort, interpolation may also spuriously fill genuine distribution gaps, and tend to underestimate the effects of the non-monotonic or discontinuous influencing factors that are responsible for these gaps, and overestimate the effects of other factors actually suppressed by these factors. These influences were most strong for species with relatively medium elevational ranges. We conclude that at the regional scale, interpolation method is a potential source of bias in identifying and explaining species richness gradients and should be used with careful consideration. It may be advantageous to adopt other robust estimation methods besides interpolation to gain a more accurate assessment of species richness and a more objective understanding of their underlying mechanisms.

2. Historical population dynamics of East Asian birds

The glacial-interglacial cycles in the Pleistocene had caused repeated range expansion and contraction of species at several regions in the world. However, it remains uncertain whether such climate oscillations had similar impact on East Asian biota, despite its widely recognized importance in global biodiversity. Here we use both molecular and ecological data on 11 East Asian avian species with various altitudinal ranges to reveal that their peculiar response to the late Pleistocene climate changes. Our ENMs consistently show that these birds contracted their ranges to the south substantially during the LIG and expanded their northern range margins through the LGM, leading to LGM ranges similar to the present ones in all 11 species. Coalescent simulations based on 25 - 30 nuclear genes retrieved signatures of significant population growth through the last glacial period across all species studied, consistent with the ENM prediction. The results strongly contrast with established views that species cyclically expanded in interglacial and contracted in glacial periods. Climate statistics suggesting that East Asia had high climatic variation at the LIG and a relatively mild climate at the LGM might explain the historical population dynamics of these birds. This is the first study based on multiple species to characterize the unique response of East Asian biota to late Pleistocene climate and implies that global warming might pose a great risk to species in this region given potentially higher climatic variation in the future analogous to that during the LIG.



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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（Highlights）

论著（Publications）

1. Andújar C, Arribas P, Gray C, Bruce C, Woodward G, **Yu DW,** Vogler AP*. Metabarcoding of freshwater invertebrates to detect the effects of a pesticide spill**. Molecular Ecology.** 2017, doi:10.1111/mec.14410.
2. Bush A, Sollmann R, Wilting A, Bohmann K, Cole B, Balzter H, Martius C, Zlinszky A, Calvignac-Spencer S, Cobbold CA, Dawson TP, Emerson BC, Ferrier S, Gilbert MTP, Herold M, Jones L, Leendertz FH Matthews L, Millington JDA, Olson J, Ovaskainen O, Raffaelli D, Reeve R, Röde, M., Rodgers TW, Snape S, Visseren-Hamakers I, Vogler AP, White PCL, Wooster MJ, **Yu DW.*** Connecting Earth Observation to High-Throughput Biodiversity Data. **Nature Ecology and Evolution.** 1:0176. doi: 10.1038/s41559-017-0176.
3. Rodgers TW., Xu C, Giacalone J, Kapheim KM, Saltonstall K, Vargas M, **Yu DW**, Somervuo P, Jansen PA, McMillan WO. Carrion fly-derived DNA metabarcoding is an effective tool for mammal surveys: evidence from a known tropical mammal community. **Molecular Ecology Resources.** 2017 , 7 (1) :6162.
4. Somervuo P*, **Yu DW*,** Xu CCY, **Ji YQ,** Hultman J, Wirta H, and Ovaskainen O. Quantifying uncertainty of taxonomic placement in DNA barcoding and metabarcoding**. Methods in Ecology and Evolution.** 2017, 8:398-407.doi: 10.1111/2041-210X.12721.
5. **Cai W**, Ma ZX, **Yang CY, Wang L, Wang WZ**, Zhao GG, Geng YP, **Yu DW***. Using eDNA to detect the distribution and density of invasive crayfish in the Honghe-Hani rice terrace World Heritage site**. Plos One.** 2017 , 12 (5) :e0177724.

1. 大尺度生物多样性监测方法的展望

大尺度实时生物多样性管理监测，对精细研究生物多样性格局动态和物种适应策略、预测生物兴衰和分布格局态势有重要意义。《中科院十三五规划纲要》将“大尺度区域生物多样性格局与生命策略”作为 60 个有望实现创新跨越的重大突破之一进行部署，旨在通过环境 DNA 条形码、大样地野外试验观测和遥感可视化技术来实现生态学和进化生物学领域的重大突破。

中国科学院昆明动物研究所 Douglas Yu 研究员提出通过将自动记录装置、高通量 DNA 测序技术、先进的生态模型和遥感技术结合起来，实现有效、实时、大尺度的生物多样性管理监测的展望。遥感数据和其他的地理数据可以得到时间、空间上连续的生物物理数据。而在样点上利用传统的生物多样性研究方法，如自动录像或图像记录设备、高通量条形码或者线粒体宏基因组技术，又可以得到物种在某些样点的生物多样性信息。但这些样点信息通常是不连续的，无法覆盖到整个景观区域。因此，可以将这些样点信息结合遥感技术来推测整个景观的生物多样性组成，并绘制出生态系统功能和生态系统服务的地图。

2. 利用环境 DNA 方法检测红河哈尼水稻梯田入侵小龙虾的分布和密度

中国红河哈尼水稻梯田景观是联合国教科文组织的世界自然遗产，但这些景观却面临着小龙虾的入侵。我们的研究测试了水样本中的环境 DNA 是否能提供一种灵敏的检测小龙虾的方法。得到结论是，重复的环境 DNA 采样方法可行，而且环境 DNA 方法能有效检测到小龙虾的地理范围，而且还可以检测到小龙虾入侵的新地方。这将有助于小龙虾入侵的控制工作，并有助于防止入侵小龙虾的进一步泛滥。

Ecology, Conservation, & Environment Center (ECEC)

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

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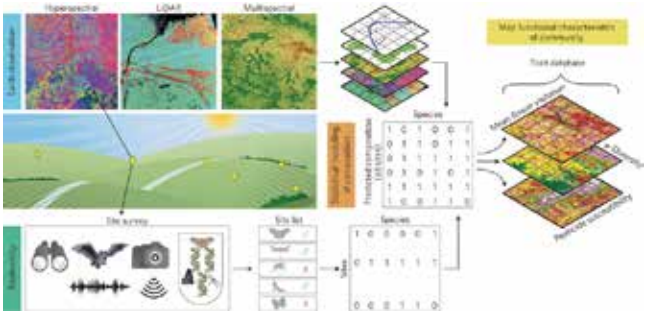
1. A science perspective: Connecting Earth Observation to High-Throughput Biodiversity Data

The global decline of biodiversity and ecosystem services has driven international commitment to better management, in particular the Convention on Biological Diversity and its 2020 Aichi Biodiversity Targets. Signatories are required to monitor and report on changes in the state of biodiversity and ecosystem services. However, without a harmonised and efficient system, signatories have struggled to monitor progress or lack thereof toward the Aichi Targets.

In our new paper, Connecting Earth Observation to High-Throughput Biodiversity Data, we describe a new approach that leverages automated recording devices (ARDs), high-throughput DNA sequencing, and ecological statistics to extract the full information content of Earth-Observation (EO) data. EO technology is providing ever more sophisticated sensors, wider data availability, higher spatial and temporal resolution, and near-continuous global coverage of a large range of biophysical parameters. In combination, ARDs and sequencing allow efficient measurement of biodiversity at high taxonomic resolution, and ecological statistics let us interpolate point samples of biodiversity to create continuous maps of species composition at landscape-scale. We conclude with an overview of approaches for implementing and institutionalising the interdisciplinary collaborations that will be needed to combine these separate fields.



2. Using eDNA to detect the distribution and density of invasive crayfish in the Honghe-Hani rice terrace World Heritage site

The Honghe-Hani landscape in China is a UNESCO World Natural Heritage site due to the beauty of its thousands of rice terraces, but these structures are in danger from the invasive crayfish Procambarus clarkii. We tested whether environmental DNA (eDNA) from paddy-water samples could provide a sensitive detection method. We conclude that a program of repeated eDNA sampling is now feasible and likely reliable for measuring crayfish geographic range and for detecting new invasion fronts in the Honghe Hani landscape, which would inform regional control efforts and help to prevent the further spread of this invasive crayfish.

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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。近几年重点开展家养动物起源与驯化机制以及动物复杂性状形成的遗传机制和高原适应的分子机制方面的研究，2017 年他们揭示了非洲家犬复杂的源流历史以及非洲家犬抵御疟原虫侵害的遗传机制，揭示了褐家鼠的东亚南部起源，发现大量神经系统相关基因在实验大鼠驯化过程中受到人工选择作用，系统阐明了家鸡矮小化的多种遗传机制，在国际权威杂志上发表了 SCI 论文 22 篇，其中 IF>10 的有 6 篇，包括 *Mol Biol Evol* (4), *Giga Science* (1)，*Cell Research* (1) 等。获第 8 届赛诺菲 -Cell Research 优秀论文奖。

重要成果（Highlights）
论著（Publications）

1. **Liu YH**[1], Wang L[1], Xu T[1], Guo XM, Li Y, **Yin TT**, Yang HC, Hu Y, **Adeola AC**, Sanke OJ, **Otecko NO**, Wang M, Ma YP, Charles OS, Sinding MHS, Gopalakrishnan S, Samaniego JA, Hansen AJ, Fernandes C, Gaubert P, Budd J, Dawuda PM, Rueness EK, Jiang LB, Zhai WW, Gilbert MTP, **Peng MS**, Xiaopeng Qi XP*, **Wang GD***, **ZhangYP***. Whole-genome sequencing of African dogs provides insights into adaptations against tropical parasites. ***Molecular Biology and Evolution***, 2017, doi:10.1093/molbev/msx258. IF14.558
2. **Wang MS**[1], **Otecko NO**[1], Wang S[1], **Wu DD**[1], **Yang MM**, Xu Y, **Murphy RW**, **Peng MS***, **Zhang YP***. An evolutionary genomic perspective on the breeding of dwarf chickens. ***Molecular Biology and Evolution***, 2017, 34:3081-3088. IF14.558
3. **Wang MS**[1], **Zeng Y**[1], **Wang X**[1], **Nie WH**, **Wang JH**, **Su WT**, **Otecko NO**, **Xiong ZJ**, Wang S, Qu KX, Yan SQ, **Yang MM**, **Wang W**, Dong Y*, **Wu DD***, **Zhang YP***. Draft genome of the gayal, *Bos frontalis*. ***Giga science***, 2017, 6(11):1-7. IF10.644
4. **Zeng L**, Ming C, **Li Y**, Su LY, Su YH, **Otecko NO**, **Liu HQ**, **Wang MS**, Yao YG, Li HP, **Wu DD***, **Zhang YP***. Rapid evolution of genes involved in learning and energy metabolism for domestication of the laboratory rat. ***Molecular Biology and Evolution***, 2017, 34:3148-3153. IF14.558
5. **Zeng L**[1], Ming C[1], **Li Y**, Su LY, Su YH, **Otecko NO**, Dalecky A, Donnellan S, Aplin K, Liu XH, Song Y, Zhang ZB, Esmailizadeh A, Sohrabi SS, Nanaei HA, **Liu HQ**,**Wang MS**, Atteynine SA, Rocamora G, Brescia F, Morand S, **Irwin DM**, **Peng MS**, Yao YG, Li HP*, **Wu DD***, **Zhang YP***. Out of southern East Asia of the brown rat revealed by large scale genome sequencing. ***Molecular Biology and Evolution***, 2017, doi:10.1093/molbev/msx276. IF14.558
6. **Li Y, Wang MS, Otecko NO, Wang W, Shi P, Wu DD*, Zhang YP***. Hypoxia potentially promotes Tibetan longevity. ***Cell Research***, 2017, 27(2):302-305. IF12.393

1. 非洲犬抵御疟疾的遗传机制

非洲具有强紫外线，疟疾高发等环境，而家犬何时迁移到非洲并适应当地环境的遗传机制尚不清楚。我们在基因组水平上，对非洲家犬的群体历史及其对非洲的热带环境适应性进化的研究发现，非洲犬在大约 1 万四千年前从欧亚大陆迁移到达非洲，并且发现非洲犬与非洲金豺有 1.88%-3.50% 的基因交流。群体遗传学分析发现 *CPT1A* 在非洲犬中受到选择作用，该基因与非洲人群对疟疾易感相关。通过疟原虫侵染小鼠巨噬细胞实验，证明了 *CPT1A* 参与巨噬细胞吞噬疟原虫的过程。通过研究非洲家犬与非洲人的趋同进化遗传机制，为探究人类适应性进化和疾病遗传基础提供模型。*Mol Biol Evol* 对此配发了同期评述报道。

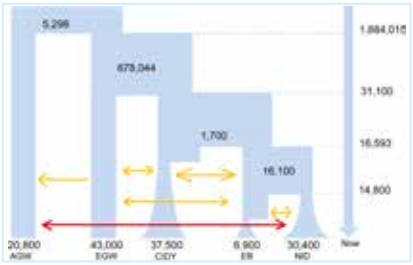

图 1. 家犬的群体历史

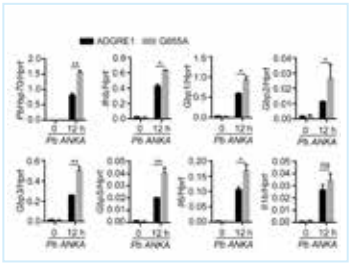

图 2. 非洲犬特有突变加强巨噬细胞 吞噬疟原虫功能

【Liu YH et al. 2017 ***Mol Biol Evol***, IF=14.558】

2. 鸡矮小化的遗传进化机制

人类的驯化和选育使得家鸡成为表型多样性最为丰富的动物之一。在体型大小方面，大型肉鸡或斗鸡（>5 kg）和小型观赏鸡（~0.5 kg）可达到 10 倍以上的悬殊差异。作为重要的经济性状，家鸡的矮小化在蛋鸡和观赏鸡选育中至关重要。矮小化的家鸡品系众多，其遗传机制是否相同呢？针对这一问题，通过对世界上体型最小的鸡 —— 塞拉玛（Serama）和我国云南著名的小型鸡 —— 大围山微型鸡和元宝鸡的群体基因组学遗传结构分析揭示，元宝鸡、塞拉玛和大围山微型鸡有着独立的遗传组分。群体历史分析显示元宝鸡和塞拉玛在选育过程中经历了强烈的瓶颈效应。选择信号和模拟计算分析锁定 *IGF1* 和 *POU1F1* 是决定塞拉玛矮小化的重要基因。相关基因均在生长发育相关通路中发挥重要的作用。这种选择信号组合的模式提示“杂种优势”效应是导致塞拉玛成为世界上体型最小鸡种的重要原因。对三个矮小化鸡种的比较分析它们矮小化的遗传机制并不相同，很可能是多次独立选育的结果。

【Wang MS et al. 2017 ***Mol Biol Evol***, IF= 14.558】

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 they focused on genomic evolution of artificial selection and molecular machenism of the comlex traits and high-altitude adaptation in animals. Within 2017, They revealed evolutionary mechanism of adaptations against tropical parasites in African dogs, and multiple genetic mechanisms of dwarfism in domesticated chickens. Out of southern East Asia of the brown rat was revealed, and rapid evolution of genes involved in learning and energy metabolism for domestication of the laboratory rat. The above research progresses were published in 22 SCI-indexed papers, including ***Mol Biol Evol*** (4), ***Gigascience*** (1), ***Cell Res*** (1).

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1. Adaptations against tropical parasites in African dogs

Africa is strong ultraviolet radiation and endemic malaria. Demographic history and adaptive evolution of African dogs is unclear. So we explored their demographic history and genetic basis of adaptation to the tropical African environment using whole genome sequencing. Admixture analysis revealed that African dog genomes contain about 1.88%-3.50% introgression from African golden wolves (*Canis anthus*). Population genetic analysis identified *ADGRE1* is one of positively selected genes. *ADGRE1* has also been found to be association with severe malaria resistance in African human populations. Functional assessments showed that *ADGRE1* provides protective host defense against *Plasmodium* infections. This result support the dogs as a model for the study of malaria control and treatment.

2. Evolutionary studies of dwarf chickens

Over the years, human have imposed strong artificial selective pressure on chicken through breeding. With regard to body size, the broiler or game fowl (>5Kg) could be 10 times heavier than ornamental chickens (<500g). Dwarfism trait has been keenly pursued for breeding layer hens and ornamental chickens. Whether they share a common genetic mechanism of body size variation is an interesting question. Therefore, we sampled and sequenced genomes for the world's smallest chicken, commonly known as Serama, and another Chinese dwarf breeds, Daweishan and Yuanbao chicken to address this question. From comparative population genomic assessments, these dwarf chickens exhibited distinct genetic background. Demographic history analysis suggested that both Yuanbao and Serama experienced strong bottlenecks during breeding. Selective sweep analyses accompanied by data simulations pointed to two genes, *POU1F1* and *IGF1*, as primary target genes underlying the small body size of Serama. Considering that Serama harbors both Malaysian and Japanese bantam ancestry, and they possess a large number of positively selected genes involved in growth and development, it suggested a likely heterotic combination of parental gene networks to produce the smallest chicken breed within a brief period of time. This research further demonstrated that the three dwarf chicken breeds exhibit parallel genetic mechanisms for small body size development.

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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。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、Mol Ecol、等一系列国际刊物发表 51 篇文章。

重要成果（Highlights）

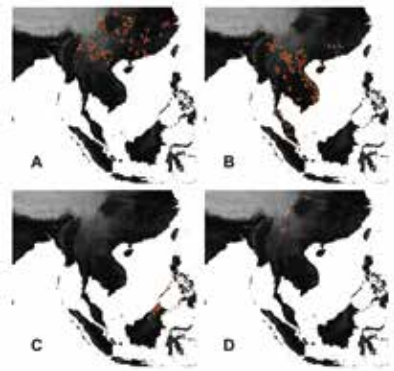
论著（Publications）

1. **Chen JM**, **Zhou WW**, Poyarkov Jr AN, Stuart LB, Brown MR, Lathrop A, Wang YY, **Yuan ZY**, **Jiang K**, Hou M, **Chen HM**, **Suwannapoom C**, Nguyen NS, Duong VT, Papenfuss JT, **Murphy WR**, **Zhang YP***, **Che J***. 2017. A novel multilocus phylogenetic estimation reveals unrecognized diversity in Asian horned toads, genus *Megophrys sensu lato* (Anura: Megophryidae). ***Molecular Phylogenetics and Evolution***, 106: 28-43.
2. **Zhou WW**, **Jin JQ**, Wu J, **Chen HM**, **Yang JX**, **Murphy RW**, and **Che J***. 2017. Mountains too high and valleys too deep drive population structuring and demographics in a Qinghai–Tibetan Plateau frog *Nanorana pleskei* (Dicroglossidae). ***Ecology and Evolution***, 1–13.
3. **Yuan ZY**[1]*, SUN R[1], **Chen JM**, Rowley JJL, Wu ZJ, Hou SB, **Che J*** 2017 A new species of the genus *Leptolalax* (Anura: Megophryidae) from Guangxi, China. ***Zootaxa***, 4300 (4): 551–570
4. **Zhao HP**, **Yang JX**, Wang CP, Li PP, **Murphy RW**, **Che J***, **Yuan ZY***. 2017. A new species of the genus *Rana* from Henan, central China (Anura, Ranidae). ***ZooKeys***, 694: 95–108.
5. **Suwannapoom C**, **Yuan ZY**, **Jiang K**, **Yan F**, **Gao W**, **Che J*** 2017 A new species of rain-poolfrog (Dicroglossidae: *Fejervarya*) from western Thailand. ***Zoological Research***, 38(5): 1-8.
6. **Sun YB*** 2017 FasParser: a package for manipulating sequence data. ***Zoological Research***, 38(2): 1-11

1. 泰国两栖爬行类多样性调查取得阶段性成果

东南亚是全球生物多样性热点区域，具有很高的物种多样性和地方特有性，同时也是高度破坏威胁的地区。自 2008 年，研究组便开始在中南半岛地区，如越南、老挝、泰国系统开展工作，着力于揭示其丰富的物种多样性，探讨物种分布格局和演化规律。通过与泰国清迈大学、Payao 大学多年的合作研究，已初步完成对泰国 41 省 10 个国家公园的联合考察，覆盖泰国境内的大部分地区，分析发现了大量隐存种和新记录种。应 Doi inthanon national park 邀请，2017-2018 年度中泰联合完成该地区两栖爬行动物本底考察。期间，中方将负责完成该国家公园两栖爬行动物名录及鉴别图册。

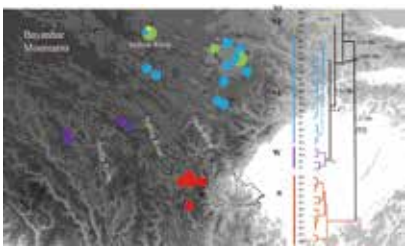
2. 多基因系统发育分析揭示角蟾属蛙类存在高度隐存多样性



中国和东南亚的生物区系有着很强的紧密性和极高的物种多样性。课题组联合多国的研究人员，将中国南方和东南亚作为完整区系整体考虑，以分布广、物种丰富、分类历史复杂的角蟾属 *Megophrys sensu lato* 为例，系统揭示了该地区部分两栖类的多样性和地理分布模式（Chen et al., 2017 *Mol Phyl Evol*）。通过广泛采样，并基于多基因数据的联合分析，第一次较为全面地构建了角蟾属及其近缘属物种的系统演化关系。

研究显示，该类群的物种多样性被严重低估。一些“广布种”很可能是多个不同物种的组合，且地理分布特征经常存在“一山多种”的情况。研究进一步显示，角蟾属是个并系，包含多个主要进化支系，这些支系具有特定的地理结构。此外，本研究对角蟾属的分类给出了建议，如婆罗蟾属（*Borneophrys*）无效，是角蟾属的同物异名。

3. 青藏高原东部山脉和河谷环境对倭蛙群体分化产生不同影响



大量证据表明，第四纪气候变化是影响现生物遗传多样性格局的主要因素。考虑到气候的作用会受到其他因素，如地理特征的影响，气候变化和地理特征如何共同影响群体分化历史和种群动态目前仍不清楚。

为此，**我们以两栖类叉舌蛙科的倭蛙（*Nanorana pleskei*）为研究对象，通过对青藏高原南、北两个区域进行群体分析和比较**（Zhou etal. 2017 Ecol Evol），**揭示横断山区的纵向岭谷促进南部群体的快速分化，而北部的河流由于没有形成深切河谷，并未对群体间基因流起到阻碍作用。**群体历史分析显示，冰期气候变化对北部群体产生了巨大的影响，而南部横断山区由于环境异质性较高，倭蛙群体受影响较小从而保持稳定。

Herpetological Diversity and Evolution

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

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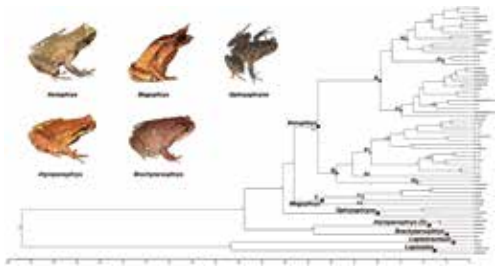
1. The current result of diversity survey of amphibians and reptiles for Thailand

The Southeast Asia is a global biodiversity hotspots area, with high species diversity and endemicity. Since 2008, our research group started to systemically work in the Indochina, especially including Vietnam, Laos and Thailand, with an attempt to systematically and comprehensively reveal the amphibian species diversity, distribution pattern and evolution in Southeast Asia.

Through years of collaborative researches with Chiang Mai University and Payao University in Thailand, we have completed investigation of 10 National parks in 41 provinces of Thailand. Our preliminary results identify numerous cryptic species as well as new species records. With invitation from Doi inthanon National park, China-Thailand will jointly complete the comprehensive investigation of amphibians and reptiles in the area between 2017 and 2018, after which we will complete the checklist and identification atlas for the National Park.

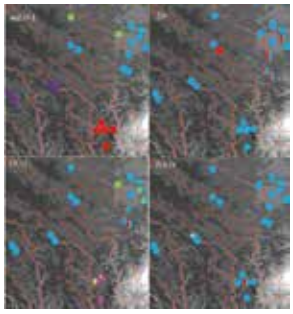
2. A novel multilocus phylogenetic estimation reveals unrecognized diversity in Asian horned toads, genus *Megophrys sensu lato*

The biodiversity of China and Southeast Asia has strong closeness and both areas possess tremendous species. To understand the amphibian diversity and its geographical distribution patterns in the whole area, **we selected the widely distributed genus, *Megophrys sensu lato* (Asian horned toads) as the research group, and made a comprehensive phylogeny using broad sampling and a multilocus approach (Chen et al., 2017; Mol Phyl Evol). Analyses strongly indicate the presence of many undescribed species. The results also suggest that *Megophrys sensu lato* is paraphyletic. Multiple mutually exclusive, geographically cohesive major clades exist in the group. Our results also indicate that *Borneophrys* is not a valid genus but rather a junior synonym of *Megophrys*.**



3. Contrasting population structure and demographic history generated by different geographic features in eastern Qinghai-Tibet Plateau

Pleistocene glacial–interglacial climatic oscillations greatly shaped the current genetic structure of many species. However, geographic features may influence the impact of climatic cycling. Distinct geographic and environmental characters between northern and southern parts of the eastern Qinghai–Tibetan Plateau (EQTP) facilitate explorations into the impacts of geographic features on species. Zhou et al. (2017 *Ecol Evol*) evaluate DNA sequence variation from both the mitochondrial and nuclear genomes in *Nanorana pleskei*. Analyses showed that **northern populations can disperse freely with population expansions, but alpine valleys isolate southern populations resulting to their more stable demographic history**. This study evidence that both geographic and environmental features drove the differences between the northern and southern EQTP.



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金洁琼 学士 实验师
Jieqiong Jin, Technician

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高 伟 Wei Gao 2015
Nneji Lotanna Micah 2015
吴云鹤 Yunhe Wu 2016
张 毅 Yi Zhang 2016
付婷婷 Tingting Fu 2014
米 雪 Xue Mi 2015
Felista Kasyoka 2016
徐 伟 Wei Xu 2016
徐 凯 Kai Xu 2016
余传鑫 Chuanxin Yu 2017
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访问学者

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进化基因组学与基因起源

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

重要成果（Highlights）

论著（Publications）

1. **Kui L**[1], **Chen HT**[1], Zhang WX, He SM, Xiong ZJ, **Zhang YS**, Yan L, **Zhong CF**, He FM, Chen JW, Zeng P, Zhang GH, Yang SC, Dong Y, **Wang W*** and Cai J*. Building a Genetic Manipulation Tool Box for Orchid Biology: Identification of Constitutive Promoters and Application of CRISPR/Cas9 in the Orchid, *Dendrobium officinale*. **Frontiers in Plant Science.** 2017, 8:664.
2. **Li XY**[1], **Liu GC**[1], Sheng WJ[1], **Dong ZW**, **Chen L**, **Zhao RP**, **Wang W***. Genome editing in the butterfly type-species *Papilio machaon*. **Insect Science**. 2017, 24:708-711.
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1. 铁皮石斛基因编辑体系

铁皮石斛作为兰科的一种，不仅具有很好的观赏价值，同时也是一种重要的药用植物。我们基于 pCambia-1301-35SN 载体成功的在铁皮石斛中建立了转基因体系，并发现 MMV、CVMV、PCISV 以及 CAMV-35S 等启动子均能在铁皮石斛细胞中高效启动基因表达，最后使用 CRISPR/Cas9 技术，成功对铁皮石斛中 5 个木质素合成通路中的基因（C3H、C4H、4CL、CCR 和 IRX）实现了基因编辑。该研究不仅为培育优良的铁皮石斛新品种提供了高效的研究工具，也对促进兰科生物学的分子遗传学研究提供了基础模型。

2. 蝴蝶模式物种 – 金凤蝶的基因编辑技术

蝴蝶具有丰富的形态多样性，特别是翅的多样性对物种形成、种群多样化、性别多型、春夏型、以及警戒色、拟态、温度调节和配偶选择的有重要作用。金凤碟 (*Papilio machaon*) 作为所有蝶类的模式物种，与柑橘凤蝶 (*Papilio xuthus*) 一起是凤蝶族 (*Papilionidae*) 的最常见的种类。我们应用最近开发的 CRISPR/Cas9 编辑技术，在成功地对柑橘凤蝶中的 3 个基因进行编辑的基础上，又实现了对所有蝴蝶的模式种金凤蝶的基因编辑。该工作进一步加强了蝴蝶作为遗传学、进化和发育研究的新模式的潜力。

3. 基因共表达网络分析揭示海参变态发育过程

海参是棘皮动物中的一大类，在其发育过程中有着非常快速和大尺度的变态过程。我们对这个过程的了解非常得少，仅仅是了解一些它的形态变化，像体长的变短、纤毛带的片段化等等。在本研究中，我们系统性的研究了日本海参 (*Apostichopus japonicus*) 从受精卵到成体的 16 个不同发育时间点的基因表达谱，基于共表达网络分析（WGCNA），我们识别了 21 个模块，并且发现了和变态过程相关性非常高的模块 (Medarkmagenta)。通过提取这个模块中的基因发现，这些基因的确特异性的在变态过程中呈现出急速的表达上升。结合变态期前后时期的差异表达和富集分析，我们最终识别了一些和海参变态过程可能相关的基因，为进一步了解海参的变态过程提供了分子基础。

4. 重要中草药 – 三七基因组的解析

三七 (*Panax notoginseng*) 是中国古代医学文献中记载的一种生长缓慢的中草药，具有止血等功效。经过几十年的研究，一些三七特有的次级代谢产物如人参皂苷、等也被分离鉴定。为了鉴定三七中的生物活性成分，并描述其生物合成途径，我们构建了三七的参考基因组。我们从头组装了三七的基因组。最终组装出的基因组大小为 2.39Gb, 包含 36,970 个蛋白质编码基因和 8,446 个非编码基因。我们也得到了 12 个全长的和植物萜类合成相关的萜类合成酶基因。本研究为三七中萜类活性成分的生物合成奠定了基础，也为在相关物种中寻找新的药物提供了遗传资源。该成果于 2017 年 6 月发表于 Molecular Plant，由基因起源与进化课题组博士研究生奎玲和云南农业大学陈玮共同负责本项目的工作，并且作为文章的共同第一作者 。

Evolutionary Genomics and Origin of New Genes

Prof. Wen Wang, Professor, Head of Evolutionary Genomics and Origin of New Genes Research Group, KIZ, CAS. Prof. Wang has been focusing on evolutionary genomics. So far, he published more than 100 papers in such scientific journals as *Science*, *Nature*, PNAS, *PLoS genetics* etc, which are totally cited more than 9760 times with a H-index of 46. He is Chief Scientist of both 973 project (Scientific and technology Ministry) and Strategic Priority Research Program B (CAS), and also leader of Innovative research group (NSFC). He received one second prize in China's National Natural Science Award in 2012 and two second prize in Yunnan Natural Science Award in 2017.

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1. Building a Genetic Manipulationg Tool Box for Orchid Biology: Identification of Constitutive Promoters and Application of CRISPR/Cas9 in the Orchid, *Dendrobium officinale*

Dendrobium officinale, a member of Orchidaceae, is highly valued for its ornamental purposes and medicinal uses. Here, we identified several highly efficient promoters for exogenous gene expression and successfully applied the CRISPR/Cas9 system for editing endogenous genes (*C3H*, *C4H*, *4CL*, *CCR*, and *IRX*) which are in the lignocellulose biosynthesis in the genome of *D. officinale*. These results showed that our two genetic manipulation tools can efficiently express exogenous genes and edit endogenous genes in *D. officinale*. These efficient research tools will not only help create novel *D. officinale* varieties, but will also facilitate the molecular genetic investigation of orchid biology.

2. Genome editing in the butterfly type-species *Papilio machaon*

Butterflies are a promising system to explore the genetic, evolutionary, and developmental mechanisms underlying morphological diversification and speciation. In particular, the extraordinarily diverse wing patterns among species, populations, sexes, and even seasonal forms and their multifunctional roles from crypsis to warning coloration, mimicry, thermoregulation, and mate selection. Using recently developed CRISPR/Cas9 technology, we succeeded in editing genes in *P. xuthus*. Here, we show that the protocol developed in *P. xuthus* efficiently works again in the butterfly type-species *P. machaon* and describe the whole protocol with great details so that the butterfly research community can easily use the protocol. This work further strengthens the potentials of butterflies as new models for genetics, evolution and development studies.

3. Weighted gene co-expression network analysis reveals potential genes involved in early metamorphosis process in sea cucumber *Apostichopus japonicus*

Sea cucumbers, one main class of Echinoderms, have a very fast and drastic metamorphosis process during their development. However, the knowledge of this process is very limited for us, just some morphological changes. Here we systematically examined the gene expression profiles of Japanese common sea cucumber (*Apostichopus japonicus*) for the first time by RNA sequencing across 16 developmental time points from fertilized egg to juvenile stage. Based on the weighted gene co-expression network analysis (WGCNA), we identified 21 modules. Among them, MEdarkmagenta was highly expressed and correlated with the early metamorphosis process from late auricularia to doliolaria larva. Furthermore, gene enrichment and differentially expressed gene analysis identified several genes in the module that may play key roles in the metamorphosis process. Our results not only provide a molecular basis for experimentally studying the development and morphological complexity of sea cucumber, but also lay a foundation for improving its emergence rate.

4. De novo genome sequence and analysis of the Chinese Herbal Plant *Panax notoginseng*

Panax notoginseng is a slow-growing plant species documented in the ancient Chinese medical literatures for its ability to ameliorate hemostasis. After decades of pharmacological research, a variety of P. notoginseng-specific secondary metabolites (notably ginsenosides, notoginsenosides and gypenosides) were isolated, identified, and implicated in conferring medicinal properties. To help identify novel bioactive compounds in *P. notoginseng* and delineate their biosynthetic pathways, We assembled a de novo draft genome of *P. notoginseng* of 2.39 Gb, with 36 790 protein-coding genes and 8446 copies of nonprotein-coding. Besides, 12 full-length *TPS* (terpene synthases) genes which were key enzymes for producing Plant terpenes in the *P. notoginseng* genome were identified. Our analysis not only lays the groundwork for studying the biosynthesis of known terpenoids in *P. notoginseng* but also provides ample genetic resources for identifying novel drug candidates in closely related Panax species.

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比较基因组学

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

重要成果（Highlights）

论著（Selected Publications）

1. Peng, Y[1], Cui, C[1], He, Y[1], Ouzhuluobu[1], Zhang, H[1], Yang, D[1], Zhang, Q[1], (19 authors), Xu, S., Chen, H., Liu, S., **Wu, T.*, Qi, X.* & Su, B.*** Down-regulation of EPAS1 Transcription and Genetic Adaptation of Tibetans to High-altitude Hypoxia. ***Mol Biol Evol*** 34, 818-830 (2017).
2. Zhang, H[1], He, Y[1], Cui, C[1], Ouzhuluobu, (22 authors), Wu, T., **Qi, X.* & Su, B.*** Cross-altitude analysis suggests a turning point at the elevation of 4,500 m for polycythemia prevalence in Tibetans. ***Am J Hematol*** 92, E552-E554 (2017).
3. Shi, L[1], Hu, E[1], Wang, Z[1], Liu, J., Li, J., Li, M., Chen, H., Yu, C., Jiang, T. & **Su, B.*** Regional selection of the brain size regulating gene CASC5 provides new insight into human brain evolution. ***Hum Genet*** 136, 193-204 (2017).
4. Bhandari, S[1], Zhang, X[1], Cui, C[1], Yangla, Liu, L., Ouzhuluobu, Baimakangzhuo, Gonggalanzi, Bai, C., Bianba, Peng, Y., Zhang, H., Xiang, K., Shi, H., Liu, S., Gengdeng, Wu, T., **Qi, X.* & Su, B.*** Sherpas share genetic variations with Tibetans for high-altitude adaptation. ***Mol Genet Genomic Med*** 5, 76-84 (2017).
5. Guo, Y.B[1], He, Y.X[1], Cui, C.Y[1], (16 authors), Zhang, X.M., Zheng, W.S., Xu, S.H., Chen, H., Zhao, S.G., Cai, Y., Liu, S.M., Wu, T.Y., **Qi, X.B.* & Su, B.*** GCH1 plays a role in the high-altitude adaptation of Tibetans. ***Zool Res*** 38, 155-162 (2017).
6. Zheng, W.S[1], He, Y.X[1], Cui, C.Y[1], (17 authors), Xu, S.H., Chen, H., Zhao, S.G., Cai, Y., Liu, S.M., Wu, T.Y., **Qi, X.B.* & Su, B.*** EP300 contributes to high-altitude adaptation in Tibetans by regulating nitric oxide production. ***Zool Res*** 38, 163-170 (2017).

1. 初步阐明 EPAS1 在高原藏族人群对低氧环境适应中的调控机制：

藏族人群对高原低氧极端环境表现出了最佳的生理适应能力，这种适应能力是通过 3 万多年的漫长的适应性选择的结果（***Qi et al Mol Biol Evol 2013***），但是这种适应性选择是如何通过基因组水平的精细调控来实现对心、肺等关键低氧敏感器官的功能适应这一遗传机制仍然不清楚。EPAS1 是低氧通路中的关键基因，其在藏族人群中受到强烈的自然选择，但其在藏族人群对高原低氧环境的适应过程中发挥怎样的生物学功能仍然不甚清楚，我们通过对 EPAS1 基因的全长精细测序发现藏族人群中受到强烈选择的变异位点都位于非编码区，提示这些藏族富集的变异很可能在藏族的转录水平参与调控。我们进一步对藏族人群中富集的 32 个 EPAS1 位点进行了大样本的遗传相关性分析、藏族胎盘组织的转录组分析、藏族新生儿脐带内皮细胞的低氧诱导实验、EPAS1 基因敲除小鼠的低氧诱导实验等综合的遗传学分析和功能验证试验，发现藏族富集的 EPAS1 的变异位点下调了 EPAS1 在脐带内皮细胞和胎盘中的表达水平；杂合 EPAS1 敲除小鼠表现出与高原藏族人群相似的对慢性低氧的钝化反应。除此之外，我们还发现 EPAS1 基因除了下调藏族人群在高原低氧环境中的血红蛋白水平外，可能还参与下调藏族人群的肺动脉压，进而实现对高原低氧环境的长期适应。研究成果发表在分子进化国际知名学术刊物 ***Molecular Biology and Evolution***，34（4）：818-830，2017），该研究成果是我们团队在藏族人群对高原低氧环境适应机制研究中的又一阶段性成果，首次鉴定出了低氧通路关键基因 EPAS1 基因的关键功能位点，为最终解析人类对高原低氧极端环境的生理适应这一复杂性状的生物学功能向前迈出了重要的一步。

2. 提出藏族人群对高原低氧环境最佳适应的海拔拐点

经过漫长的自然选择的洗礼，世居青藏高原的藏族人群已经对高原低氧极端环境获得了很好的生理适应能力。与移居高原的平原汉族人群相比，藏族人群在生理上表现为具有较高的通气量、较低的肺动脉压和相对较低的血红蛋白浓度。其中，血红蛋白浓度能间接反映人群对高原低氧环境中的适应情况，即藏族人群在高原低氧环境中维持较低的血红蛋白浓度，降低红细胞增多症的风险，这种较低的血红蛋白浓度主要是通过下调低氧诱导因子基因的表达水平来实现的。但是我们经过对本项目样本库中的 20 多个地理区域的不同海拔藏族人群的各项血液、生理和生化指标数据，涵盖从最低海拔（墨脱县，1900 米）到极限高海拔（浪卡子县普玛江塘乡，5018 米）的世居藏族人群。我们系统分析了这些藏族人群的血红蛋白浓度随海拔高度变化的模式，发现藏族人群的血红蛋白浓度和红细胞增多症检出率在 4500 米左右是一个拐点，4500 米以上呈现快速增长。研究结果提示，藏族人群通过调控血红蛋白浓度来适应高原低氧环境的调控机制在 4500 米以上的极限高海拔低氧环境中可能不再有效。据此，我们首次提出 4500 米可能是世居藏族人群对高原低氧环境最佳适应的临界海拔，初步回答了藏族人群究竟能适应多高海拔的问题。这项研究成果发表于美国血液学杂志 ***American Journal of Hematology*** 92(9):E552-E554(2017)。

3. 脑容量调控基因 CASC5 在现代人进化过程中对脑容量的调控机制

人类起源过程中大脑容量的急剧扩增一直是灵长类脑进化研究关注的核心问题。以前的研究主要是比较人类与非人灵长类脑容量的差异及其遗传调控机制，对近期人类进化过程中群体水平脑容量变化的遗传分析少有涉及。我们在近期的研究中发现，脑容量调控基因 CASC5 在现代人的起源过程中积累了 8 个氨基酸突变，这些突变在非人灵长类和古人类（尼安德特人和丹尼索瓦人）中均不存在，是现代人特有的变异位点。其中，2 个突变位点在现代人中已经固定下来，而其他 6 个位点在人群中仍然是多态的；更有意思的是，有 4 个多态位点在东亚人群中呈现高频率，但在欧洲和非洲人群中频率很低。进一步的分子进化分析表明，CASC5 基因在东亚人群中受到达尔文正选择的作用，但在非洲和欧洲群体中没有发现选择信号。遗传关联分析显示这些东亚人群富集的位点在汉族人群中与大脑灰质体积显著相关，突变型等位基因的携带者具有更大的灰质体积。该研究结果提示，在近期人类大脑进化过程中，CASC5 基因对现代人大脑形态结构的变化可能发挥重要作用。研究成果发表在国际核心期刊 ***Human Genetics 136, 193-204 (2017)***。

Comparative Genomics

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

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1. Down-regulation of EPAS1 Transcription and Genetic Adaptation of Tibetans to High-altitude Hypoxia

Tibetans are well adapted to the hypoxic environments at high altitude, yet the molecular mechanism of this adaptation remains elusive. We reported comprehensive genetic and functional analyses of EPAS1, a gene encoding hypoxia inducible factor 2α (HIF-2α) with the strongest signal of selection in previous genome-wide scans of Tibetans. We showed that the Tibetan-enriched EPAS1 variants down-regulate expression in human umbilical endothelial cells and placentas. Heterozygous EPAS1 knockout mice display blunted physiological responses to chronic hypoxia, mirroring the situation in Tibetans. Furthermore, we found that the Tibetan version of EPAS1 is not only associated with the relatively low hemoglobin level as a polycythemia protectant, but also is associated with a low pulmonary vasoconstriction response in Tibetans. We propose that the down-regulation of EPAS1 contributes to the molecular basis of Tibetans' adaption to high-altitude hypoxia. ***Peng et al. Mol Biol Evol*** 34, 818-830 (2017)

2. Cross-altitude analysis suggests a turning point at the elevation of 4,500 m for polycythemia prevalence in Tibetans

Tibetans are well adapted to hypoxic environment at high altitude. Compared with lowlanders moving to high altitude, Tibetans have relatively low hemoglobin concentrations that is considered a protection from high altitude polycythemia (overproduction of red cells). But how high can Tibetans live remains an open question. We analyzed hemoglobin profiles of nearly 9,000 Tibetan individuals from 20 geographic populations permanently residing at elevations from 2,227m to 5,018m. With the use of a nonlinear regression model, we identified an elevation turning point around 4,500m showing sharp increases of hemoglobin concentration and polycythemia incidence. This elevation turning point likely marks the altitude limit for Tibetans. ***Zhang et al. Am J Hematol 92, E552-E554 (2017).***

3. Regional selection of the brain size regulating gene CASC5 provides new insight into human brain evolution

Human evolution is marked by a continuedenlargement of the brain. Previous studies on human brainevolution focused on identifying sequence divergences ofbrain size regulating genes between humans and nonhumanprimates. However, the evolutionary pattern of thebrain size regulating genes during recent human evolutionis largely unknown. We conducted a comprehensive analysisof the brain size regulating gene CASC5 and found thatin recent human evolution, CASC5 has accumulated manymodern human specific amino acid changes, including twofixed changes and six polymorphic changes. Among humanpopulations, 4 of the 6 amino acid polymorphic siteshave high frequencies of derived alleles in East Asians,but are rare in Europeans and Africans. We proved that this between-population allelic divergence was caused byregional Darwinian positive selection in East Asians. Furtheranalysis of brain image data of Han Chinese showedsignificant associations of the amino acid polymorphic siteswith gray matter volume. Hence, CASC5 may contributeto the morphological and structural changes of the humanbrain during recent evolution. The observed between-populationdivergence of CASC5 variants was driven by naturalselection that tends to favor a larger gray matter volume inEast Asians. ***Shi L. et al. Human Genetics 136, 193-204 (2017).***

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彭应梅　Yingmei Peng, 2008
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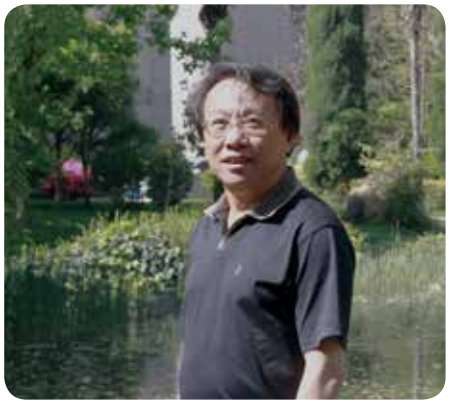

生物信息学与系统生物学

黄京飞，研究员，博士生导师，云南省遗传学会副理事长。主要从事蛋白质相互作用网络及其功能的演化；基于蛋白质进化的干扰肽的设计；复杂疾病机理及其潜在药物靶点的发现研究， 先后在 Mol. Biol. Evol.，FEBS Lett.，PLoS ONE，BMC Bioinformatics，BMC Evol Biol，Mol BioSyst, Bioinformatics 等刊物发表论文 90 余篇。曾获中国科学院自然科学三等奖和云南省自然科学一等奖各 1 项。培养博士、硕士研究生 20 余名。

实验室主页：http://bsb.kiz.ac.cn/

重要成果（Highlights）

论著（Publications）

1. **Li WX**[1], He K[1], Tang L[1], **Dai SX**, **Li GH**, Lv WW, **Guo YC**, **An SQ**, Wu GY, Liu D*, **Huang JF***. Comprehensive tissue-specific gene set enrichment analysis and transcription factor analysis of breast cancer by integrating 14 gene expression datasets. **Oncotarget**. 2017, 8(4): 6775-86.
2. **Wang Q**[1], **Li WX**[1], **Dai SX**, **Guo YC**, **Han FF**, **Zheng JJ**, **Li GH***, and **Huang JF***. Meta-Analysis of Parkinson's Disease and Alzheimer's Disease Revealed Commonly Impaired Pathways and Dysregulation of NRF2-Dependent Genes. **Journal of Alzheimer's Disease**. 2017, 56(4): p. 1525-1539.
3. **Liu JQ**[1], **Dai SX**[1], **Zheng JJ**[1], **Guo YC**, **Li WX**, **Li GH***, and **Huang JF***. The identification and molecular mechanism of anti-stroke traditional Chinese medicinal compounds. **Scientific reports.** 2017, 7: p. 41406.
4. **Li WX**[1], Cheng F, Zhang AJ, **Dai SX**, **Li GH**, Lv WW, Zhou T, Zhang Q, Zhang H, Zhang T, Liu F, Liu D*, **Huang JF***. Folate Deficiency and Gene Polymorphisms of MTHFR, MTR and MTRR elevate the Hyperhomocysteinemia Risk **Clin Lab**. 2017, 63(3):523-533.

1. 从传统中草药中发掘抗癌植物和化合物研究

现如今，尽管癌症治疗取得了重大进步，癌症依然是全球范围内严重危害人类健康的疾病。最常见和有效的癌症治疗手段有手术治疗、化学疗法和放射疗法。但是这些治疗手段都存在这许多限制和缺点。因此，我们需要不断的研发新的、有效的和负担得起的抗癌药物。中国的传统中药数据库记录了超过 2000 种药用植物。许多药用植物来源的化合物已经用于治疗脾癌、肝癌、儿童白血病、肺癌、卵巢癌、睾丸癌和膀胱癌等多种癌症。因此，传统中草药无疑是发掘新颖抗癌药物的宝贵资源库。遗憾的是，在传统中草药中只有小部分的药用植物被充分系统地研究过。针对这一现状，我们利用实验室前期开发的抗肿瘤药物预测平台 CDRUG 对传统中草药数据库中的所有药用植物及其化合物的抗癌潜力进行了系统的评估和发掘。我们从中预测出 5278 个抗癌化合物，其中前 346 个化合物在 60 个细胞系测试实验中表现出超强的抗癌活性。进一步的分析表明有 3952（75%）个化合物和已经上市的抗癌药物具有高度的结构相似性。基于上述结果，我们利用活性富集方法鉴别出 57 种具有潜在抗癌活性的药用植物。这些植物广泛分布于植物界的 28 个科和 46 个属，这极大的拓宽了抗癌药物的筛选范围。最后，我们构建了抗癌植物和上市抗癌药物的连接网络。该网络凸显了这些植物对抗癌药物研发的支持作用并提示这些植物具有不同的抗癌分子机制。该研究预测出来的大量抗癌化合物和多种抗癌植物为抗癌药物研发提供了一个有吸引力的起点和广阔的范围。

2. 抗中风靶标在年龄和性别中的基因表达异质性研究

中风（stroke）也叫脑卒中，作为全球范围的高发病率、高致死率的疾病，中风的发病率一直以来均排在前十名。仅亚洲的中风死亡率就占居全球中风死亡率的 2/3，在中国，每年都有近 2000 人死于中风；在西方国家中风死亡率也排在前三。此外，中风的发病年龄也横跨青年、中年、老年，甚至是儿童和青少年。 其中，缺血性中风占中风的绝大多数约 85%，以往的研究报道缺血性中风的发生率，患病率和死亡率受到性别的影响，但是关于抗中风靶标基因的性别异质性的研究较少。针对这一现状，我们通过整合缺血性中风转录组学数据，结合汤森路透 Integrity 数据库中的抗中风靶标基因，系统地分析了抗中风靶标基因在男性和女性人群，以及老年和中青年人群的差异。分析发现男性中风患者相比于正常男性的失调基因跟女性中风患者相比于正常女性的失调基因有着很大的差异。我们比较了男性和女性正常人群的差异基因并证实了以上失调基因的差异是由疾病状态引起的而非性别因素。通过 KEGG 富集分析我们发现男性和女性中风患者表现出严重的免疫相关通路损伤。进一步，我们揭示了大量免疫相关的靶标基因在男性和女性中呈现相反的表达趋势（如 IL1A，IL6，IL8 等）。此外这些靶标基因在不同年龄阶段的人群中也有较大的差异。目前已经有一些针对这些靶标基因的药物已经上市或处于研发阶段。因此，在今后的中风治疗中，需要考虑到中风的性别和年龄异质性。我们的研究对今后缺血性中风的基础研究和临床试验有一定的指导意义。

Bioinformatics and system biology

Prof. Jing-Fei Huang, Principle Investigator, Deputy Director, Kunming Institute of Zoology, Chinese Academy of Sciences. The research is mainly focused on the structure basis of protein functional evolution, the evolutionary mechanism of protein/gene, protein interaction network and functional evolution, disturbing peptide design based on protein evolution, the mechanism of complex disease and potential drug target discovery. More than 90 papers have been published in Mol. Biol. Evol., FEBS Lett., Structure, Acta Crystall., J. Mol. Struct., J. Theor. Biol., J. Mol. Model., Mammalian Genome, PLoS ONE, BMC Bioinformatics, BMC Evol Biol, Mol. BioSyst and Bioinformatics.

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1.In silico identification of anti-cancer compounds and plants from traditional Chinese medicine database

There is a constant demand to develop new, effective, and affordable anti-cancer drugs. The traditional Chinese medicine (TCM) is a valuable and alternative resource for identifying novel anti-cancer agents. In this study, we aim to identify the anti-cancer compounds and plants from the TCM database by using cheminformatics. We first predicted 5278 anti-cancer compounds from TCM database. The top 346 compounds were highly potent active in the 60 cell lines test. Similarity analysis revealed that 75% of the 5278 compounds are highly similar to the approved anti-cancer drugs. Based on the predicted anti-cancer compounds, we identified 57 anti-cancer plants by activity enrichment. The identified plants are widely distributed in 46 genera and 28 families, which broadens the scope of the anti-cancer drug screening. Finally, we constructed a network of predicted anti-cancer plants and approved drugs based on the above results. The network highlighted the supportive role of the predicted plant in the development of anti-cancer drug and suggested different molecular anti-cancer mechanisms of the plants. Our study suggests that the predicted compounds and plants from TCM database offer an attractive starting point and a broader scope to mine for potential anti-cancer agents.

2. Integrated analysis of ischemic stroke datasets revealed sex and age difference in anti-stroke targets

Ischemic stroke is a common neurological disorder and the burden in the world is growing. This study aims to explore the effect of sex and age difference on ischemic stroke using integrated microarray datasets. The results showed a dramatic difference in whole gene expression profiles and influenced pathways between males and females, and also in the old and young individuals. Furthermore, compared with old males, old female patients showed more serious biological function damage. However, females showed less affected pathways than males in young subjects. Functional interaction networks showed these differential expression genes were mostly related to immune and inflammation-related functions. In addition, we found ARG1 and MMP9 were up-regulated in total and all subgroups. Importantly, IL1A, ILAB, IL6 and TNF and other anti-stroke target genes were up-regulated in males. However, these anti-stroke target genes showed low expression in females. This study found huge sex and age differences in ischemic stroke especially the opposite expression of anti-stroke target genes. Future studies are needed to uncover these pathological mechanisms, and to take appropriate pre-prevention, treatment and rehabilitation measures.

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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“真核细胞进化基因组学”。以处在真核细胞进化的关键地位的单细胞生物（代表如贾第虫、衣藻、眼虫、领鞭毛虫等原生生物）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与利用等应用基础研究。

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重要成果（Highlights）

1. **Ye Q-Q,** Tian H-F, **Chen B, Shao J-R,** Qin Y, **Wen J-F*.**Giardia's primitive GPL biosynthesis pathways with parasitic adaptation'patches': implications for Giardia's evolutionary history and for finding targets against Giardiasis. **Scientific Reports.** 2017, 7(1):9507.
2. **Lv Zhangxia†, Shao J-R†, Xue M, Ye Q-Q, Chen B,** Qin Y, **Wen J-F*.** A New Species of Giardia (Sarcomastigophora: Hexamitidae) likely Specifically Parasitizing Hamsters. **Parasites & Vectors (in press)**
3. **Chen B, Shao J-R,** Zhuang H-F, **Wen J-F*.** Evolutionary dynamics of triosephosphate isomerase gene intron location pattern in Metazoa: A new perspective on intron evolution in animals. **Gene.** 2017,602 :24-32

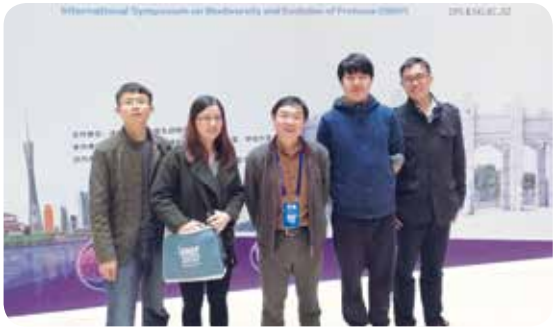
1. 贾第虫一具有最窄宿主范围的新种的发现及其意义

我们在仓鼠亚科啮齿动物体内发现了一种滋养体尺寸比其它种的贾第虫都更大并且拥有最低的长宽比的贾第虫，对其 beta-giardin 和 small subunit rRNA 两个基因克隆测序后进行系统发生分析，发现其与现有的贾第虫有明显的区别。结合形态和分子等方面的证据，我们确定了这是与所有六种已知贾第虫有显著区别的一新种贾第虫，并命名为仓鼠贾第虫（Giardia cricetidarum）。该新种长约 14 微米，宽约 10 微米，能够在光学显微镜下与其它种的贾第虫明显的区分开来。野外调查指出该物种仅寄生在仓鼠亚科物种体内，对仓鼠近缘的哺乳动物的人工感染实验进一步证明了该物种专性地寄生于仓鼠亚科啮齿动物体内。其特别的感染特性指出其对仓鼠的感染过程中演化出了其独特的优势，从而使其能够专性并且非常成功的寄生于仓鼠亚科啮齿动物体内。已知蓝氏贾第虫（G. intestinalis）拥有最广的宿主范围，它能寄生于几乎所有脊椎动物体内，但平均感染率较低；而仓鼠贾第虫只专性的寄生于仓鼠亚科啮齿动物体内，但在一个群体内可达到接近于百分之百的感染率；结合寄生于不同范围的哺乳动物的其它贾第虫，它们可以共同构建出一个模型系统可用于研究贾第虫的进化趋异现象和宿主适应策略。

2. 基因重叠引起贾第虫中内含子的保留以及对内含子的进化和功能的启示

根据目前的分析研究我们可知剪接体内含子在早期的真核生物中是含量丰富的，随着基因组进化过程中内含子的不断丢失，导致一些现存的真核生物中只有极少量的内含子。尽管有很多人对内含子丢失进行了大量的研究，但是丢失的原因仍然不清楚。我们的工作是以贾第虫为研究对象，通过分析它这种极少内含子的现状来探索另一相反的问题—少量的内含子是如何保留下来的。通过调查发现，尽管贾第虫一直受到内含子丢失的强大的选择压力，但是它还是有获得了新的内含子，极少量的古老的和新出现的内含子才保留下来。除此之外没有发现其他与内含子保留相关的任何的信息。我们发现并证实一些内含子基因与其互补链中的无内含子的基因形成一种基因重叠，并且对应的内含子是完全位于重叠区域。所以，我们推测内含子的保留并不一定与它自身的功能有关联，而是由它自身以外的因素控制，来自基因或者其他基因组功能元件的“重叠限制”至少是其中的一种原因。我们的研究结果不仅可以解释为什么不存在无内含子的真核生物也可为探索新的基因组功能元件提供宝贵的线索，此外也提示内含子本身的“功能限制”不一定可以直接影响到内含子的丢失和获得，或者是说内含子的功能或者其发挥功能的方式不是我们现在所理解的这样。

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 specific metabolic pathways.

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1. A New Species of Giardia and its Value for the Study of Host Parasitism Strategy of Giardia

Giardia are flagellated protozoan parasites that infect humans and many other vertebrates worldwide. Their diverse host ranges and specificities reflect an extensive divergence of host parasitism strategy among them, which contributes to their successful parasitism in such an extremely wide range of vertebrates. Although many species in various animals were reported, currently only six species of *Giardia* has been considered valid. It has already been more than a quarter of century since the last new species *G. ardeae* was re-identified.Here, we report a new specifically hamster-parasitizing species, *Giardia cricetidarum*. Its trophozoites are pear-shaped and have a usual length of about 14mm and a usual width of about 10mm, and thus are generally larger but dumpier than all the described species. But its ovoid cysts, with a usual length of about 10mm and a usual width of about 10mm, are not morphologically distinguishable from others. Molecular phylogenetic analyses based on *b-giardin* and *small subunit rRNA* loci both demonstrated *G. cricetidarum* is genetically distinct from all the current valid *Giardia* species. Investigation of host range indicated it was only found in hamsters (including *Phodopus sungorus*, *P. campbelli*, and *Mesocricetus auratus*), while all the other described mammal-parasitizing species (*G. muris*, *G. microti*, and *G. intestinalis*) each also have other hosts. Artificial infective experiment further demonstrated it can only infect hamsters rather than any nearly-related rodents. Besides, its "all or none" prevalence pattern in hamster populations, strong positive detection in infected hamsters, and rare coinfection with other *Giardia* in a common hamster, all suggest it has some advantages in parasitizing hamsters over other *Giardia*. Therefore, our work has identified a new species of hamster-specific *Giardia*, which has the narrowest host range among all the known mammal-parasitizing *Giardia*. The new species, together with the three other mammal-parasitizing *Giardia* with differently wider host ranges, may be able to be used as a model system for the study of evolutionary divergence of host parasitism strategy of *Giardia*.

2. Sense-antisense gene overlap causes the retention of the few introns in Giardia and the implications for intron evolution and function

Spliceosomal intron has been speculated to be abundant in early eukaryotes with subsequent genome evolution dominated by intron loss, and thus very few introns in some modern eukaryotes must be the consequence of massive loss. Unfortunately, the causes of the loss remain elusive despite extensive research. Here, by investigating the extremely few introns in Giardia lamblia, we explore the reverse question – how these few introns can be retained. Our investigation finds that despite of constant selective pressure of intron loss in Giardia's evolution, intron gain still occurred and a few of both ancient and newly-emerged introns can still be retained. Furthermore, not finding any special features or functional importance of these introns responsible for their retention, we notice some intron-containing genes form sense-antisense gene pairs with the genes on their complementary strands, and that the introns exactly reside in the overlapping regions. These observations suggest the retention of introns is not necessarily due to functional constraint of the introns themselves but due to the causes outside of introns, and "overlap constraint" imposed by genes or other genomic functional elements is at least an important one of the reasons. These findings can not only explain why there exist no eukaryotes without any introns and might provide a valuable clue to find new genomic functional elements, but implicate that "functional constraint" of introns themselves is not necessarily directly associated with intron loss and gain, or that the real functions or functioning manners of introns are still outside of our current knowledge.

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进化与功能基因组学

施 鹏，研究员，中科院昆明动物研究所副所长，“遗传资源与进化国家重点实验室”主任，进化与功能基因组学科组负责人。2008 年入选中科院“百人计划”，2013 年获国家杰出青年基金，2014 年获科技部中青年科技创新领军人才，2016 年入选中组部万人计划，2017 年入选人社部“国家百千万人才”。长期从事进化基因组学和功能基因组学研究。本研究室的研究兴趣集中在以下两个方向：（1）利用新一代测序技术，运用自然选择理论在基因组范围内探讨基因型和表型的关系；结合生物信息学和功能实验的方法来研究动物适应环境的分子机制；（2）通过对非模式生物的基因组研究，从新的视角理解人类长寿、心血管疾病和肿瘤的发病机理及新的疾病相关基因资源的挖掘。 Email: ship@mail.kiz.ac.cn Tel: 0871-68125411

重要成果（Highlights）

论著（Publications）

1 **Liu Z**#, Zhang JZ*, Most m^{6}A RNA modifications in protein-coding regions are evolutionarily unconserved and likely nonfunctional, ***Molecular Biology and Evolution***, doi:10.1093/molbev/msx320, 2017/12, (5-Year IF=14.558)

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1. 蛋白编码区中大部分 RNA m^{6}A 修饰在进化上是非保守并且可能是没有功能的

N6- 甲基腺嘌呤（m^{6}A) 是许多真核生物中最为普遍的 mRNA 转录后修饰。尽管近期在转录组水平上 m^{6}A 修饰图谱绘制，m^{6}A 修饰“写入”，“读取”，和“擦除”相关蛋白的鉴定，以及 m^{6}A 在可变剪接，RNA 稳定性的维持，翻译和其他过程中的作用等各个方面取得了快速进展，但是对于大多数观察到的 m^{6}A 修饰是否真正具有功能还并不清楚。为解决这个问题，我们分别分析了酵母和人类蛋白编码区中 m^{6}A 位点的保守程度。在可比条件下，m^{6}A 位点在酵母中总体上并不比未被甲基化的 A 位点更加保守，而在哺乳动物中略微保守。此外，酵母和人类中的 m^{6}A 位点与可比较的未甲基化的 A 位点的单核苷酸多态性（SNP）密度或 SNP 位点频谱都没有显着差异。具有 m^{6}A 修饰位点的基因以及其中的 m6A 修饰位点均可检测到纯净化选择信号，但在基因水平，受到纯净化选择的基因不超过 20%。以上结果表明大多数蛋白编码区中的 m^{6}A 修饰是无功能的和非适应性的，可能是由 m^{6}A 甲基转移酶的脱靶效应随机引起的。另外，我们的分析也否定了最近得出的人类进化中新近产生的 m^{6}A 修饰受到正选择的结论。对于那些少数进化保守的 m^{6}A 位点，有证据表明其中很大一部分可能是具有特定功能，在未来可以优先对这些 m^{6}A 位点进行功能研究。综上，本研究的发现对于理解 m^{6}A 修饰和其他转录后修饰的生物学意义具有重要指示。该研究结果于 2017 年 12 月发表在 ***Molecular Biology and Evolution*** 上。

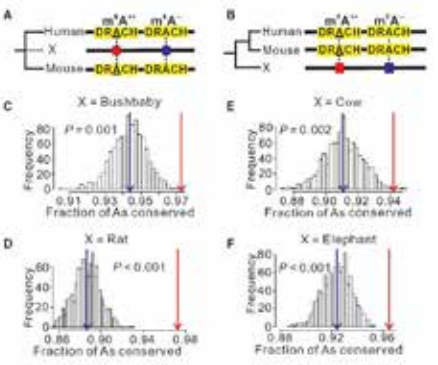

Figure1.(A) A schematic diagram illustrating the comparison between S. cerevisiae m6 A+ and m6 A- sites (B-C) Frequency distribution of the fraction of conserved S. cerevisiae m6 A- sites

2. CDKN2B 缺失对胰腺癌发生非常重要，而并非因其与 CDKN2A 共置使共同缺失没有意义

胰腺癌是最致命的恶性肿瘤之一，然而导致成人胰腺癌发生的遗传事件仍不清楚。

在动物模型中，这些遗传改变发生在成年动物身上可以更准确地反映人类癌症的特征。在这项研究中，CDKN2B 在诱导胰腺癌的过程中是必不可少的，其通过致癌基因 KRAS 表达、TP53 和 CDKN2A 失活起作用。KRAS 基因的表达激活转化生长因子 -β 信号和 CDKN2B 表达，伴随着 CDKN2A 导致细胞衰老及 KRAS 介导的转化。这些结果表明，CDKN2B 失活在胰腺癌的发生中的关键作用，同时提供了一个有用的成年动物慢病毒基因操作模型。该研究结果于 2017 年 7 月发表在 ***Oncogene*** 上。

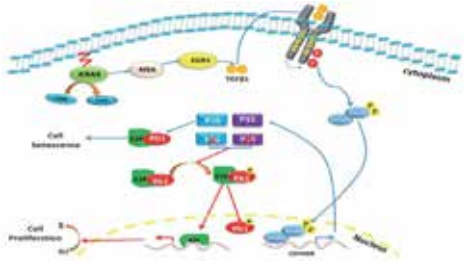

Figure 2. The KRAS/TGF-β/p15Ink4b pathway controls the cell fate

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. Most m^{6}A RNA modifications in protein-coding regions are evolutionarily unconserved and likely nonfunctional

Methylation of the adenosine base at the nitrogen-6 position (m^{6}A) is the most prevalent internal posttranscriptional modification of mRNAs in many eukaryotes. Despite the rapid progress in the transcriptome-wide mapping of m^{6}As, identification of proteins responsible for writing, reading, and erasing m^{6}As, and elucidation of m^{6}A functions in splicing, RNA stability, translation, and other processes, it is unknown whether most observed m^{6}A modifications are functional. To address this question, we respectively analyze the evolutionary conservation of yeast and human m^{6}As in protein-coding regions. Relative to comparable unmethylated As, m^{6}As are overall no more conserved in yeasts and only slightly more conserved in mammals. Furthermore, yeast m^{6}As and comparable unmethylated As have no significant difference in single nucleotide polymorphism (SNP) density or SNP site frequency spectrum. The same is true in human. The methylation status of a gene, not necessarily the specific sites methylated in the gene, is subject to purifying selection for no more than ~20% of m^{6}A-modified genes. These observations suggest that most m^{6}A modifications in protein-coding regions are nonfunctional and nonadaptive, probably resulting from off-target activities of m^{6}A methyltransferases. In addition, our reanalysis invalidates the recent claim of positive selection for newly acquired m^{6}A modifications in human evolution. Regarding the small number of evolutionarily conserved m^{6}As, evidence suggests that a large proportion of them are likely functional; they should be prioritized in future functional characterizations of m^{6}As. Together, these findings have important implications for understanding the biological significance of m^{6}A and other posttranscriptional modifications

2. CDKN2B deletion is essential for pancreatic cancer development instead of unmeaningful co-deletion due to juxtaposition to CDKN2A

Pancreatic cancer is among the deadliest malignancies; however, the genetic events that lead to pancreatic carcinogenesis in adults remain unclear. In vivo models in which these genetic alterations occur in adult animals may more accurately reflect the features of human cancer. In this study, we demonstrate that inactivation of *Cdkn2b (p15ink4b)* is necessary for induction of pancreatic cancer by oncogenic KRAS^{G12D} expression and inactivation of *Tp53* and *Cdkn2a* in adult mouse pancreatic ductal cells (P60 or older). KRAS^{G12D} overexpression in these cells activated transforming growth factor-β signaling and expression of CDKN2B, which, along with CDKN2A, led to cellular senescence and protected cells from KRAS-mediated transformation via inhibition of retinoblastoma phosphorylation. These results show a critical role of CDKN2B inactivation in pancreatic carcinogenesis, and provide a useful adult animal model by genetic engineering via lentiviral delivery.

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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*、*Mol Biol Evol*、*PNAS*、*Theranostics* 及 *Hum Mol Genet* 等国际重要 SCI 期刊上发表论文 80 余篇，论文被各类 SCI 刊物累计引用 3000 余次，H 指数 28。主持有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。Email: kongqp@mail.kiz.ac.cn

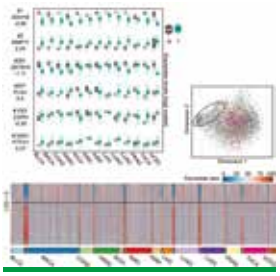
重要成果（Highlights）

论著（Publications）

1. **Li QG**[1], **He YH**[1], **Wu H**[1], Yang CP[1], **Pu SY**, Fan SQ, Jiang LP, Shen QS, **Wang XX**, **Chen XQ**, **Yu Q**, Li Y, Sun C, Wang XT, Zhou J, Li HP, Chen YB*****, **Kong QP***. A Normalization-free and nonparametric method sharpens large-scale transcriptome analysis and reveals common gene alteration patterns in cancers. **Theranostics**, 2017, **7**: 2888. (5-Y IF: 9.22)
2. **Pu SY**[1], **Yu Q**[1], **Wu H**, **Jiang JJ**, **Chen XQ**, **He YH***, **Kong QP***. ERCC6L, a DNA helicase, is involved in cell proliferation and associated with survival and progress in breast and kidney cancers. **Oncotarget**, 2017, **8**:42116-42124. (5-Y IF: 5.31)
3. **Wang XX**, **Xiao FH**, **Li QG**, **Liu J**, **He YH***, **Kong QP***. Large-scale DNA methylation expression analysis across 12 solid cancers reveals hypermethylation in the calcium-signaling pathway. **Oncotarget**, 2017, **8**:11868-11876 . (5-Y IF: 5.31)
4. **Li YC**[1], **Wang HW**[1], **Tian JY**, **Li RL**, **Rahman Z**, **Kong QP***. Cultural diffusion of Indo-Aryan languages into Bangladesh: A perspective from mitochondrial DNA. **Mitochondrion**, 2017, In press. (5-Y IF: 3.67)

1. 基于组学数据研究肿瘤发生发展的分子机制

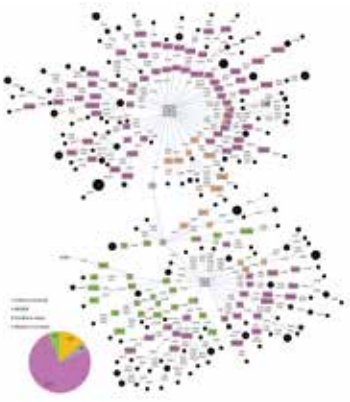
肿瘤是一种病因复杂且异质性极高的疾病，发病机制尚不完全清楚。目前肿瘤组学数据大量积累，但肿瘤组织高度异质性、批次效应等因素是肿瘤数据分析的重要难题。针对此，我们开发了一种新的适用于大样本高通量数据的分析方法（CVAA），并利用此对 TCGA 数据库中 12 种肿瘤的 RNA-seq 进行分析，成功鉴定到大量肿瘤差异基因，且不同肿瘤之间存在很多共同的基因转录紊乱水平（Li, He, and Wu et al. 2017, Theranostics）。



其中，*ERCC6L* 基因在 12 种肿瘤中都非常一致地显著高表达，通过体内体外实验发现沉默 *ERCC6L* 可显著抑制乳腺癌细胞和肾癌细胞的增殖及裸鼠移植瘤的生长（Pu and Yu et al. 2017, Oncotarget）。同时，我们还发现多种肿瘤类型的钙信号通路均发生显著高甲基化，并伴随调控基因表达水平降低（Wang et al. 2017, Oncotarget）。

2. 印欧语系向孟加拉传播遵循文化传播模式

作为印欧语系最东部的一个分支，孟加拉语的形成被认为与雅利安人入侵南亚（2000 BCE）密切相关。源于欧亚西部的印欧语系 - 雅利安语支与当地的土著语言发生融合后，最终形成了孟加拉语。语言学、历史学等研究认为，雅利安人的入侵只涉及到少部分人的迁徙，并且印欧语系传播至孟加拉只是语言上的转变（即文化传播模式）。为了验证这一观点，我们分析了孟加拉国的 240 个孟加拉语个体的 mtDNA 数据。结果发现孟加拉语人群与南亚土著人群有着较近的遗传关系。该群体中的南亚土著类群比例（~76%）远远高于欧亚西部类群（~6%），并且年龄相对古老（5-40 kya），比雅利安人入侵的时间要早得多。我们的研究提示，伴随雅利安人入侵进入该地区的西欧亚遗传组分非常少，从而从遗传学的角度支持文化传播模式（Li and Wang et al. 2017, Mitochondrion）。



3. 长寿老人转录组研究

百岁老人不但拥有常人难以企及的年龄，更可延缓甚至规避一些重大老年疾病，是研究人类健康衰老的典范。然而早期基因组范围研究并未发现长寿老人携带有大量的健康保护性突变。鉴于基因异常表达与年龄以及老年病发生的密切关系，我们利用 RNA-seq 技术获得并分析了 800 余例长寿家系样本（百岁老人、F1 后代和 F1 后代配偶）的外周血转录数据。结果发现百岁老人确实拥有独特的基因表达模式，其对人类健康衰老至关重要；同时，该基因表达模式可以一定程度遗传给后代（未发表数据）。

Human Evolution and Disease Genomics

Prof. Qing-Peng Kong, Principle Investigator, Kunming Institute of Zoology, Chinese Academy of Sciences.
The main research interests of my laboratory are: (1) tracing the origin and evolutionary history of modern humans and (2) disclosing the molecular mechanism of healthy aging by studying longevity individuals. Our research group has already published over 80 papers on the international peer-reviewed journals such as *Am J Hum Genet, PNAS, Mol Biol Evol*, *Theranostics* with total citations over 2,900 times.
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1. Insights into the mechanism of tumorigenesis based on omics data

Tumor is one complex disease with high heterogeneity, its pathogenesis is still very unclear. With the accumulation of massive tumor genome and transcriptome analysis data, it is a perfect opportunity for us to deeply understand the molecular mechanisms of cancer development. However, the heterigenetity of tumor and batch effects in data brought lots of difficulties in large-scale data analysis. In view of this, we have developed a new CVAA method for large sample high throughput data and used this method to analyze 12 tumor RNA-seq in the TCGA database, successfully identified a large number of tumor-differentiated genes, and there are many common gene transcriptional disruption levels among different tumors (**Li, He, and Wu et al. 2017, Theranostics**). Furthermore, we found that *ERCC6L*, a newly discovered DNA helicase, is highly expressed in 12 solid cancers, *ERCC6L* silencing can significantly inhibited the proliferation of breast and kidney cancer cells. The xenograft experiment also showed that silencing of *ERCC6L* strikingly inhibited tumor growth. In addition, higher *ERCC6L* expression was found to be significantly associated with worse clinical survival in breast and kidney cancers **(Pu and Yu et al. 2017, Oncotarget)**. In addition, we also found that the genes located on calcium signaling pathway tend to be hypermethylated in multiple types of tumors, suggesting the close relationship between calcium signal and tumorigenesis (**Wang et al. 2017, Oncotarget**).

2. Cultural diffusion of Indo-Aryan languages into Bangladesh

Although both linguistic and historical studies indicated only a small group of Aryans had been involved into the diffusion of Indo-Aryan languages into Bangladesh, no genetic studies had been carried out to prove this notion. By studying mitochondrial DNA variants of 240 Bengali speakers in Bangladesh, among which 23 mitogenomes are completely sequenced, we found a high proportion of South Asian components in this group. By contrast, only a small proportion of lineages can be traced back to western Eurasia, which could be attributed to recent gene flow. Our results implied a cultural diffusion of the Indo-Aryan languages into Bangladesh (**Li and Wang et al. 2017, Mitochondrion**).

3. Large-scale of transcriptomes study of longevity population

Centenarians live longer and markedly delay even escape some serious age-related diseases, thus are regarded as good subjects to study underlying mechanisms of healthy aging. However, previous genome-wide variation scanning studies revealed that longevity individuals carry very few health-protective mutations, suggesting the importance and necessity of exploration on other layers, such as gene expression. Aberrant gene expression is closely associated with age/age-related diseases, we obtained and analyzed about 800 transcriptomes from longevity families including centenarians, their F1 offspring and spouses of offspring. The results revealed that centenarians indeed harbor unique transcriptional characteristics, which functions in influencing human health. Moreover, this transcriptional pattern can partially passes on to their offspring (unpublished data).

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计算生物与医学生态学

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

重要成果（论文、软件、专利）

Publications & Patents

1. **Ma ZS*** (2017) The P/N (Positive-to-negative links) ratio in complex networks— a promising in silico biomarkers for detecting changes occurring in the human microbiome. *Microbial Ecology*. DOI: 10. 1007/s00248-017-1079-7.
2. **Ma ZS*** & Ye DD (2017) Trios— promising in silico biomarkers for differentiating the effect of disease on the human microbiome network. *Scientific Reports*. 7: 13259
3. **Ma ZS*** & **Li LW** (2017) Quantifying the human vaginal community state types (CSTs) with the species specificity index. *Peer J*. 5:e3366.
4. **Ma ZS*** (2017) Measuring Microbiome Diversity with Hill Numbers. *Metagenomics: Perspecitives, Methods, and Applications*. Elsevier Inc.
5. Dai L, Kou HD, **Xia Y**, Wen XJ, Gao JP, **Ma ZS*** (2017) Does colorectal cancer significantly influence the assembly of gut microbial communities? *Peer* J. 5: e3383,
6. Chen HJ, Peng ST, Dai L, Zou Q, Yi B, Yang XH, **Ma ZS*** (2017) Oral microbial community assembly under the influence of periodontitis. *PloS One*. 2(8): e0182259.
7. Wei L, Xing PW, Su R, Shi G, **Ma ZS***, Zou Q* (2017) CPPred-RF: A Sequence-based Predictor for Identifying Cell-Penetrating Peptides and Their Uptake Efficiency. *Journal of Proteome*. 16: 2044−2053.
8. Zou Q, Wan S, Zeng X, **Ma ZS** (2017) Reconstructing evolutionary trees in parallel for massive sequences. BMC Systems Biology, 11(S6)
9. 马占山等《生物信息学：计算技术和软件导论》科学出版社。
10-12. 三项菌群生物信息学 / 医学生态学 分析发明专利受理：专利受理号如下：
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《生物信息学：计算技术和软件导论》

序

生物信息学是生命科学与信息（计算）科学的交叉学科，现已成为现代生命科学和生物技术领域的基础学科之一，大数据时代的来临更是将其推向了现代科技的前沿。在国内外生物信息学迅猛发展的今天，《生物信息学计算技术和软件导论》一书的出版，对国内生物信息学的科研和教学具有重要的现实意义。该书主要从计算技术和软件的视角综述了生物信息学中计算、遗传和统计等基础领域的一些最新重要进展（基础篇）；同时较全面系统地介绍了各种组学技术所涉及的生物信息数据分析和建模技术（技术篇）。通过该书，读者可了解生物信息学和计算生物学领域的前沿科技。编著者来自中国科学院五个相关研究所（昆明动物研究所、数学与系统科学研究院、上海计算生物学研究所、西双版纳植物园和沈阳应用生态研究所）、沈阳药科大学，以及多家国外著名大学和科研机构（伦敦大学学院、阿尔伯塔大学、加拿大国家科学研究委员会、加拿大国家纳米技术研究所和马里兰大学），在生物信息学和计算生物学领域具有较高的造诣。主编马占山研究员在美国爱达荷大学获得计算机科学和昆虫学双博士，并具有在美国硅谷近十年的计算机高级工程师经历，是中国科学院遗传资源与进化国家重点实验室于 2010 年从美国爱达荷大学通过 “百人计划” 引进的 PI(Principal Investigator)。引进后在中科院昆明动物研究所建立了 “计算生物与医学生态学实验室”，并在三代基因测序软件、人类微生物群系宏基因医学生态学等领域取得了一系列重要突破。

跨学科障碍或许是当今生物信息学领域面临的最大的挑战之一。传统上，生命科学多以实验和归纳推理为主，而计算和数理科学则以理论和演绎推理为主。该书基础篇虽侧重于介绍计算和数理科学领域的前沿发展，但想必也能够为生物学家理解和掌握。而技术篇不仅为生物学家详细介绍了组学中重要的生物信息学分析技术和相关的资源（软件及数据库），同时也为计算和数理学者提供了深入了解生物学研究的恰当切入点。该书特别值得一提的是对国内外在生物信息学专业课程设置的比较分析和建议。毕竟，专业人才培养应该是减缓并最终消除跨学科障碍的大计！

20 世纪末叶展开的信息革命为开启 21 世纪生命科学世纪奠定了良好的技术基础。生命的进化史和未来的延续本质上是信息的遗传、变异和进化。生物信息学的重要性就在于它能够为人类认识、保护和永续利用地球上的生物资源，以及为自身的保健和疾病诊治提供有效的信息处理理论、技术和工具。本人愿《生物信息学计算技术和软件导论》一书的出版发行能够为推进中国生物信息学和计算生物学的发展有所贡献！

张亚平

2017 年 6 月于北京

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Bioinformatics

Computing and Software

Zhanshan（Sam）Ma *Editor*

Chinese Academy of Sciences

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Computational Biology and Medical Ecology

Prof. **Zhanshan (Sam) Ma,** Principle Investigator, received his double PhDs in Computer Science, and Entomology in 2008, and 1997, respectively, both from the University of Idaho (UI), USA. In November 2010, he was retained as a Professor and Principal Investigator by Kunming Institute of Zoology (KIZ), the Chinese Academy of Sciences (CAS) through "The Elite 100 Scientists Program" of the CAS. Prior to joining in KIZ, he was a Research Scientist (in Computational Biology & Computer Science) at UI. He was a senior network and software engineer from 1998 to 2006 in the computer industry in Silicon Valley, USA. Dr. Ma has been keeping dual track publishing in both Computer Science and Biology with more than 80 peer-refereed papers in premier platforms such as *IEEE Transactions on Reliability*, *Science Translational Medicine*, *The ISME Journal*. He was a member of London-based "*Faculty 1000 of Biology and Medicine*" and the editor-in-chief of *I. J. Network Science*.

精准诊断微生物群系相关疾病的核心使能技术

计算生物与医学生态学科组于 2017 年发布了两项生物信息技术（算法和软件），这两项技术可用于精准诊断菌群相关疾病指标的研发，也可以用于其它环境微生物群系监测的研究。其技术报告以 The P/N (Positive-to-Negative Links) ratio in complex networks—a promising in silico biomarker for detecting changes occurring in the human microbiome 和 Trios—promising in silico biomarkers for differentiating the effect of disease on the human microbiome network 为题，分别发表在 Microbial Ecology 和 Scientific Reports 上。两项技术的国家发明专利已进入实质审核阶段。

现今仍然有一类疾病（例如：乳腺炎、BV、IBD、肥胖、牙周炎等），由于对其发病机制缺乏完整的了解，使得临床诊断存在诸多障碍。它们具有一些共同特征：用一通俗说法，就是与人体“菌群失调（Dysbiosis）”密切关联，类似于自然生态系统（例如：森林、湖泊）失衡可能会引发生态灾害。“人体菌群”或者更准确的应该称作“人体微生物群系（Microbiome）”是指分布在人体体内（肠道、生殖道、呼吸道、口腔）和体表（皮肤）的大量微生物（包括细菌、病毒、噬菌体、质粒等）。如果单指细菌，则“菌群”这一传统使用名词可以继续使用。如果包括了病毒、噬菌体、质粒等，则“微生物群系”应该是更加恰当的名词。另目前中文翻译中大量使用了“微生物组”一词，但如果考虑：与传统上类似的“（动植物）区系（Biomes）”一词使用，以及与“微生物宏基因组（Metagenomics）”区别；中文其它生物“组”学也都对应英文“Omics”；Omics 通常也指对生物大分子（基因、宏基因，蛋白质等）“组”的研究。则“微生物群系（Microbiome）”或许更为恰当。

人类自进入工业化时代以来，现代化的生活方式（特别是饮食习惯的改变）可能为人类微生物群系带来了深刻的变化，这些改变很大程度上是不利于健康的。肥胖、糖尿病、痛风、IBD 等免疫代谢相关疾病的高发构成了一张可能仍在不断加长的疾病清单。许多科学家将这类疾病称之为菌群相关疾病 (Microbiome Associated Diseases：MAD)。然而，针对 MAD 的大规模、深入研究仅仅是过去 10 年间的事。由于受到菌群检测技术的限制，长期以来对此类疾病病因的研究往往迷失了方向；其中一些疾病的病因至今仍然未知。例如，有些疾病被认为是感染性疾病（例如乳腺炎、BV、牙周炎），但医学界却找不出确切的病原菌。又例如，有些疾病被笼统归之为代谢性疾病（例如肥胖、IBD），但确切的发病机制往往并不清楚。正是 10 年前美国“人体微生物群系研究计划”（HMP）以及欧盟“人体肠道微生物群系研究计划”（MetaHIT）等所采用的宏基因组学研究技术将 MAD 疾病的研究推向了医学前沿。但是对寻找 MAD 疾病“病原”和诊断标准的研究仍然鲜有重大突破。巨大的挑战例如：与传统感染性疾病不同，通常不存在单一的“敌人”（病原菌）。即使存在“敌人”，敌人也非常“狡猾”，他们可能形成机会性的邪恶联盟。学科组在 2015 年首次揭示的乳腺炎发病机制就是其实例之一。这些机会性邪恶联盟往往“潜伏”在健康人体菌群内，一旦机体发生有利于他们扩张的环境，则迅速“兴风作浪”。

虽然从人类微生物群系计划一开始，科学家就已近认识到了 MAD 疾病乃至微生物群系研究本质上是一生态学问题，并从以研究动植物为对象的宏观生态学汲取了大量理论、方法和技术。人体微生物群系生态学被认为是进入了黄金时代；但这些进展并没有解决 MAD 疾病的诊断和病因研究中的根本性挑战！例如，几乎所有人体菌群研究都进行多样性分析、多样性指数计算。现实中，这些多样性指数对于疾病诊断的意义有限。鉴于生态学分析技术的局限性，科学家对应用复杂网络科学研究菌群生态网络也展开了大量研究。虽然网络科学在过去 10 多年间被认为是许多自然科学和社会科学领域最重要的技术之一，然而在 MAD 疾病诊断领域却进展甚微。由于先前所定义的复杂网络特征忽略了菌群网络中特殊节点的作用，以及其相互作用方式；结果是，这些特征要不就是在疾病和健康样本之间无显著差别，要不就是“七上八下”。学科组研发团队制定了如下策略寻找全新的网络特征，包括（1）“承认”代表特殊微生物种类的网络节点（例如，最高丰度物种、最高优势度物种、网络枢纽节点等）可能具备的特殊作用；（2）区分种间相互作用的模式（相生、相克或阴、阳关系）；（3）选取尽可能简单的特征。

以上策略有效地揭示了人体微生物群系网络内部相互作用的三条基本原理：其一、物种生来并不平等，特殊物种可能具有特殊的诊断价值；其二、相生相克或阴阳平衡程度应具有重要诊断价值；其三、奥卡姆剃刀原理（以简御繁）。正是基于此三项原理，研发团队定义了两类生物信息标记（指标）算法。一类是菌群网络中 12 种三角（基序）关系（trios），另一类是菌群网络中正负比例。三角关系虽然简单，但往往是决定系统格局和稳定性的重要因素。国际关系中曾经的中美苏“三角关系”可能就是三角关系影响系统格局的例子之一。团队定义的 12 种三角关系应该足以描述影响复杂网络系统格局和稳定性的要素；而正负比例指标显然受到了传统中医阴阳平衡思想的启示。团队通过分析公共数据库中已经发表的菌群相关疾病的研究数据，示范了两项生物信息诊断技术的有效性。当然，新诊断技术的适用性和有效性并非限于所检验过的这些疾病。事实上，学科组所建立的原理、算法和软件为用户研发其它菌群（微生物群系）相关疾病的个性化精准诊断提供了全套分析和计算技术。据了解，目前尚无其它类似能够用于研发可靠、特异的菌群相关疾病诊断指标的通用技术（算法和软件）。因此，新技术的发布为菌群相关疾病的精准诊断和其他环境微生物群系监测的研究提供了一项前景良好的核心使能技术。

神经系统的发育机制与演化

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

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重要成果（Highlights）

论著（Publications）

1. **Ma P[1]*, Ren B[1], Yang X[1],** Sun B, **Liu X, Kong Q, Li C, Mao B***, ZC4H2 stabilizes Smads to enhance BMP signalling, which is involved in neural development in Xenopus . **Open Biol**. 2017, 7: 170122.
2. **Liu X[1], Xia Y[1],Tang J, Ma L, Li C, Ma P*, Mao B***, Dual roles of Akirin2 during Xenopus neural development, **J Biol Chem**. 2017,292:5676-5684.
3. **Sun J[1], Wang X[1], Shi Y, Li J, Li C, Mao B***, EphA7 regulates Claudin6 and pronephros development in Xenopus**. Biochem Biophys Res Commun**. doi:10.1016/j.bbrc.2017.12.027.
4. An T, Gong Y, Li X,Kong L, **Ma P**, Gong L, Zhu H,Yu C, Liu J,Zhou H, **Mao B**, Li Y* . USP7 inhibitor P5091 inhibits Wnt signaling and colorectal tumor growth. **Biochemical Pharmacology**. 2017,131:29-39.

1. Akirin2 调控神经系统发育的分子机制

发现 Akirin2 在非洲爪蛙发育中的神经系统特异表达，并参与了早期神经前体细胞的维持以及神经元分化过程的调控。生化实验表明，Akirin2 通过参与不同的蛋白复合体来分别参与对神经祖细胞维持以及神经元分化过程的调控，具体表现为：在神经前体细胞中，Akirin2 与 BAF 染色质重塑复合物的亚基 BAF53a 及其互作因子 Geminin 相互作用，拮抗 Geminin 对 Sox2 表达诱导，以便维持适当的神经前体细胞的数目；在分化中的神经元中，Akirin2 作为共同转录因子通过影响 NeuroD 的表达来调控 N-tubulin 的表达水平，进而参与了神经分化过程的调控。 Akirin2 在脊椎动物中高度保守，本研究为揭示了其在早期神经系统发育中的新功能。

2. ZC4H2 调控 BMP 信号通路并参与神经系统发育

ZC4H2 是一个非常保守的小核蛋白，与人类神经系统相关疾病的发生密切相关，但关于其在神经系统发育中的功能一直未知。我们的研究发现：在非洲爪蛙的胚胎发育过程中，ZC4H2 是一个母源性表达的基因，随后在发育中的神经系统中特异表达。功能实验表明，ZC4H2 参与了非洲爪蛙早期胚胎神经诱导过程；且体内和体外的实验都证明 ZC4H2 可以正调控 BMP 信号通路。进一步的生化实验表明，ZC4H2 通过直接与 Smad1/5 蛋白相互作用，竞争性抑制了其与泛素连接酶 Smurf1/2 的结合，从而抑制了 Smad1/5 蛋白的泛素化降解途径进而促进了其蛋白稳定性。另外在对人类神经系统相关疾病中鉴定出的 ZC4H2 的突变的研究发现，ZC4H2 可能是通过对 BMP 信号通路的调控参与了人类神经系统的发育过程。 本研究首次揭示了 ZC4H2 调控早期胚胎发育的分子机制。

图 1　ZC4H2 调控爪蛙胚胎神经系统发育及其分子机制。

Fig.1　Roles and mechanisms of ZC4H2 in neural development in Xenopus.

Mechanisms of Neural Patterning and Evolution

Prof. Bingyu Mao, Principal Investigator, Ph. D. (1998, Shandong University, China). The molecular mechanisms of neural patterning and how these mechanisms evolved during vertebrate origin are the focuses of our lab. We use mouse, the amphibian *Xenopus* and the cephalochordate amphioxus as our model animals.
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1. Dual roles of Akirin2 protein during Xenopus neural development

The newly identified nucleoprotein Akirin has been shown to modulate the innate immune response through epigenetic regulation and to play important roles in other physiological processes, but its role in neural development remains unknown. We show that Akirin2 is required for neural development in Xenopus and knockdown of Akirin2 expands the expression of the neural progenitor marker Sox2 and inhibits expression of the differentiated neuronal marker N-tubulin. Akirin2 acts antagonistically to Geminin, thus regulating Sox2 expression, and maintains the neural precursor state by participating in Brg1/Brm-associated factor (BAF) complex mediated by BAF53a. Additionally, Akirin2 also modulates N-tubulin expression by acting upstream of NeuroD and in parallel with Ngnr1 during terminal neuronal differentiation. Thus, our results reveal a novel model in which Akirin2 precisely coordinates and temporally controls Xenopus neural development.

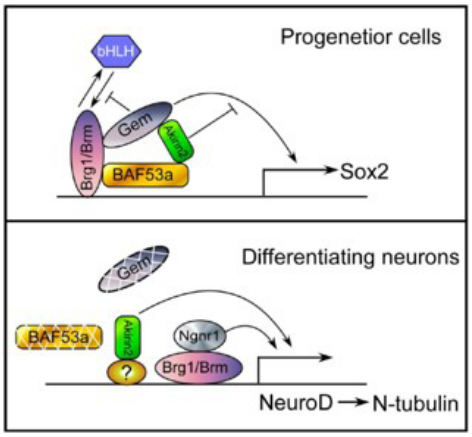

图 2. Akirin2 调控神经前体 细胞的维持及神经元分化的分子机制

Figure 2. Akirin2 maintains the neural precursor state and modulates neuronal differentiation through different protein complexes.

2. ZC4H2 stabilizes Smads to enhance BMP signalling

ZC4H2 is a small nuclear protein associated with intellectual disability and neural development in humans. We report that ZC4H2 is highly expressed in the developing neural system and is involved in neural patterning and BMP signalling in Xenopus. Knockdown of ZC4H2 led to expansion of the expression of the pan neural plate marker Sox2 in Xenopus embryos. In mammalian cells, ZC4H2 promotes BMP signalling and is involved in BMP regulated myogenic and osteogenic differentiation of mouse myoblast cells. Mechanistically, ZC4H2 binds and stabilizes Smad1 and Smad5 proteins through reducing their association with the Smurf ubiquitin ligases and thus their ubiquitination. We also found that a group of ZC4H2 mutations, which have been isolated in patients with intellectual disorders, showed weaker Smad-stabilizing activity, suggesting that the ZC4H2–Smad interaction might contribute to proper neural development in humans.

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哺乳动物胚胎发育

郑 萍，博士，研究员，课题组长。2009 年入选中国科学院“百人计划”。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。

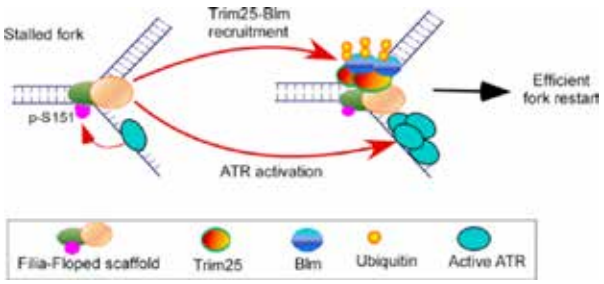
重要成果（Highlights）

论著（Publications）

1. **Li CH**, Yan LZ, **Ban WZ**, Tu Q, Wu Y, **Wang L**, Bi R, **Ji S**, Ma YH, **Nie WH**, Lv LB, Yao YG*, Zhao XD*, **Zheng P***. Long-term propagation of tree shrew spermatogonial stem cells in culture and successful generation of transgenic offspring. **Cell Res**, 2017, 27(2):241-252.
2. **Wang XY**[1], Liu DH[1], **He DJ**, Suo SB, Xia X, **He XC**, Han JD*, **Zheng P***. Transcriptome analyses of rhesus monkey pre-implantation embryos reveal a reduced capacity for DNA double strand break (DSB) repair in primate oocytes and early embryos. **Genome Res**, 2017, 27:567-579.
3. **Zhao B**[1], **Zhang WD**[1], **Cun YX**, **Li JZ**, **Liu Y**, Gao J, Zhu HW, Zhou H, Zhang RG, **Zheng P***. Mouse embryonic stem cells have increased capacity for replication fork restart driven by the specific Filia-Floped protein complex. **Cell Res**, 2017 Nov 10. doi: 10.1038/cr.2017.139. [Epub ahead of print]

1. 发现小鼠多能干细胞利用特殊机制高效化解 DNA 复制压力

干细胞如何在快速自我更新中维持遗传物质的稳定是发育生物学中远未清楚的重要科学问题。复制压力是内源性 DNA 损伤和基因组不稳定的主要来源。发现多能干细胞有高效的复制压力处理能力，能有效重启受阻复制叉。并发现它们通过在复制叉上增设干细胞特异性 Filia-Floped 脚手架蛋白，脚手架以类似海绵的作用，大量富集复制叉维护和修复因子，从而高效重启受阻复制叉。该研究首次指出干细胞以特殊机制高效化解复制压力，维持遗传物质稳定性。



The working model of Filia–Floped on replication forks

【Zhao B et al. Cell Res, 2017 Nov 10, Epub ahead of print, IF=14.33】

2. 发现灵长类和小鼠早期胚胎多能细胞具不同的全能性变化特征

小鼠早期胚胎多能细胞在着床前呈 naïve pluripotency 状态（具发育全能性），在着床后过渡到 primed pluripotency 状态（具局限的发育能力）。但是，灵长类早期胚胎多能细胞的多能性变化特征并不清楚。通过单细胞 RNA-seq，我们分析了猕猴着床前 7 个发育阶段胚胎细胞的转录组 [包括 16 细胞期、早桑椹胚期、晚桑椹胚期、早期囊胚 (EB)、中期囊胚 (MB)、晚期囊胚 (LB) 和孵化囊胚 (HB)]，发现猕猴早期胚胎多能细胞的全能性变化特征与小鼠显著不同：naïve pluripotency 状态仅短暂存在于着床前囊胚期的早期 (EB) 和中期 (MB)，在囊胚后期 (LB) 即转变为 primed pluripotency 状态（图 1）。这一发现提示，选择早期和中期囊胚，将可能成功分离和建立具 naïve pluripotency 特征的灵长类胚胎干细胞系（投稿中）。

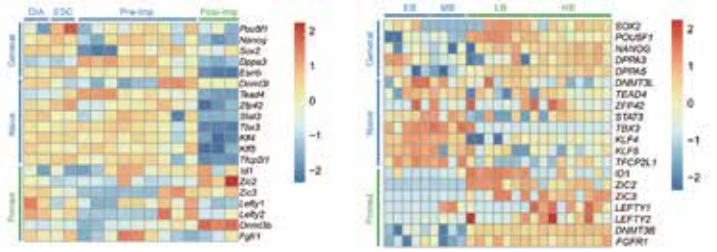


图 1. 不同状态多能性的标记基因在猕猴和小鼠上胚层细胞中呈现不同的表达变化模式 。

Mammalian Embryonic Development

Prof. Ping Zheng, Principal Investigator, joined in Kunming Institute of Zoology, Chinese Academy of Sciences in 2009. The laboratory studies how stem cells safeguard their genomic stability, and the biology of germ-line stem cells in male and female. We use mouse, monkey and tree shrew as animal models.

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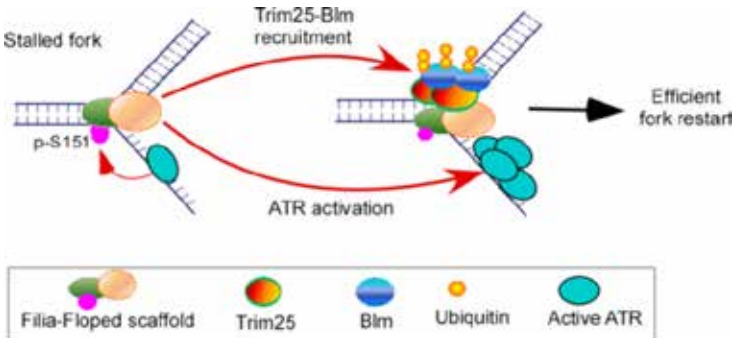
1. Unique mechanisms of DNA replication stress response in embryonic stem cells

How pluripotent stem cells (PSCs) maintain genomic stability during the rapid self-renewal remains a key unresolved question. Here we report that mouse embryonic stem cells (ESCs) are superior to differentiated cells in resolving replication stress. Specifically, ESCs utilize a unique Filia-Floped protein complex-dependent mechanism to efficiently promote the restart of stalled replication forks in maintaining the genomic stability. ESC-specific Filia-Floped complex resides on replication forks and act as a functional scaffold, which promotes the stalling fork restart through a dual mechanism: enhancing the recruitment of Blm to replication forks and stimulating the ATR kinase activation. This study for the first time reveals that ESCs utilize an additional and unique regulatory layer to efficiently promote the stalled fork restart and maintain genomic stability.



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2. Pluripotency dynamics in rhesus monkey early embryos

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

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表观遗传与发育调控

焦保卫，博士，研究员，博士生导师。“青年千人计划”引进人才。云南省细胞生物学学会第五届理事会秘书长。长期从事发育及生殖生物学研究，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中的调控机制及其进化意义。还通过一系列新基因的发现和功能研究揭示了鱼类生殖生长的新格局。已经在 Cell 等杂志发表论文 17 篇。目前学科组以小鼠等动物为对象研究发育与进化的遗传印迹调控，主要从事乳腺干细胞的调控、X 染色体失活机制及进化意义、发育过程印迹基因的功能等研究。

重要成果（Highlights）

论著（Publications）

1. **Yang X**, Wang H, **Jiao B***. Mammary gland stem cells and their application in breast cancer. Oncotarget. 2017 Feb 7;8(6):10675-10691.
2. Lv C, Li F, Li X, Tian Y, Zhang Y, Sheng X, Song Y, Meng Q, Yuan S, Luan L, Andl T, Feng X, **Jiao B**, Xu M, Plikus MV, Dai X, Lengner C, Cui W, Ren F, Shuai J, Millar SE, Yu Z. MiR-31 promotes mammary stem cell expansion and breast tumorigenesis by suppressing Wnt signaling antagonists. Nat Commun. 2017 Oct 19;8(1):1036. doi:10.1038/s41467-017-01059-5.

1. 乳腺干细胞及其在乳腺癌中的应用

乳腺是一种特殊的器官，含有两种不同的上皮细胞：内层的腔上皮细胞和外层的肌上皮细胞。乳腺干细胞是一中动态变化的细胞，具有自我更新和分化成所有乳腺上皮细胞的能力。这些上皮细胞对于青春期乳腺的形成以及怀孕期乳腺的扩增具有重要作用。近年来，研究者们主要集中于理解在乳腺发育以及乳腺癌的转变过程中乳腺干细胞是如何进行调控的，因此，我们论述了乳腺干细胞的发现以及信号通路、微环境、非编码 RNA 对乳腺干细胞的调控作用。另外，我们也讨论了乳腺干细胞作为乳腺癌起源的证据和靶向乳腺癌干细胞的治疗前景。【Yang X et al. 2017 Oncotarget, IF=5.415】

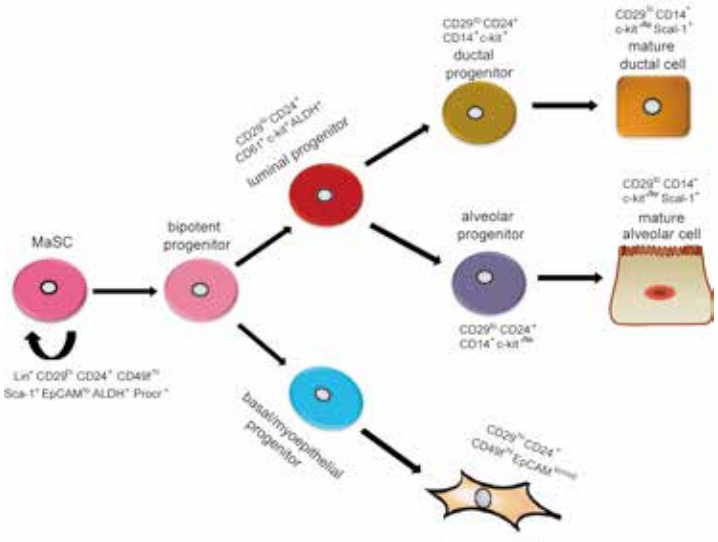

图 1. 乳腺干细胞的等级分化模型和各亚群分离标志物

2. 印迹基因对乳腺发育的影响

印迹基因 (imprinted gene) 为父母源等位基因中呈现出单侧表达的等位基因。研究发现，印迹基因不仅在早期胚胎发育过程中扮演重要作用，哺乳动物的成体发育、某些遗传疾病及癌症的发生都与印迹基因密切相关。 我们将以杂交子一代小鼠不同发育时期的乳腺作为研究对象，探讨基因印迹在调控乳腺发育方面的作用及其相关作用机制。

3. lncRNA 对乳腺发育的影响

长链非编码 RNA（lncRNA）是一类转录本长度超过 200 核苷酸的功能性 RNA 分子。它们缺乏编码成蛋白的功能，但能以多种方式调控生命活动。我们首先通过转录组学等技术筛选得到一些影响乳腺发育的相关 lncRNAs，希望对这些相关的 lncRNAs 在乳腺发育的作用进行深入全面的探讨。

Epigenetic and Developmental Regulation

Prof. Baowei Jiao, Principal Investigator, joined in Kunming Institute of Zoology, Chinese Academy of Sciences since July of 2013. 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.
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Research Interests:

Mammary gland stem cells and their application in breast cancer

The mammary gland is an organ comprising two primary lineages, specifically the inner luminal and the outer myoepithelial cell layers. Mammary gland stem cells (MaSCs) are highly dynamic and self-renewing, and can give rise to these mammary gland lineages. The lineages are responsible for gland generation during puberty as well as expansion during pregnancy. In recent years, researchers have focused on understanding how MaSCs are regulated during mammary gland development and transformation of breast cancer. Here, we summarize the identification of MaSCs, and how they are regulated by the signaling transduction pathways, mammary gland microenvironment, and non-coding RNAs (ncRNAs). Moreover, we debate the evidence for their serving as the origin of breast cancer, and discuss the therapeutic perspectives of targeting breast cancer stem cells (BCSCs).

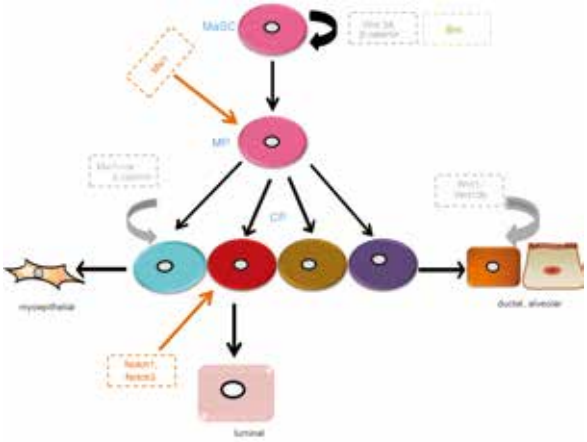

Figure 2: Main regulators of MaSCs in different signaling pathways.

The impact of imprinted genes on breast development

In genomic imprinting, genes within a discrete domain are coordinately regulated and expressed according to parent of origin. Researches show that imprinted genes do not only play an important role in the process of early embryonic development, they are also closely related to the adult mammalian development, certain genetic diseases and cancers. We will investigate the role of breast development and its mechanisms by using mammary tissue at different stages of hybrid F1 mouse.

The influence of lncRNA on breast development

lncRNA is an RNA molecule that is longer than 200 nucleotides and that is not translated into a protein. lncRNAs of all kinds have been implicated in a range of developmental processes and diseases, but knowledge of the mechanisms by which they act is still surprisingly limited. We will expect to get some lncRNAs related to breast development by transcriptomics technology screening, and then carry out a comprehensive discussion of the role of these related lncRNAs on mammary gland development.

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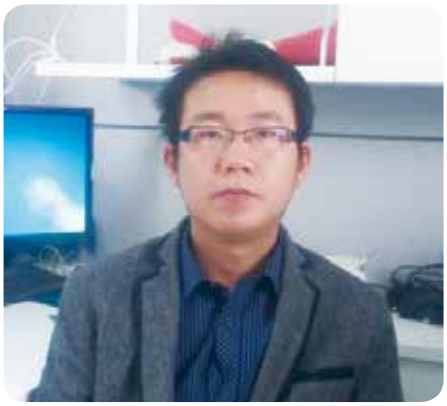

进化与发育转录组学

吴东东，博士，研究员， PI，昆明动物研究所青年科学家小组组长。2011 年 1 月于中科院昆明动物研究所获得博士学位，并破格晋升为副研究员，2012 年被聘为项目研究员，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）。以第一作者或共同通讯作者在 ***Nat Genet, Cell Res, Mol Biol Evol, PloS Genet, J Mol Cell Biol, Hum Mol Genet*** 等杂志发表论文 30 余篇。

重要成果（Highlights）

论著（Publications）

1. **Zeng L**[1],Ming C, Li Y, Su LY,Su YH, **N O**. Otecko, **Liu HQ**,**Wang MS**, Yao YG,Li HP,**Wu DD**,*and Zhang YP*.Rapid Evolution of Genes Involved in Learning and Energy Metabolism for Domestication of the Laboratory Rat. ***Molecular Biology and Evolution***. 2017, doi:10.1093/molbev/msx238.
2. Li Y[1],**Wang MS**, **N O Otecko**,**Wang W**,**Shi P**, **Wu DD***, Zhang YP*. Hypoxia potentially promotes Tibetan longevity. ***Cell Research***. (2017) 27:302-305.
3. **Wang MS**[1], **N O. Otecko**[1],Wang S [1],**Wu DD**[1],**Yang MM**,Xu YL, R W. Murphy,**Peng MS**,* and Zhang YP*. An Evolutionary Genomic Perspective on the Breeding of Dwarf Chickens. ***Molecular Biology and Evolution***. 2017,34(12):3081–3088
4. **Zeng L**[1], Ming C[1], Li Y, Su LY, Su YH, **N O. Otecko**, A Dalecky, S Donnellan, K Aplin, Liu XH, Song Y, Zhang ZB, A Esmailizadeh, S S. Sohrabi, H A Nanaei, **Liu HQ**, Wang MS, S A Atteynine, G Rocamora, F Brescia, S Morand, D M. Irwin, **Peng MS**, Yao YG, Li HP,***Wu DD**,* and**Zhang YP** *. Out of Southern East Asia of the Brown Rat Revealed by Large-Scale Genome Sequencing. ***Molecular Biology and Evolution***.2017,doi:10.1093/molbev/msx276.
5. **Wang MS**[1], Zeng Y[1], Wang X[1], WH Nie, JH Wang, Su WT, **N O. Otecko**, Xiong ZJ, Wang S, Qu KX, Yan SQ, **Yang MM**, **Wang W**, Dong Y *, **Wu DD** *, and **Zhang YP***. Draft genome of the gayal,Bos frontalis. ***GIGAScience***. 2017,doi:10.1093/gigascience/gix094.
6. Xu HB[1], Li YX[1], Li Y, Otecko NO, **Zhang YP**, Mao B*, **Wu DD***. Origin of new genes after zygotic genome activation in vertebrate. ***Journal of Molecular Cell Biology***. Accepted.
7. **Ye LQ**[1], Zhao H[1], Zhou HJ[1], Ren XD[1], Liu LL, Otecko NO, Wang Zb, **Yang MM**, **Zeng L**, Hu XT, Yao YG, **Zhang YP***, **Wu DD** *. The RNA editome of Macaca mulatta and functional characterization of RNA editing in mitochondria. ***Science Bulletin*** 2017, 62:820-830 (cover)
8. Wang YM[1], Xu HB, **Wang MS, Otecko NO**, **Ye LQ**, **Wu DD***, **Zhang YP** *. Annotating long intergenic non-coding RNAs under artificial selection during chicken domestication. BMC Evol Biol. 2017, 17(1):192.

1. 实验大鼠被成功驯化的遗传机制

实验大鼠作为一种广泛使用的模式动物，由野生褐家鼠驯化而来，也是一种家养动物。与其野生祖先褐家鼠相比，实验大鼠在形态、行为及生理方面发生了很大的变化，然而实验大鼠的起源以及导致其被驯化成功的机制尚不清楚。本研究通过比较野生褐家鼠和实验大鼠的基因组和转录组数据，解析了实验大鼠的起源和驯化遗传机制。利用群体遗传学方法，例如 FST 以及 cross-population extended haplotype homozygosity (XP-EHH) 等，在全基因范围内扫描了野生褐家鼠与实验大鼠群体之间出现分化的区域，发现大量神经系统基因在大鼠驯化过程中受到人工选择作用，例如在学习记忆方面起重要作用的 FOXP2 和 B3GAT1，以及节律相关基因 CLOCK。有意思的是这些基因在实验大鼠的神经组织中的表达水平显著上调，有助于提高学习记忆能力。研究人员推测学习记忆能力的提高可能是实验大鼠被成功驯化的关键。另外，基于转录组分析及 qPCR 数据揭示能量代谢相关基因在实验大鼠大脑组织中显著上调，这些都为我们进一步揭示实验大鼠驯化的遗传机制奠定了良好的基础。

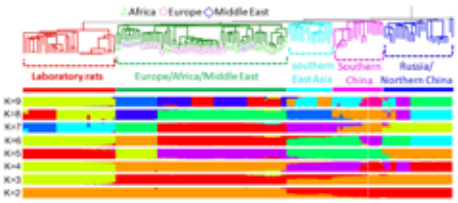

图 1. 实验大鼠与野生褐家鼠的系统发育关系及群体结构

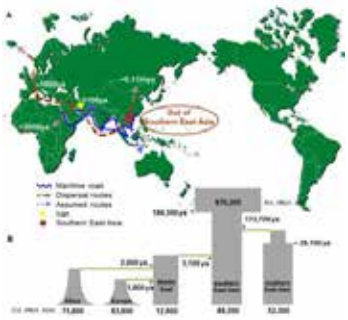

图 2. 褐家鼠的传播路线及群体历史

2. 褐家鼠的东亚南部起源

褐家鼠是重要的伴人鼠类之一，除两级冰盖之外，几乎遍布全球，在人类活动区域非常常见。褐家鼠也是最主要的害鼠之一，携带多种病毒，传染类似鼠疫等的传染性疾病。关于褐家鼠的起源及扩散问题，学术界目前仍存在争议。大量的历史及研究基本确定褐家鼠是起源于亚洲，但是具体起源区域及迁徙路线尚无定论。本研究利用高通量大规模测序平台对全球多地区 110 个褐家鼠样本进行测序，解析和阐明了褐家鼠的东亚南部起源及迁移问题。这项研究从群体遗传学角度和计算生物学角度揭示了褐家鼠的东亚南部起源，并描绘了其从起源地往东亚北部以及欧洲 / 非洲 / 中东的两条主要扩散路线。对其迁出时间进行的推断显示：褐家鼠在 ~173,000 年前从东亚南部迁往东亚北部；在 ~3,100 年前，由东亚南部往中东迁徙，紧接着在 ~2,000 年前往非洲迁徙，~1,800 年前迁往欧洲。这推翻了人们之前认为褐家鼠起源于东亚北部的这一假说。同时，在褐家鼠的迁徙过程中，很多与免疫系统相关的基因受到了快速进化。

Evolutionary and Developmental Transcriptomics

Prof. 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, CAS in 2011. He performed studies of artificial selection on domestic animals, particularly high altitude adaptation of domestic animals in Tibet. He has published more than 30 research papers in *Nat Genet, Cell Res, Mol Biol Evol, PloS Genet, J Mol Cell Biol, Hum Mol Genet,* etc, as first author or co-corresponding author.
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1. Rapid evolution of the laboratory rat

The laboratory rat, widely used in biomedical research, is domesticated from wild brown rat. The origin and genetic mechanism underlying domestication of the laboratory rat remain largely elusive. In the present study, large scale genomes supported a single origin for the laboratory rat, possibly from a sister group to wild rats from Europe/Africa/Middle East. Genomic and transcriptomic analyses uncovered many artificially selected genes (e.g. FOXP2, B3GAT1, and CLOCK) involved in the nervous system. These genes associate with learning ability and regulation of circadian rhythm, which likely enabled the successful domestication of the laboratory rat. Particularly, many genes, including mitochondrial genes responsible for energy metabolism, displayed a substantially increased expression in the brain of laboratory rats compared to wild rats. Our findings demystify the origin and evolution of this model animal, and provide insight into the process of its domestication.

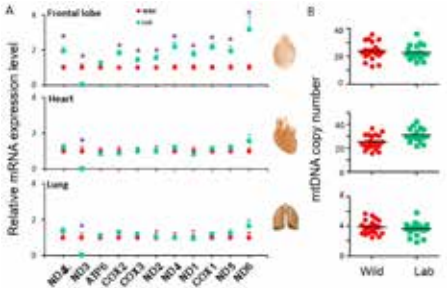

Fig 3. Relative mRNA expression levels of mitochondrial coding genes (A) and mtDNA copy number (B) in wild brown and laboratory rats.

2. Out of southern East Asia of the brown rat revealed

The geographic origin and migration of the brown rat (*Rattus norvegicus*) remain subjects of considerable debate. In this study, we sequenced whole genomes of 110 wild brown rats with a diverse world-wide representation. We reveal that brown rats migrated out of southern East Asia, rather than northern Asia as formerly suggested, into the Middle East and then to Europe and Africa, thousands of years ago. Comparison of genomes from different geographical populations reveals that many genes involved in the immune system experienced positive selection in the wild brown rat.

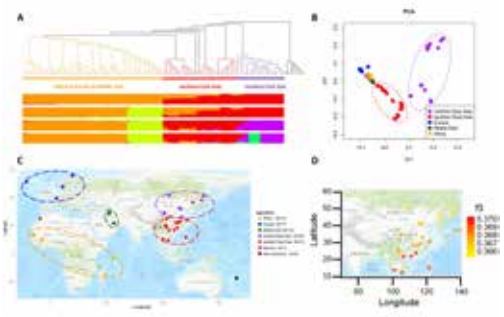

Fig 4. Out of southern East Asia origin of wild brown rats.

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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。中国科学院“百人计划”引进人才。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、eLife 等国际学术期刊发表论文 11 篇。目前实验室以小鼠、树鼩和猕猴为模型，主要研究：（1）神经突触生理功能及病理活性的调控机制；（2）中枢神经系统进化发育的遗传基础；（3）灵长类神经环路的进化与高级认知功能的关系和机制。

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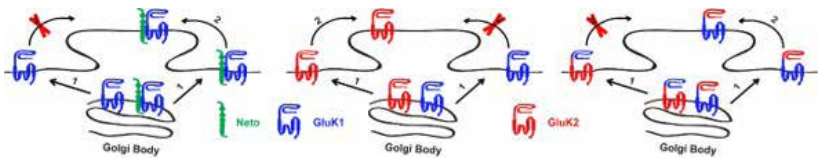
重要成果（Highlights）

论著（Publications）

1. **Sheng N**, Shi YS, Nicoll RA. (2017) Amino-terminal domains of kainate receptors determine the differential dependence on Neto auxiliary subunits for trafficking. ***Proc. Natl. Acad. Sci. U. S. A.*** 114: 1159-1164.
2. **Sheng N**, Yang J, Silm K, Edwards RH, Nicoll RA. (2017) A slow excitatory postsynaptic current mediated by a novel metabotropic glutamate receptor in CA1 pyramidal neurons. ***Neuropharmacology*** 115: 4-9
3. Lomash RM, **Sheng N**, Li Y, Nicoll RA, Roche KW. (2017) Phosphorylation of the kainate receptor (KAR) auxiliary subunit Neto2 at Serine 409 regulates synaptic targeting of the KAR subunit GluK1. ***J. Biol. Chem.*** 292:15369-15377.

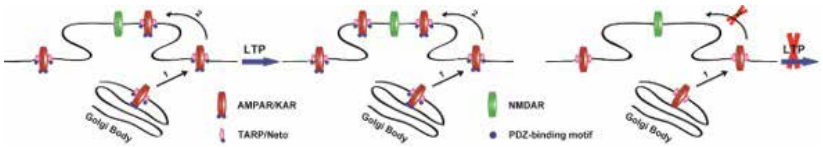
1. 红藻氨酸受体的突触转运调控

谷氨酸受体是中枢神经系统中介导兴奋性突触传递的主要离子通道类型，其在突触部位的定位和活性调控是实现大脑功能的生理基础。我们以小鼠和大鼠脑片为研究系统，结合神经电生理、神经药理学、分子细胞生物学等研究手段，深入研究了其家族成员红藻氨酸受体的突触转运和生物物理活性的调控机制。我们发现其成员 GluK1 和 GluK2 的突触转运依赖于不同的分子机理，GluK1 依赖于其辅基 Neto 蛋白，而 GluK2 自身具有突触转运能力且不受 Neto 蛋白调控。进一步的结果表明，这种差异性是由 GluK1 和 GluK2 的胞外 N 端结构域所决定的。相关工作发表于 **Sheng N et al. 2015 eLife** 和 **Sheng N et al. 2017 PNAS**。目前，我们将进一步研究红藻氨酸异质性复合受体的突触转运机制以及辅基等结合蛋白对其活性的调控。



2. LTP 神经突触后分子机制

突触可塑性是学习记忆的神经生理基础，在此过程中，谷氨酸受体家族成员 AMPA 受体在突触中的表达水平存在变化且依赖于神经元活性。利用 AMPA 受体的条件性基因敲除小鼠（*GluA1*$^{fl/fl}$*GluA2*$^{fl/fl}$*GluA3*$^{fl/fl}$），结合早期胚胎宫内电转、海马脑片和神经电生理，我们揭示了长时程增强（LTP）产生的突触后分子机制。发现谷氨酸受体和其辅基所形成的复合物，与突触后支架蛋白中 PDZ 结构域之间的相互作用是 LTP 所必须的。相关工作正在被审稿中。



3. 突触传递异常与神经系统疾病

神经突触功能异常是神经疾病和神经退行性疾病发生的重要原因之一。利用神经电生理和神经药理学等手段，我们发现当谷氨酸回收循环系统发生异常并导致其组织中浓度增加时，海马锥体神经元中一种新型的代谢性谷氨酸受体会被激活，且介导一慢速电流，提示该代谢性谷氨酸受体可能在中风等神经疾病中发挥一定作用。相关工作发表于 **Sheng N et al. 2017 Neuropharmacology**。目前，我们利用疾病遗传分析与神经系统疾病相关的致病敏感基因，并进一步研究其在突触传递中的功能机制，从而建立突触病理与相关神经疾病和神经退行性疾病的关系。

4. 中枢神经系统进化发育的分子机制

关于神经系统疾病的研究目前大都以啮齿类动物为模型，但是在临床上以此为基础的药物研发的失败率非常的高，其中主要原因之一是：与啮齿类动物相比，灵长类（包括人）的大脑中的细胞类型和结构复杂度等都有不同程度的增加，并且进化出与高级认知功能相关的关键脑区及神经环路。我们拟以小鼠、树鼩和猕猴为模型，通过进化基因表型系统生物学分析，结合发育生物学、神经电生理、显微成像、光遗传学等技术手段，研究特定关键脑区的神经细胞发育进化的遗传机制，以及突触和神经环路的进化与高级认知功能的关系和机制。

Synaptic Function and Mechanism

Prof. Nengyin Sheng, Principal Investigator, joined in Kunming Institute of Zoology, Chinese Academy of Sciences in 2017. The research of Sheng's lab focuses on central nervous system (CNS) and will study the following topics using mice, shrew and rhesus monkey as model systems: (1) The synaptic mechanisms underlying physiology and neuropathology; (2) The genetic bases underlying evolution and development of CNS; (3) The evolution of neural circuit in primate and its relationship with higher cognition function.
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1. The regulation of kainate receptors (KARs) synaptic trafficking

Glutamate receptors are the major functional channels to mediate excitatory synaptic transmission in the central nervous system, and their proper expression at synapses and biophysical properties regulation are the physiological bases for brain function. Using mice and rat brain slices as model systems and combining the techniques including electrophysiology, neurological pharmacology, molecular and cellular biology, we studied the regulatory mechanisms for KARs synaptic trafficking and their biophysical properties modulation. We found that the synaptic targeting of its two members GluK1 and GluK2 is through distinct molecular bases. Synaptic expression of GluK1 receptor is depended on its auxiliary subunits Neto proteins, whereas GluK2 itself harbors synaptic trafficking ability and is independent on Neto proteins. Furthermore, it was found that the underlying difference is determined by the excellular amino-terminal domains of GluK1 and GluK2. The results of these studies have been published as ***Sheng N et al. 2015 eLife*** and ***Sheng N et al. 2017 PNAS***. Currently, we are further studying the molecular mechanisms for synaptic trafficking of heteromeric KAR complexes, as well as their biophysical properties regulation by auxiliary subunits and other interacted proteins.

2. The postsynaptic mechanism for LTP

Synaptic plasticity is the neural physiological basis for learning and memory, and in this process the expression level of AMPA receptors at postsynapses are changed in a neuronal activity-depended manner. Using conditional knock-out mice of AMPA receptors ($GluA1^{fl/fl}GluA2^{fl/fl}GluA3^{fl/fl}$) as a model and combining the techniques including *in utero* electroporation, hippocampal slice culture and electrophysiology, we determined the postsynaptic mechanism for long-term potentiation (LTP). And it was found that LTP requires the PDZ-domain mediated interaction between postsynaptic scaffold proteins and the complexes of glutamate receptors/auxiliary subunits. This work is under review now.

3. Synaptic pathology and neurological or neurodegeneration diseases

The malfunction of synapses is regarded as one most important factor involved in neurological and neurodegeneration diseases. Using electrophysiology and neural pharmacology as tools, we identified a slow excitatory postsynaptic current mediated by a novel metabotropic glutamate receptor in hippocampal pyramidal neurons. The current is present when the glutamate concentration is aberrantly increased in the tissue because of its uptake and recycle system turbulence, suggesting the potential involvement of this novel mGlu receptor in neurological disease such as stoke. This work has been published as ***Sheng N et al. 2017 Neuropharmacology***. Currently, we are trying to identify novel pathogenesis sensitive genes underlying neurological diseases through genetic analyses, and then further study their function and mechanisms for synaptic transmission. The long-term goal for this study is to determine the functional relationship between synaptic pathology and neurological/neurodegeneration diseases.

4. The molecular bases for CNS evolution and development

At present most of the studies of neurological diseases are based on rodent as models. However, their developed drugs are mostly failed during clinical trials. One underlying major reason is that the cell types and structure complex of primates (including human) brains are increased significantly, compared to that of rodent. Moreover, novel brain regions, as well as the neural circuits, are formed during evolution, which is critical for higher cognition function. We are trying to use mice, shrew and rhesus monkey as model systems and establish techniques including evolutionary genotype-phenotype system biology, developmental biology, electrophysiology, high-resolution microimaging, optogenetics. Our long-term goals are to study the genetic bases for the evolution and development of the neural cells in specific and critical brain regions and identify the functional relationship and mechanism between evolution of synapses & neural circuits and higher cognition function.

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Xu Sha
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叶雅馨 研究实习员
Ye Yaxin
Research Trainee

研究生 (GraduateStudents）

唐　杰 Tang Jie 2017 硕士

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）。2017 年，课题组利用群体遗传学研究揭示了非洲化蜜蜂攻击性强度快速降低的演化机制，通过基因组研究揭示了鸟类特异性保守序列的重要作用，发起并启动了全球蚂蚁基因组联盟计划。同时，初步建立了法老蚁的 CRISPR/Cas9 基因组编辑技术平台。2017 年，在 *Nat commun* (2), *PNAS* (1) , *GigaScience* (3) 等国际刊物发表 SCI 文章 9 篇。 http://zhanggjlab.cn/en/index.html

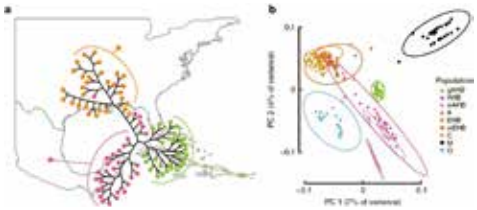
重要成果（Highlights）

论著（Publications）

1. Avalos A[1], **Pan H**[1], Li C, Acevedo Gonzalez J, Rendon G, Fields C, Brown P, Giray T, Robinson G*, Hudson M*, **Zhang G*.** A soft selective sweep during rapid evolution of gentle behaviour in an Africanized honeybee. ***Nat Commun***. 2017, 8:1550.
2. Seki R[1], **Li C**[1], **Fang Q**, Hayashi S, Egawa S, **Hu J**, **Xu L**, **Pan H**, Kondo M, Sato T, Matsubara H, Kamiyama N, Kitajima K, Saito D, **Liu Y**, Gilbert M, Zhou Q, Xu X, Shiroishi T, Irie N*, Tamura K*, **Zhang G***. Functional roles of Aves class-specific cis-regulatory elements on macroevolution of bird-specific features. ***Nat Commun***. 2017, 8: 14229.
3. Boomsma J, Brady S, Dunn R, Gadau J, Heinze J, Keller L, Moreau C, Sanders N, Schrader L, Schultz T, Sundstrom L, Ward P, Wcislo W, **Zhang G***. The GAGA Consortium & Forum The Global Ant Genomics Alliance (GAGA) ***Myrmecol News***. 2017, 25(2):61-66 .
4. Hargreaves A, Zhou L, Christensen J, Marlétaz F, Liu S, Li F, Jansen P, Spiga E, Hansen M, Pedersen S, Biswas S, Serikawa K, Fox B, Taylor W, Mulley J, **Zhang G***, Heller R*, Holland P*. Genome sequence of a diabetes-prone rodent reveals a mutation hotspot around the ParaHox gene cluster. ***PNAS***. 2017, 114(29):7677-7682 .
5. Mak S[1], Gopalakrishnan S[1], Carøe C[1] , Geng C[1], Liu S, Sinding M, Kuderna L, Zhang W, Fu S, Vieira F, Germonpré M , Bocherens H, Fedorov S, Petersen B, Sicheritz-Ponten T, Marques-Bonet T, **Zhang G**, Jiang H, Gilbert M. Comparative performance of the BGISEQ-500 versus Illumina HiSeq2500 sequencing platforms for palaeogenomic sequencing. ***GigaScience***. 2017, 6(8): 1-13.
6. Gao J*[1], **Li Q***[1], Wang Z*[1], Zhou Y, Martelli P, Li F, **Xiong Z**, Wang J, Yang H, **Zhang G***. Sequencing, *de novo* assembling and annotating the genome of the endangered Chinese crocodile lizard *Shinisaurus crocodilurus*. ***GigaScience***. 2017, 6(7):1-6.

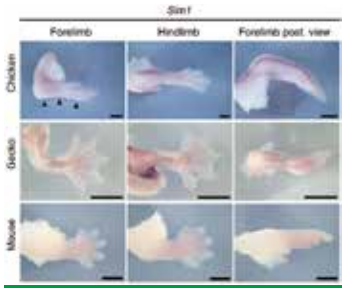
1. 群体遗传学研究揭示非洲化蜜蜂攻击性强度快速降低的演化机制

非洲化蜜蜂（Africanized honeybee, AHB），是 1956 年巴西一实验室的非洲蜜蜂逃逸后与当地的欧洲蜜蜂（European-derived honeybee, EHB）发生杂交后产生的具有极强攻击性的杂交种。在波多黎各岛上传代 12 年后攻击性强度急剧下降，变成了温和的非洲化蜜蜂（gentle Africanized honeybee, gAHB）。为了研究蜜蜂攻击行为快速演化的分子机制，本课题组对 EHB，AHB 和 gAHB 开展了群体遗传学研究。证实了波多黎各的 gAHB 群体起源于同一批 AHB 和 EHB 的杂交后代群体，gAHB 的遗传背景大部分与 AHB 类似，但在许多控制攻击行为的相关基因中，gAHB 群体更接近 EHB。同时，这些攻击行为相关基因在 gAHB 中快速形成了许多自身特有的单体型。以上结果表明，非洲化蜜蜂的攻击能力在演化过程中受到了柔性选择（soft selection），这种选择可能是蜜蜂与岛屿环境中高度密集的人群共存下选择的结果。【Avalos and Pan et al. 2017 ***Nat Commun***】



2. 基因组研究揭示鸟类特异性保守序列的重要作用

从非鸟类恐龙到鸟类演化的过程中，鸟类展现出了许多特异性的特征，如飞行的能力和与飞行相关的翅膀，但是我们对这一过程中的遗传机制知之甚少。我们通过比较 48 种鸟和 9 种非鸟类脊椎动物的基因组，鉴定出了占到鸟类基因组 1% 的鸟类特异性保守的原件（ASHCEs），而且许多 ASHCEs 展现出不同的组蛋白修饰，可能与四肢的发育有关。我们进一步比较了四足动物之间在胚胎期的基因表达，发现 ASHCE 相关的基因在鸟类翅膀发育中有着特殊的作用。最终我们找出了由 ASHCE 调控的，对鸟类飞羽形成有着重要作用的 *Sim1* 基因。该研究表明鸟类借助于非编码序列来实现对基因功能的特异性调控，展现出特异性的生理特征，而不是新基因等原件。该研究集合了基因组学、发育生物学、演化生物学和古生物学等多个学科，强调了顺式调控原件在物种演化中的重要作用。【Seki and Li et al. 2017 ***Nat Commun***】



3. 启动全球蚂蚁基因组联盟计划（GAGA）

2017 年 7 月，全球蚂蚁基因组联盟计划在 *Myrmecological News* 杂志发起并启动。本计划将构建全球蚁科属级代表物种的基因组图谱，提供最全面的蚂蚁基因组多样性数据。通过比较分析，我们将可以理解蚂蚁演化的全球性趋势，并找到当今蚂蚁物种的多样性及其令人惊叹的适应性背后的遗传基础。

本项目预期在系统发育框架下从全球范围内选取约 300 个有代表性行为生态特征的蚂蚁物种进行基因组分析，将会极大促进蚂蚁（乃至其他物种）生物学的研究，同时为未来数十年学术界回答不同的科学问题提供了大量的基础数据。【Boomsma et al. 2017 ***Myrmecol News***】

Biodiversity Genomics Lab

Prof. Guojie Zhang, visiting professor, head of Biodiversity Genomics Group, Kunming Institute of Zoology, CAS; full professor in University of Copenhagen and Associate Director of the China National GeneBank. He has been served as peer reviewer for ***Nature***, ***Science***, ***Genome Research***, ***Current Biology*** and several grant-giving agencies. He has more than 100 publications, including ***Science***, ***Nature***, ***Cell***, ***Nature Genetics***, ***Nature Communication***, ***PNAS***, ***Current Biology***. In 2017, we focused on the progress of rapid evolution of gentle behavior in an Africanized honeybee, the functional roles of ASHCEs, and GAGA (the Global Ant Genomics Alliance) program. At the mean time, we firstly built the CRISPR/Cas9 genome editing system in the ant species *Monomorium pharaonis*. In 2017, we published 9 high impact factor SCI papers, including ***Nat commun*** (2), ***PNAS*** (1), and ***GigaScience*** (3).

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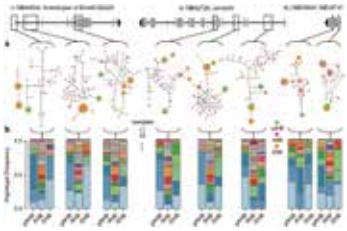
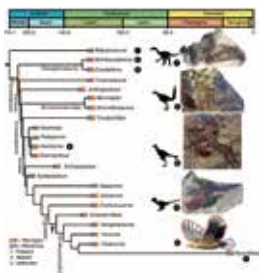
1. Population genomic study explores evolution of gentle Africanized honeybee

Africanized bees are the offspring of African honey bees and their European counterparts. They were set out to produce a desirable mix of traits from the gentle European bees and their African counterparts, which were more aggressive, disease-resistant and adapted to a tropical climate. Africanized honey bees arrived in Puerto Rico in the 1990s, and evolved into the gentle within three decades and dominated the island today. Here, we sequenced the genomes from gAHB, EHB and AHB, and discovered that the genomes of gAHB are mostly resembled to AHB. However, specific regions of the DNA, had shifted in the gentle bees, reflecting more of their European heritage (EHB). And we described a soft selective sweep, acting at multiple loci across the genome, that occurred during, and may have mediated, the rapid evolution of a behavioural trait.



2. Functional roles of Aves class-specific cis-regulatory elements on macroevolution of bird-specific features



During the transition from non-avian dinosaurs to birds, birds had shown numerous evolutionary innovations such as self-powered flight and its associated wings with flight feathers. But little is known about the genetic basis of this process.By analyzing the genome of 48 avian and 9 non-avian vertebrate species, we identified millions of avian-specific highly conserved elements (ASHCEs) which represented nearly 1% of the avian genome and predominantly (>99%) reside in non-coding regions. Many ASHCEs show differential histone modifications that may participate in regulation of limb development. We demonstrated how ASHCE driven avian-specific expression of *Sim1*. These findings demonstrate regulatory roles of ASHCEs in the creation of avian-specific traits, and highlight the importance of cis-regulatory rewiring during macroevolutionary changes.

3. The Globe Ant Genome Alliance (GAGA) has been launched and started

GAGA has been launched and started via an open access publication in Myrmecological News in 2017, and its website has become relatively completed (http://antgenomics.dk/). This global project on ant genomics will provide a comprehensive dataset of the genomic diversity of the world's ant genera. Based on the comparative analysis of these data, we will be able to understand global trends of ant evolution and narrow down the genetic features that have been particularly relevant for the diversification and astonishing evolutionary success of ants. Based on recent experience with global-scale bird genome sequencing (B10K), we expect that obtaining and analyzing ~300 genomes of ant species from across the world will allow major advances in ant (and, indeed, non-ant) biology and will provide the scientific community with a trove of data that will be mined in the service of diverse questions for decades to come.

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重要基金项目 Key Projects and Fundings

我国重要家养动植物在人工选择下进化的遗传和基因组机制，973 项目；执行年限：2013-2017；项目负责人：王文；金额：683.1 万（留室经费）。

The Genetic and Genomic Mechanisms of the Evolution of Important Domesticated Plants and Animals in China during Artificial Selection. National Basic Research Program (973) project, Period: 2013-2017; Head of project, Wen Wang; Amount: RMB 6.83 million of the lab.

基于自然保护区的 DNA 条形码，科技基础工作专项；执行年限：2012-2017；项目负责人：Douglas W Yu；金额：808 万元。

DNA Barcoding Based on Nature Conservation Areas; The Special Foundation for Technology Basis Work, Period, 2012-2017; Head of project, Douglas W. Yu; Amount: RMB 8.08 million.

自噬和 DNA 损伤修复维持 PSC 稳态的机制研究，科技部“干细胞与转化研究”重点专项子课题；执行年限：2016-2020；项目负责人：郑萍；金额：239.5 万元。

The Roles of Autophagy and DNA Damage Repair in the Maintenance of Pluripotent Stem Cell. Key project from the “Stem cell and Transformation Research” National Key Research and Development Program of China. Period, 2016-2020; Head of project, Ping Zheng; Amount: RMB 2.395 million.

继发性卵巢早衰致病因素及分子机制研究，科技部“生殖健康及重大出生缺陷防控研究”重点专项子课题；执行年限：2017-2020；项目负责人：郑萍；金额：153 万元。

Pathogenic Factors and Molecular Mechanism of Secondary Premature Ovarian Failure. Key project from the “Prevention and Control of Reproductive Health and Major Birth Defects”, National Key Research and Development Program of China. Period, 2017-2020; Head of project, Ping Zheng; Amount: RMB1.53 million.

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“典型脆弱生态修复与保护研究”重点专项子课题；执行年限：2017-2020；项目负责人：蒋学龙；金额：340 万元。

Formation Mechanism and Evolutionary Motivation of Origin and Geographical Pattern of Animal Diversity. Key project from the “Study on Typical Fragile Ecological Rehabilitation and Protection” National Key Research and Development Program of China. Period, 2017-2020; Head of project, Xuelong Jiang; Amount: RMB3.4 million.

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“干细胞与转化研究”重点专项子课题；执行年限：2016-2021；项目负责人：焦保卫；金额：175 万元。

In VivoStudies on the Behavior of Cells Post Transplantation Based on Multimode Molecular Imaging. Key project from the “Stem cell and Transformation Research” National Key Research and Development Program of China. Period, 2016-2021; Head of project, Baowei Jiao; Amount: RMB1.75 million.

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，农业部转基因生物新品种培育重大专项子课题；执行年限：2016-2020；项目负责人：高云；金额：658.9 万。

Cloning and Functional Verification of Important Breeding Genes of Muscle Growth and Fat Deposition Traits of Pig, Cattle and Sheep. Major projects on Transgenic of Ministry of Agriculture, Period, 2016-2020; Head of project, Yun Gao; Amount: RMB 6.589million.

基因组中新遗传结构的起源与动物的适应进化，国家自然科学基金创新研究群体；执行年限：2017-2019；项目负责人：王文；金额：525 万元。

Evolutionary Origins of New Genetic Structure in Genome and Animals' Adaptive Evolution. NSFC Science Fund for Creative Research Groups, Period, 2017-2019; Head of project, Wen Wang; Amount: RMB5.25million.

哺乳动物适应性进化的遗传学机制，国家杰出青年基金，执行年限：2014-2017；项目负责人：施鹏；金额：320 万元。

Genetic Mechanisms of Adaptive Evolution in Mammals. National Science Fund for Distinguished Young Scholars, Period, 2014-2017; Head of project, Peng Shi; Amount: RMB2.0 million.

家犬在人工选择下的微进化研究，国家自然科学基金“微进化过程的多基因作用机制”重大研究计划重点项目；执行年限：2016-2018；项目负责人：王国栋；金额：336 万。

Microevolution Studies in Dogs under Artificial Selection. Key project of "Polygenic mechanism of micro-evolution" major research program of National Science Foundation of China, Period, 2016-2018; Head of project, Guodong Wang; Amount: RMB 3.36million.

高山倭蛙适应高原极端环境的遗传机制研究，国家自然科学基金微进化重大研究计划；执行年限：2015-2017；项目负责人：车静；金额：150 万。

Genetic Mechanism of Dwarf frog to Adapt to the Extreme Environment of Altitude Alpine. Major Research Plan of Microevolution of National Science Foundation of China, Period, 2015-2017; Head of project, Jing Che; Amount: RMB1.50 million.

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，国家自然科学基金重大研究计划；执行年限：2017-2019；项目负责人：宿兵；金额：289 万。

Molecular Mechanisms and Functions of EPAS1 and EGLN1 in Hypoxia Adaptation of Tibetan Population. Major Research Plan of National Science Foundation of China, Period, 2017-2019; Head of project, Bing Su; Amount: RMB 2.89 million.

棘皮动物及脊索动物发育进程中的进化遗传程度的研究，国家自然科学基金组织间合作研究 —NSFC-JST 项目 (中日)；执行年限：2015-2018；项目负责人：王文；金额：200 万。

Evolutionary Genetic Studies on the Development of Echinoderms and Chordates. NSFC Foundation between Funding organizations -NSFC-JST project. Period, 2015-2018; Head of project, Wen Wang; Amount: RMB2.00 million.

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，国家自然科学基金国际 (地区) 合作与交流项目；执行年限：2016-2020；项目负责人：Douglas W Yu；金额：161 万

Ecological and Socio-Economic Effects of Death of Forest Trees in Mountainous Areas under Climate Change. NSFC International (Regional) Cooperation and Exchanges Programs. Period, 2016-2020; Head of project, Douglas W Yu; Amount: RMB1.61 million.

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，国家自然科学基金国际 (地区) 合作与交流项目；执行年限：2017-2021；项目负责人：孔庆鹏；金额：235 万。

Tracing the Origin of Native Americans based on Mitochondrial and Y Chromosomal Sequence Variations. NSFC International (Regional) Cooperation and Exchanges Programs. Period, 2017-2021; Head of project, Qingpeng Kong; Amount: RMB2.35 million.

基于 Hedgehog 信号通路和纤毛形成的抗肿瘤化合物的发现与机制研究；国家自然科学基金 - 云南省联合基金；执行年限：2014-2017；项目负责人：毛炳宇；金额：200 万。

Screening and Mechanism Study of Anti-tumor Compound Based on the Hedgehog Signaling Pathway and Cilia Formation. NSFC Joint Funds of China-Yunnan Province; Period, 2014-2017; Head of project, Bingyu Mao; Amount: RMB 2.0 million.

两栖爬行类多样性与进化，国家自然科学基金委优秀青年科学基金；执行年限：2017-2019；项目负责人：车静；金额：130 万元。

Herpetological Diversity and Evolution. National Science Foundation for Outstanding Young Scholars of China; Period, 2017-2019; Head of project, Jing Che; Amount: RMB 1.3 million.

动物复杂性状的进化解析与调控；中国科学院战略性先导科技专项（B 类）；执行年限：2014-2019；项目负责人：王文、施鹏；金额：2.226 亿元。

Evolutionary Analysis and Functional Regulation of Animal Complex Traits; Strategic Priority Research Programs (B) of Chinese Academy of Sciences (CAS), Period, 2014-2019; Head of project, Wen Wang, Peng Shi; Amount: RMB222.6 million.

猪脂肪沉积等优质高产分子模块解析，中科院分子模块设计育种先导专项（A 类）子课题；执行年限：2013-2017；项目负责人：张亚平；金额：1900 万元。

Molecular Module Analysis of Pig high-yielding Characters including Fat Deposition. Project of the CAS Strategic Priority Research Programs (A) on “Designer Breading by Molecular Modules” , Period, 2013-2017; Head of project, Yaping Zhang; Amount:RMB19.0 million.

西南分子育种基地的完善与能力提升，中科院分子模块设计育种先导专项（A 类）子课题；执行年限：2013-2017；项目负责人：高云；金额：1200 万元。

Improvement and Capacity Building of Southwest Molecular Breeding Base. Project of the CAS Strategic Priority Research Programs (A) on “Designer Breading by Molecular Modules”, Period, 2013-2017; Head of project, Yun Gao; Amount: RMB12.0 million.

家犬基因组拼装注释和群体基因组分析，中国科学院战略性先导科技专项（B 类）；执行年限：2017-2019；项目负责人：张亚平；金额：220 万元。
Genome Assembly, Annotation, and Analysis of Domestic Dog; Strategic Priority Research Programs (B) of Chinese Academy of Sciences (CAS), Period, 2017-2019; Head of project, Ya-Ping Zhang; Amount: RMB 2.2 million.

东非动物多样性格局，中国科学院境外机构建设项目；执行年限：2016-2020；项目负责人：蒋学龙；金额：500 万元。

Animal Diversity of East African, Project for International Institutions Construction of Chinese Academy of Sciences. Period,2016-2020; Head of project, Xuelong Jiang; Amount: RMB 5 million.

非洲家禽的分子进化与基因组多样性研究，中国科学院境外机构建设项目；执行年限：2016-2020；项目负责人：彭旻晟；金额：400 万元。

Molecular Evolution and Genomic Diversity of African Poultry. Project for International Institutions Construction of Chinese Academy of Sciences. Period, 2016-2020; Head of project, Minsheng Peng; Amount: RMB 4 million.

锐目猎犬的人工选择和遗传基础研究，中科院国际合作项目；执行年限：2015-2017；项目负责人：王国栋；金额：100 万。

Artificial Selection and Genetic basis of Ruimu Bound. International cooperation projects of Chinese Academy of Sciences. Period,2015-2017; Head of project, Guodong Wang; Amount: RMB1.00 million.

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；执行年限：2017-2019；项目负责人：Douglas W Yu；金额：100 万。

Study the impact of climate change on the entire ecological community using mitochondrial metagenomic methods, International cooperation projects of Chinese Academy of Sciences, Period: 2017-2019; Head of project, Douglas W Yu; Amount: 1 million.

西南家猪分子育种基地智能化系统，中国科学院科研平台建设项目；执行年限：2016-2017；项目负责人：高云；金额：460 万。

Intelligent System of Southwest Pig Molecular Breeding Base. Scientific Research Platform Construction project of Chinese Academy of Sciences. Period,2016-2017; Head of project, Yun Gao; Amount: RMB 4.6 million.

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；执行年限：2017-2019；项目负责人：高云；金额：223 万。

Upgrade and Reconstruction of Animal Information Management System of Southwest China Wildlife Germplasm Bank. Major technological infrastructure maintenance projects of CAS. Period, 2017-2019; Head of project, Yun Gao; Amount: RMB 2.23 million.

建立哀牢山自然保护区快速生物多样性监测方法，中科院前沿科学重点研究项目；执行年限：2017-2019；项目负责人：Douglas W Yu；金额：400 万。
Establishment of a Rapid Biological Diversity Monitoring Method in Ailao Mountain Nature Reserve. CAS Frontier Key Program. Period,2017-2019; Head of project, Douglas W Yu; Amount: RMB 4 million.

健康长寿人群基因组表观修饰模式及功能利用研究，中科院前沿重点研究项目；执行年限：2016-2020；项目负责人：孔庆鹏；金额：250 万。

Pattern and Function of Epigenetic Modifications in Chinese Centenarians. CAS Frontier Key Program.Period,2016-2020; Head of project, Qingpeng Kong; Amount: RMB 2.5 million.

云南省高端科技人才引进计划；执行年限：2015-2019；项目负责人：郑萍；金额：260 万。

Projects for Recruited Top Talent of Sciences and Technology of Yunnan Province, Period: 2015-2019; Head of project, Ping Zheng; Amount: RMB 2.6 million.

基于角蟾科生命之树研究东南亚物种多样性格局的形成，中科院东南亚生物多样性研究中心；执行年限：2017-2019；项目负责人：周炜帏；金额：100 万。

Study on the Formation of Species Diversity in Southeast Asia Based on the Tree of Megophryidae. Southeast Asia Biodiversity Research Center of Chinese Academy of Sciences. Period: 2017-2019; Head of project, Weiwei Zhou; Amount: RMB 1 million.

X 失活对乳腺干细胞的调控机制及其在乳腺癌中的应用研究，云南省高端科技人才引进计划；执行年限：2015-2019；项目负责人：焦保卫；金额：210 万。

Projects for Recruited Top Talent of Sciences and Technology of Yunnan Province, Period: 2015-2019; Head of project, Baowei Jiao; Amount: RMB 2.1 million.

基因大数据信息技术及其应用研究，云南省科技入滇专项；执行年限：2017-2019；项目负责人：马占山；金额：138 万。
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134. **Zou Q**, Wan SX, Zeng XX*, **Ma ZS***. Reconstructing evolutionary trees in parallel for massive sequences. ***BMC Syst Biol***. 2017, 11(Suppl 6):100.

135. **Zheng WS**[1], **He YX**[1], Cui CY[1], Ouzhu L, Deji Q, **Peng Y**, Bai CJ, Duoji Z, Gongga L3, Bian B, Baima K, Pan YY, Qula, Kang M, Ciren Y, Baima Y, Guo W, Yangla, **Zhang H**, **Zhang XM**, **Guo YB**, Xu SH, Chen H, Zhao SG, Cai Y, Liu SM, Wu TY, **Qi XB*, Su B*.** EP300 contributes to high-altitude adaptation in Tibetans by regulating nitric oxide production. ***Zool Res***. 2017,38, 163-170.

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137. 孔德军，杨晓君 *. 绿孔雀及其在中国的保护现状 . 生物学通报 . 2017, 52(1): 9-12.

138. 肖志术 *，李学友，向左甫，李明，蒋学龙， 张礼标．中国兽类多样性监测网络的建设规划与进展．生物多样性 .2017,25(3):237-245.

说明："[1]" 为并列第一作者，"*" 为通讯作者

Note:[1]These authors contributed equally to this work,[*]as the corresponding author.

获奖 Awards

2017 **王文，相辉，李昕，陈垒**，董扬。云南省自然科学奖二等奖（家蚕等鳞翅目昆虫茧丝进化机制及基因资源挖掘）

2017 **Wen Wang, Hui Xiang, Xi Li, Lei Chen**, Yang Dong. Second Prize for Natural Science of Yunnan province (Evolution Mechanism and Genetic Resources Exploration of Lepidoptera insects such as Silkworm).

2017 胡凤益，**王文**，张石来，**徐讯，吕俊**。云南省自然科学奖二等奖（水稻适应进化的基因组变异机制研究）

2017 Fengyi Hu, **Wen Wang**, Shilai Zhang, **Xun Xu**, **Jun Lv**. Second Prize for Natural Science of Yunnan province (Study on the Mechanism of Genome Variation in Rice Adaptive Evolution).

2017 耿嘉蔚，**张志刚**，吴韬，**施鹏**，唐晓丹，董树强，范红。云南省科技进步奖三等奖（消化系统疾病患者肠道微生物组结构的时空变化研究及应用）

2017 Jiawei Geng, **Zhigang Zhang**, Tao Wu, **Peng Shi**, Xiaodan Tang, Shuqiang Dong, Hong Fan. Third Prize for Science and Technology Progress of Yunnan Province.

2017 **杨君兴，李再云，潘晓赋，陈小勇，崔桂华**。云南省专利奖三等奖（滇池金线鲃的人工训养方法）。

2017 **Junxing Yang**, **Zaiyun Li**, **Xiaofu Pan**, **Xiaoyong Chen**, **Guihua Cui**. Third prize for Patent Award of Yunnan Province.

2017 施鹏研究员入选 “2017 年国家百千万人才工程 ”，并被授予 “ 有突出贡献中青年专家 ” 荣誉称号

2017 Prof. Peng Shi was selected as “the National key Talent Project in 2017” and was awarded the honorary title of “ Young Experts with Outstanding Contributions”.

2017 施鹏、孔庆鹏入选 “ 云岭英才 ” 计划

2017 Prof. Peng Shi and Qingpeng Kong were selected into the “Yunling Excellence” program of Yunnan Province.

2017 孔庆鹏研究员团队入选 2017 年云南省创新团队（培育对象）

2017 The team of “research on the mechanism of health aging molecular mechanism and application” leading by Prof. Kong Qingpeng was selected as innovation team (nurturing object) of Yunnan Province in 2017.

2017 王慧入选 “ 云岭青年人才 ” 计划

2017 Hui Wang was selected into the “Yunling Young talent” program of Yunnan Province.

2017 吴东东研究员荣获中科院 2017 年度青年创新促进会优秀会员，何锴、王明山入选中科院青年创新促进会会员

2017 Prof. Dongdong Wu was awarded the outstanding members of Youth Promotion Association of CAS in 2017. Kai He and Mingshan Wang were selected into the members of Youth Promotion Association Chinese Academy of Sciences.

2017 杨召辉博士学位论文获评云南省优秀博士学位论文，导师宿兵研究员被评为云南省优秀研究生指导教师

2017 Zhaohui Yang’s doctoral thesis won the Outstanding Doctoral Dissertation Award of Yunnan Province. Prof. Bing Su was awarded Outstanding Graduate Student’s Instructor of Yunnan Province.

2017 王鑫轶、李媛媛荣获中科院院长奖学金优秀奖

2017 Xinyi Wang and Yuanyuan Li won” the President Outstanding-Scholarship of CAS.

2017 王鑫轶、李媛媛荣获朱李月华优秀博士生奖 ; 江建军荣获地奥奖学金一等奖

2017 Xinyi Wang and Yuanyuan Li won “Zhu Li Yuehua Outstanding PhD Graduate Scholarship of CAS”. Jianjun Jiang won the first prize of “Diao Scholarship”.

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339种动物的细胞系2108株10000余份。大多数为哺乳动物的细胞系，其中包括60种国家级重点保护动物的细胞系。目前，昆明细胞库是国家实验细胞资源共享服务平台、中国科学院生物遗传资源库、中国西南野生生物种质库的成员单位之一，也是遗传资源与进化国家重点实验室的成员单位之一。

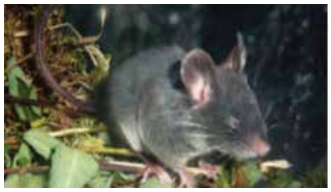
重要成果（Highlights）

论著（Publications）

1. Liu L, Zhang J,Rheindt FE, Lei F, Qu Y, Wang Y, Zhang Y, Sullivan C, **Nie W**, **Wang J**, Yang F, Chen J, Edwards SV, Meng J, Wu S. 2017. Genomic evidence reveals a radiation of placental mammals uninterrupted by the KPg boundary. PNAS,114 (35): E7282-E7290.
2. Liu L, Zhang J, Rheindt FE, Lei F, Qu Y, Wang Y, Zhang Y, Sullivan C, **Nie W**, **Wang J**, Yang F, Chen J, Edwards SV, Meng J, Wu S. 2017. REPLY TO GATESY AND SPRINGER: Claims of homology errors and zombie lineages do not compromise the dating of placental diversification. PNAS, 114(45): E9433-E9434.
3. Li C, Yan L, Ban W, Tu Q, Wu Y, Wang L, Bi R, Ji S, Ma Y, **Nie W**, Lv L, Yao Y, Zhao X, Zheng P. 2017. Long-term propagation of tree shrew spermatogonial stem cells in culture and successful generation of transgenic offspring. Cell Research, 27(2): 241-252.
4. Wang M, Zeng Y, Wang X, **Nie W**, **Wang J**, **Su W**, Otecko NO, Xiong Z, Wang S, Qu K, Yan S, Yang M, Wang W, Dong Y, Wu W, Zhang Y. 2017. Draft genome of the gayal, Bos frontalis. GIGA Science, 6:1-7.
5. Poplavskaya NS, Romanenko SA, Serdyukova NA, Trifonov VA, Yang F, **Nie W**, **Wang J**, Bannikova AA, Surov AV, Lebedev VS. 2017. Karyotype Evolution and Phylogenetic Relationships of Cricetulus sokolovi Orlov et Malygin 1988 (Cricetidae, Rodentia) Inferred from Chromosomal Painting and Molecular Data.Cytogenet Genome Res, 152:65–72.

1. 细胞资源的收集和保藏

2017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108株，其中包括猪尾鼠、电鳗、巨暹罗鲤、穗须原角鲃等10种野生动物的细胞系20株，建立家猪、家蚕、小耳猪和独龙牛等家养动物的正常细胞系19株，EBV转化的人淋巴细胞系30株以及人和实验动物的正常细胞系和肿瘤细胞系39株。复苏和扩增各类动物细胞系375株次。

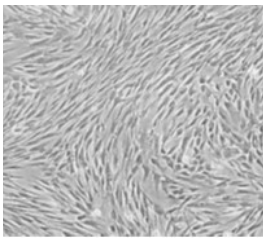


2. 对外服务

在2017年度，昆明细胞库为全国各地的398家单位，其中高等院校228家，科研院所72家，企业98家的研究人员提供各类野生和家养动物细胞系、人及常见实验动物的各类正常组织来源的细胞系及肿瘤细胞系共计398株次。除提供细胞服务外，我们还提供了核型分析技术服务40次和STR检测35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. 猕猴不同组织来源细胞系的建立

猕猴是常用的灵长类实验动物。不同组织来源的细胞系是在体外开展相关的功能研究和药物实验的重要材料。为满足课题组的研究需求，2017年度细胞库开展了猕猴不同组织来源的细胞系的建系工作。从一只测序猕猴体内获得七种组织材料，成功建立了七株来自猕猴的皮肤、肾、脾、骨骼肌、大网膜、睾丸、附睾的细胞系。另外，还建立了猕猴的关节滑膜和关节软骨细胞系。这些细胞系的建立丰富了细胞库保藏猕猴细胞的种类。



4. 猪尾鼠体细胞系的建立

猪尾鼠是啮齿目刺山鼠科一个特殊的类群。本年度，细胞库完成了两种猪尾鼠三个个体的不同组织来源细胞系的建立工作，最终成功建立并冻存了九株猪尾鼠细胞系，并完成了相关的细胞遗传学分析工作。

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 2108 cell lines from 339 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 2017, 108 cell lines from various wild and domestic animals had been established and frozen. Among these cell lines, 20 cell lines were derived from 10 species of wild animals such as Chinese pygmy dormouse, Isok barb, Giant barb, and American electric eel etc; 19 cell lines were established from domestic animals such as domestic pigs, small-ear pigs, silkworms, and mithans; 30 cell lines were obtained by EBV-transferred human lymphocytes; and 39 cell lines were normal cell lines and tumor cell lines from human and experimental animals. Three hundred and seventy-five of frozen-stored cell lines were also resuscitated and subcultured.

2. Cell lines service and technical service

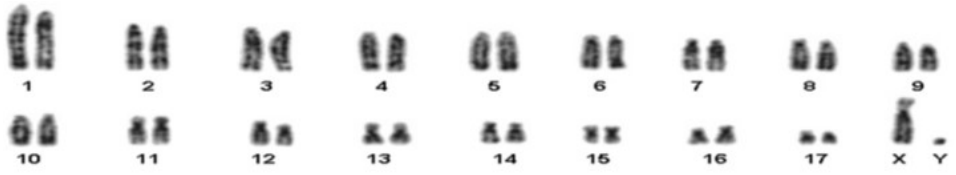
In this year, 398 cell lines, 40 times of karyotype analysis and 35 times of STR test had been provided for the researchers not only at State key laboratory of genetic resources and evolution, but also at other 72 scientific research institutions, 228 Chinese universities, and 98 enterprises . In addition, we also had provided a lot of cell culture technical advisory services by using the telephone and the email.

3. The establishment of the cell lines of different tissues of macaque

Rhesus monkeys are commonly used primates.The cell lines from different tissues of the rhesus monkey are important materials for the relevant functional research and drug experiments in vitro. To meet the needs of the research groups, the cell bank carried out the construction of the cell lines of different tissues of macaque in 2017. Seven different tissue materials (skin, kidney, spleen, skeletal muscle, large omentum, epididymis and testicular) were obtained from the rhesus monkey, which successfully established seven strains of cell lines. In addition, cell lines of synovial membrane and articular cartilage from the rhesus monkey have been established. The establishment of these cell lines enriched the types of the rhesus monkey cell lines preserved in our cell bank.

4.The establishment of somatic cell lines from the Chinese pygmy dormouse

The Chinese pygmy dormouses are a special group of rodents, belonging to Typhlomys, Platacanthomyidae. In this year, cells from three individuals of two species of Chinese pygmy dormouses were cultured, and nine cell lines were successfully established. The related cytogenetic analysis was completed.



G-banded karyotype of *Typhlomys daloushanensis* (2n=36)

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生命条形码南方中心

South China DNA Barcoding Center

生命条形码南方中心，成立于 2011 年 1 月，专门从事 DNA 条形码相关的科学研究、技术革新和应用推广。根据国重室的相关规定，目前生命条形码南方中心的工作任务主要为：与国家重点实验室课题组合作，服务国重室的各项科研任务；开展 DNA 条形码分子实验和数据提交汇总；管理国家大科学工程中国西南野生生物种质资源库，进行无脊椎动物资源的采集和保藏；管理云南濒科委司法鉴定中心，进行分子鉴定；以及国重室领导交办的其他工作

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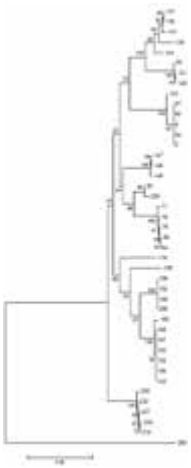
重要成果（Highlights）

论著（Publications）

1. Brennan IG, Bauer AM, Van Tri N, **Wang YY4, Wang WZ**, Zhang YP, Murphy RW. 2017. Barcoding utility in a mega-diverse, cross-continental genus: keeping pace with Cyrtodactylus geckos. Sci Rep. 7:5592.
2. Chatmongkon SUWANNAPOOM, Ya-Jiang WU, **Xing CHEN**, Adeniyi C. ADEOLA, Jing CHE, and **Wen-Zhi WANG***. 2017. The complete mitochondrial genome of the Thailand Red Junglefowl (Gallus gallus) and a phylogenetic analysis. Zoo Res. Revised.
3. **Zhang H M***. Odonata fauna of Dai-Jingpo Autonomous Prefecture of Dehong in the western part of the Yunnan Province, China - a brief personal balance from seven years of surveys and workshop report on current studies. 2017. International Dragonfly Fund - Report, 103: 1-49.
4. **Zhang H M***, Guan Z Y & WANG W Z, 2017. Updated information on genus *Gomphidictinus* (Odonata: Gomphidae) in China with description of *Gomphidictinus tongi* sp. 2017. Nov.. Zootaxa, 4344 (2): 321–332.
5. DOW R. A. **& Zhang H M***, 2017 *Yunnanosticta* gen. nov, from Yunnan, a new genus from the Sinostictinae, with the description of two new species (Odonata: Zygoptera: Platystictidae). 2017. Zootaxa, in press.
6. 张浩淼 .《中国蜻蜓大图鉴》（重庆大学出版社）
7. 张浩淼 .《新昆虫记－蜻蜓王国的神秘航线》（湖北科技出版社）

1. 蜻蜓目 DNA 条形码

2017 年中心启动蜻蜓目的基因组研究计划，开展利用 DNA 条形码数据对我国蜻蜓多样性的认识。目前已经收集到中国各地区的研究用标本超过 800 种，将对标本进行细致的分类整理，建立中国蜻蜓目的 DNA 条形码数据库。已经开展了环尾春蜓属 *Lamelligomhus*、小叶春蜓属 *Gomphidia*、类春蜓属 *Gomphidictinus* 和基色　属 *Archineura* 的基因测序工作，包括 12S，16S, 28S, Histone 3，COI，ITS 六个基因测序。样品共 161 个，2 科 5 属 27 种，共完成条形码实验 966 个。成功获得 829 个序列。



2017 年中心完成了国际蜻蜓研究基金会（IDF）的合作项目，并发表研究报告 - 云南德宏州的蜻蜓区系研究。这份报告是第一份有关滇西德宏州的蜻蜓区系研究报告。这份调查共记录云南德宏蜻蜓 174 种，其中包括了大量的中国新纪录和未知物种。例如：中国类春蜓属研究，发表新种童氏类春蜓 *Gomphidictinus tongi*；建立新属云扁螅属 *Yunnanosticta*，并发表云扁螅属 2 新种，韦氏云扁螅 *Yunnanosticta wilson* 及蓝颈云扁螅 *Yunnanosticta cyaneocollaris* 。

2. 基于线粒体基因组探讨白垩纪－第三纪事件对长纺蛛多样化的影响

白垩纪 - 第三纪时期，有花植物的适应辐射，促进了完全变态昆虫的多样化。同时，随着地表游猎昆虫的大爆发 (距今 125-90 Ma) 为蜘蛛提供了丰富的食物资源，推动了游猎蜘蛛的多样化。白垩纪 - 第三纪事件作为复杂生殖器类蜘蛛从结网到游猎演化的关键因素，造就了当前蜘蛛目中最广的多样化事件（RTA 分支多样化）。长纺蛛作为复杂生殖器类结网园蛛和地表游猎的 RTA 分支之间的中间过渡类群，既有树栖游猎又有地表结网的类群。但是长纺蛛在蜘蛛目的系统地位，起源时间和地点以及演化方向等问题，一直悬而未决。本研究将联合非洲长纺蛛分类学权威专家 Dr. Foord，首次利用高通量测序手段获得 15 属 25 种长纺蛛线粒体基因组数据，结合化石证据和相关地质年代时间节点，构建长纺蛛系统发育关系，重建祖先区域和特征。同时运用生态位模型，探讨长纺蛛多样化的可能进化驱动力。最终尝试解答白垩纪 — 第三纪事件是否影响，如何影响长纺蛛多样化?

目前该项目已完成长纺蛛蜘蛛转录组和线粒体基因组测序实验，正在进行数据分析和文章撰写。邀请南非合作者 Dr. Stefan 参加第四次亚洲蛛形学会（重庆），并获得了新鲜的非洲区系长纺蛛样品，相关分子实验正在开展。挖掘公共数据库已发表数据，建立和更新了蜘蛛生命树。基于新的蜘蛛生命树探讨 EPA（Evolutionary Phylogenetic Placements）在蜘蛛目的适用性，以及相较于常规 Blasthits 方法的优势。相关研究内容以摘要和会议报告在第四次亚洲蛛形学会进行了汇报。

South China DNA Barcoding Center

Established in 2011, the Center is the first and only facility focus on DNA barcoding in China. The initialization of SCDBC commercial using DNA barcoding technology and high-throughput barcoding laboratory construction and operation. In the year of 2017, the SCDBC collected more than 5K specimens in wild field, took pictures for over 3200 specimens, got almost 5K standard DNA barcodes. This year we using DNA Barcoding data to understand the diversity of dragonflies in China, get know Urban butterfly species diversity. And make great progress.

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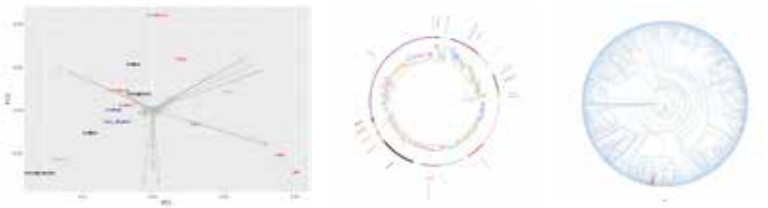
1. Strengthening the Spider Tree of Life Trough Phylogenetic Placement

We retrieved protein-coding genes of 1198 spider species (703 genera; 115 families except Synaphridae) from Machida et al. (2017) and Genbank database, to strengthen spider phylogenetic analyses. Our used two supermatrices with curated (after removal of the hypervariable expansion segments) and non-curated alignmentsdataset for our dataset that included 15 mitochondrial genes and 3 nuclear genes.

We used Evolutionary Placement Algorithm (EPA) to place sequence data from Coddington et al. (2016) (848 species from 49 families, 313 genera) on the two different reference trees (non-curated and curated ML trees). Our placement results suggested: (i) EPA is a reliable tool in identifying the higher spider taxa and outperforms the blast-hits method; (ii) even if some raw sequences have mistaken taxonomic annotations, EPA performs better than the blast-hits method; and (iii) EPA can become a quick and reliable tool for spider identification with applications in ecology.



2. Urban butterfly species diversity

Beijing is the capital city of China with more than 21 million people and is the third most populous city in the world. The many parks in Beijing can be refuges for ecological important animals such as butterflies. In June and July 2017, scientists from Kunming Institute of Zoology (Dr. Sing Kong-Wah) and China Agricultural University (Dr. John James Wilson, Mr. Yang Xianzhe), conducted butterfly surveys at parks in Beijing to investigate which butterflies share the se spaces with people in the city. The highest butterfly species richness was recorded in Beijing Botanical Garden that located whereas lowest species richness was observed in Zhong Shan Park. Parks that outside the inner city where surrounding have more natural environment support higher butterfly species richness. The findings will help policy makers facing the challenge of monitoring and managing biodiversity in megacities so as to promote beneficial interactions and co-existence between urban insects and the public.

公园 (Park)	物种数量 (# species)
北京植物园 (BBG) Beijing Botanical Garden	18
南海子公园 (NHZ) Nan Hai Zhi Park	11
奥林比克公园 (OFP) Olympic Forest Park	9
景山公园 (JSP) Jing Shan Park	6
天坛公园 (TTP) Tian Tan Park	6
颐和园 (YHY) Yi He Yuan	6
圆明园 (YMY) Yuan Ming Yuan	6
朝阳公园 (CYP) Chao Yang Park	5
柳荫公园 (LYP) Liu Yin Park	4
中山公园 (ZSP) Zhong Shan Park	1

Butterflies in Beijing's Parks

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Li-fen Xie, Engineer

博士后（Postdoctoral Fellows）

SING KONG WAH, 2017

中心实验室

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

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

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三大技术平台

一、基因组学分析平台

1. Ion Torrent 测序系统

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

2. Miseq 测序仪

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

3. 单细胞自动制备

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

4. 高通量单细胞基因分型系统

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

5. QuantStudio 12K Flex 实时定量 PCR 仪

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

二、蛋白质组学分析平台

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

三、显微影像分析平台

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

Core Facility

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

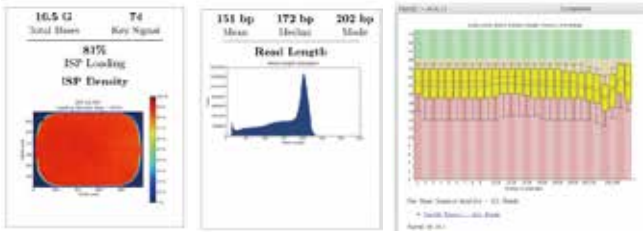
http://www.kiz.cas.cn/gre/gre6/gre61/

The Three Technical Platforms

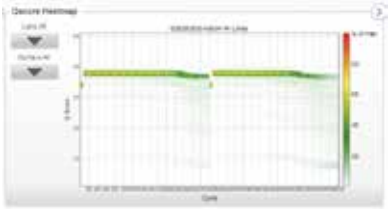
I. Genomic Analysis Platform

1. Ion Torrent Sequencers

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



2. Miseq Sequencer



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

3. C1 Single-Cell Preparation System

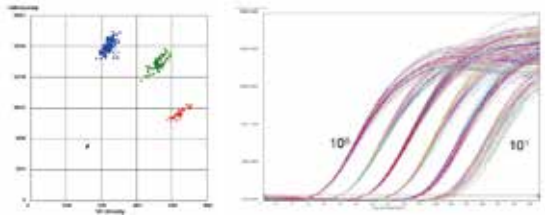
The C1 system enables cell capture, lysis, and preparation of individual cells for genomic applications. The system is an electrically and pneumatically operated desktop instrument. It has a built-in vacuum pump to hold the IFC in position. The embedded PC inside the system regulates all the functions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

4. Biomark HD Real-time PCR System

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

5. QuantStudio 12K Flex Real-Time PCR System

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

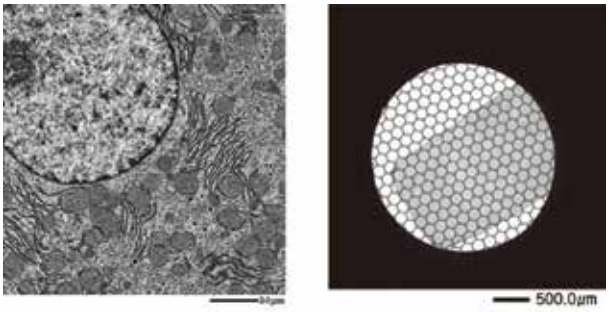


II. Proteomic Analysis Platform

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

III. Micro-imaging Analysis Platform

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



参加学术会议 (Attended Scientific Meetings)

序号	报告名称	报告人	会议名称	地点	会议时间
1	高原哺乳动物基因组及其生态适应	施鹏	2017 动物学前沿论坛	昆明	2 月 17 日
2	“ 定量 ” 代谢网络模拟新方法及在重度烧伤中的应用	李功华	第四届生物信息学会议	长沙	4 月 21-22 日
3	利用 Anti-HIV-Predictor 进行药物重定位和发掘新型抗 HIV 药物	代绍兴	第四届生物信息学会议	长沙	4 月 21-22 日
4	Outbred genome sequencing and CRISPR/Cas9 gene editing in butterflies	李学燕	The 4th Asia-Pacific Drosophila Research Conference (AP-DRC4)	日本	5 月 6 日 -5 月 13 日
5	全基因组水平揭示褐家鼠的起源和进化	吴东东	中国植物保护协会 2017 年度工作会议暨全国青年植保科技创新学术研讨会	杭州	6 月 28 日
6	SINO-BON Bird tracking in China	伍和启	Argos 野生动物追踪网络东亚地区第二届技术研讨会	韩国仁川	7 月 3-5 日
7	Mitochondrial Dna, Y-Chromosome and Mc1r Data Shed Light on Ancestry of Nigerian Indigenous Pig	Adeola, A. Charles	the 36th International Society for Animal Genetics Conference	爱尔兰都柏林	7 月 16-21 日
8	普洱 - 勐养亚洲象种群与当地居民冲突热点分析	黄程	亚洲象保护学术研讨会	景洪	8 月 12 日
9	西黑冠长臂猿近 30 年生境破碎化研究：至 2050 年在土地利用与气候变化的影响下的分布变化	程峰	中国动物学会灵长类学分会成立大会暨 2017 年学术年会	西安	8 月 19-22 日
10	西黑冠长臂猿行为对食物季节性变化的适应策略	宁文鹤	中国动物学会灵长类学分会成立大会暨 2017 年学术年会	西安	8 月 19-22 日
11	Low Genetic Diversity and Post-LGM Expansion of Assam Macaque (*Macaca assamensis*) in Foothills f Nepal Himalaya	Laxman Khanal	中国动物学会灵长类学分会成立大会暨 2017 年学术年会	西安	8 月 19-22 日
12	中国绿孔雀现状	杨晓君	第 14 届中国鸟类学大会暨第 12 届海峡两岸鸟类学术研讨会	西安	9 月 21-24 日
13	The genetic consequence of Quaternary climatic change on southern Asian birds	董锋	第 14 届中国鸟类学大会暨第 12 届海峡两岸鸟类学术研讨会	西安	9 月 21-24 日
14	狩猎、传统文化与鸟类多样性保护	吴飞	第 14 届中国鸟类学大会暨第 12 届海峡两岸鸟类学术研讨会	西安	9 月 21-24 日
15	百岁老人长寿基因研究	孔庆鹏	中国抗衰老科技与健康精准干预峰会	深圳	9 月 22-24 日
16	更新世气候变迁对于喜马拉雅山鸟类群落组成的影响	董锋	首届青藏高原动物多样性与适应进化研讨会	保定	9 月 25-27 日
17	西藏自治区鸟类多样性	伍和启	首届青藏高原动物多样性与适应进化研讨会	保定	9 月 25-27 日

18	Transcriptomic insights into the protective factors in Chinese centenarians	孔庆鹏	全国老年基础与转化医学论坛	深圳	10 月 12-15 日
19	TDP43 promotes progression of triple negative breast cancer in cooperation with SRSF3	焦保卫	第六届国际乳腺癌干细胞高峰论坛	湛江	10 月 14-15 日
20	两栖爬行类多样性与进化研究组进展	车静	中国动物学会两栖爬行动物学分会 2017 年学术研讨会	昆明	10 月 26-29 日
21	Selection and environmental adaptation along a path to speciation in the Tibetan frog Nanorana parkeri	张宝林	中国动物学会两栖爬行动物学分会 2017 年学术研讨会	昆明	10 月 26-29 日
22	Evolution of Asian metacarpal-tuberculed toads (Leptolalax)	陈进民	中国动物学会两栖爬行动物学分会 2017 年学术研讨会	昆明	10 月 26-29 日
23	Evaluating the effects of transposable element on the evolution of Protein-Coding Genes	孙艳波	中国动物学会两栖爬行动物学分会 2017 年学术研讨会	昆明	10 月 26-29 日
24	Peptide diversity in amphibian skins	郝雪	中国动物学会两栖爬行动物学分会 2017 年学术研讨会	昆明	10 月 26-29 日
25	Taxonomic revision of the genus Mesechinus (Mammalia: Erinaceidae) with description of a new species from Yunnan, China	陈中正	第十三届全国野生动物生态与资源保护学术研讨会暨第六届中国西部动物学学术研讨会	成都	10 月 27-30 日
26	Riverine Barrier Effects on Population Genetic Structure of Hanuman Langur in Nepal Himalaya	Laxman Khanal	第十三届全国野生动物生态与资源保护学术研讨会暨第六届中国西部动物学学术研讨会	成都	10 月 27-30 日
27	中国啮齿类一属、种新纪录	成市	第十三届全国野生动物生态与资源保护学术研讨会暨第六届中国西部动物学学术研讨会	成都	10 月 27-30 日
28	亚洲鼩鼱物种多样性与地理分布格局	万韬	第十三届全国野生动物生态与资源保护学术研讨会暨第六届中国西部动物学学术研讨会	成都	10 月 27-30 日
29	International Seminar of “Interdisciplinary & Frontier Research on Healthy Aging”	孔庆鹏	全国老年基础与转化医学论坛	深圳	11 月 10-11 日
30	几种腔道寄生原虫微氧环境适应的趋同进化	叶青青	中国动物学会原生动物学分会第十九次学术讨论会	广州	11 月 17-21 日
31	贾第虫一新种的发现及贾第虫宿主适应策略的探讨	吕章夏	中国动物学会原生动物学分会第十九次学术讨论会	广州	11 月 17-21 日
32	衣滴虫异养生长的形成机制	李毓劲	中国动物学会原生动物学分会第十九次学术讨论会	广州	11 月 17-21 日
33	卫星跟踪技术在黑颈鹤和水鸟保护中的应用	伍和启	第六届黑颈鹤保护网络年会	会泽	12 月 11-13 日
34	黑颈鹤夜栖地类型与分布	卢光义	第六届黑颈鹤保护网络年会	会泽	12 月 11-13 日
35	表观遗传学在家养动物驯化过程中的作用	周中银	学术交流	安徽	12 月 16 日
36	三代基因测序软件与人体微生物群系医学生态学	马占山	中科院生命和信息领域前沿交叉学术研讨会	深圳	12 月 26-27 日
37	iHuman: 人体数字模拟与精准医疗	李功华	中科院生命和信息领域前沿交叉学术研讨会	深圳	12 月 26-27 日

开放课题（Open Projects）

课题编号	负责人	职称	负责人单位	课题名称	资助经费（万元）
GREKF17-01	赵 卉	副研究员	云南大学	人 TBC1D8B 基因在癌症中的功能研究	10
GREKF17-02	郎大田	讲 师	昭通学院	鲸偶蹄目核糖核酸酶基因（RNASEA）超家族分子进化研究	10
GREKF17-03	何 德	副教授	西南林业大学	绿藻 FBPase 的分布及其与异养生长的进化	10
GREKF17-04	龚 理	助理研究员	浙江海洋大学	鲽形目鱼类系统发育基因组学研究	10
GREKF17-05	李 君	副主任医师	西藏阜康妇产儿童医院分院	解析藏族人群精子的遗传背景对青藏高原低氧极端环境中男性生殖能力的影响	10
GREKF17-06	石德利	教授	山东大学	ZC4H2 稳定 RNF220 的分子机制及其在神经发育中的功能研究	10
GREKF17-07	王 茉	中级	西南林业大学	爬鳅属、间吸鳅属和华平鳅属的系统进化和生物地理研究	10
GREKF17-08	郭玉红	副教授	贵州师范学院	钝头蛇科蛇类的分类和系统演化研究	10
GREKF17-09	袁 治	副主任医师	云南省第一人民医院	长寿人群口腔等微生物分布规律及模式研究	10
GREKF17-10	李 磊	研究员	中国科学院动物研究所	猴囊胚的体外培养和发育初探	10
GREKF17-11	易 斌	讲师	红河学院	微生物群落的生态位 — 中性混合效应研究	10
GREKF17-12	戴传银	副教授	贵州师范学院	捕捉和城市化对灰喉鸦雀种群遗传多样性的影响	10
GREKF17-13	朱 浩	研究员	南方医科大学	对进化与基因组印迹相互作用的初步分析	10
GREKF17-14	闫守庆	副教授	吉林大学	蓝狐高脂肪日粮适应的遗传基础研究	10
GREKF17-15	杨鸿波	副研究员	贵州省分析测试研究院	猛犸象与亚洲象的比较基因组学研究	10
				合计	150

邀请学术报告（Invited Lectures）

序号	邀请专家	单位	报告日期	报告题目
1	张国捷	University of Copenhagen, Denmark	3 月 27 日	From mutations to macroevolution,what we learned from biodiversity genomics
2	王旭	Cornell University, USA	4 月 11 日	Transcriptome and allele frequency responses to selection for tame/aggressive behaviors in silver foxes (vulpes vulpes)
3	和庆钢	浙江大学	4 月 26 日	F-18 标记芳香类 PET 分子探针的方法学研究进展
4	Su Zhengchang	University of North Carolina, USA	6 月 13 日	Comparative Differential Gene Expression in Oocyte-to-Embryo Transition in Mouse and Rat revealed by single-cell RNA-seq
5	Chun-Fang (Fanli) Xu	Pharmaceutical R&D	6 月 29 日	The application of genetics and genomics in drug discovery and development
6	Ru-gang Zhang	University of Pennsylvania, USA	7 月 12 日	Epigenetics, cancer and cellular senescence
7	金子兵	温州医科大学	7 月 13 日	重大致盲性眼病的遗传解析：Bed-To-Bench 研究
8	John-James Wilson	University of Guelph, Canada	7 月 19 日	Application of DNA barcodes in wildlife conservation in Tropical East Asia
9	汪兆琦	University of Jena, Germany	8 月 21 日	Epigenetic modulation of neuro(de)generation
10	Stefan Hendrik Foord	University of Venda, South Africa	10 月 9 日	Phylogenetic and functional perspectives on b-diversity: the case of spiders and ants along elevation
11	Christof Niehrs	Institute of Molecular Biology，Mainz，Germany	10 月 18 日	Novel regulators of Wnt-LRP6 signaling involved in embryonic development
12	Stephen Jackson	the University of New South Wales, Australia	10 月 26 日	Taxonomy of Australian Mammals
13	Olivier Hanotte	International Livestock Research Institute，University of Nottingham, UK	10 月 26 日	ILRI’s LiveGene program overview and research highlights
14	韩建林	International Livestock Research Institute，University of Nottingham, UK	10 月 26 日	Molecular insight on the domestication, dispersal and adaptation of sheep
15	Nabiev Loik Cangalievici	Academy of Sciences Institute of Zoology and Parasitology，Tajikistan	11 月 6 日	塔吉克斯坦野生动物资源和保护区现状、保护与利用
16	Najmudinov Tojiddin	Academy of Sciences Institute of Zoology and Parasitology，Tajikistan	11 月 6 日	塔吉克斯坦两栖和爬行动物资源现状、保护与利用
17	吴刘仓	昆明理工大学	11 月 7 日	偏 t 正态数据下联合位置、尺度与偏度模型的变量选择
18	李永昆	云南大学	11 月 21 日	生态系统的动力学分析
19	Herve Yesou	SERTIT, France	11 月 23 日	Exploiting satellite imagery for water bodies monitoring: Example of Poyang case

在读研究生及博士后
Graduate Students and Postdoctors

序号	导师姓名	硕士生	博士生	博士后
1	张亚平	汪轩，马成，许明敏，周其俊，伍胤桥，周博闻，刘露（安徽大学联培）	杨阳，胡靖扬，尹婷婷，曾琳，黄翠萍，李建波，吕梦蝶，王运梅，沈全宽，耿伟航，NEWTON OTIENO OTECKO，马云飞，HADI CHARATI，SABER KHEDERZADEH，DAVID HERIEL MAUKI，戴珊珊，黎武略，颜晨	倪刚
2	彭旻晟	Felista Kasyoka Kilunda，Said Ismail Nganga		
3	王国栋	林娜（安徽大学联培），张湘泉		
4	杨君兴	殷艳慧，牛诚祎，吴安丽	杨坤凤，张源伟，Marco Endruweit，杜丽娜，孙超	
5	车静	米雪，徐伟，余传鑫，徐凯，杨春华（安徽大学联培）	张宝林，陈进民，高伟，付婷婷，吴云鹤、张毅，LOTANNA MICAH NNEJI，MD MIZANUR RAHMAN	
6	焦保卫	郭璐，马玉洁，成美，杨旭，陈微（安徽大学联培），李玲玲（中科大联培）	柯浩，赵丽娜，徐海波，赵丽敏，杨星	
7	孔庆鹏	葛明侠，杨杏丽，董蕾，王昊天，郭荣慧，顾康蜀云	余琴，刘耀文，田娇阳，吴焕，江建军，夏王晓，李曼，ZIA UR RAHMAN	
8	毛炳宇	任碧玉（安徽大学联培），李雨薇，朱良	祁飞燕，张龙龙	
9	宿兵	周亚楠，黄俊，张栋秦，胡庭，孟晓宇，胡艳，周斌，曾雪芮	杨晏冬，罗鑫，和耀喜，姜瑾，袁佳妙，郑王山	
10	祁学斌	岳天		
11	王文	刘威，王宝，何金武	奎玲，向志丹，李永鑫，任彦栋，王筱，陈海涛，曾严	刘斌，吴江鸿，苏蕊
12	文建凡	邱兰，邓琪	吕章夏，薛敏，叶青青	
13	郑萍	孙春丽，李聪，李秀峰，宁雨琪，周漫漫（中科大联培），刘焱（中科大联培）	何大健，陈忠良，张伟道，李竞争，姜方洁	
14	马占山	李杰，李文迪，肖琬蒙	夏尧，李连伟	
15	施鹏	陈杰，郭媛婷，吴群富，雷孟龙，杨丽丽，雷青（苏州大学联培），华绒（苏州大学联培），杨陆	罗杰，郑智中，李媛媛，朱磊，张涛，刘奇，陈艳艳	
16	黄京飞	李慧娟，陈碧雯（苏州大学联培），徐婉	郑俊娟，王倩	
17	蒋学龙	牛晓炜，甘霖，于秋鹏，胡文强，成市（安徽师大联培），KENNETH OTIENO ONDITI	宋文宇，Laxman Khanal，李权，宁文鹤，黄程	陈顺德

18	Douglas W Yu	罗明洁	杨洋，王晓阳，蔡望	Sing Kong Wah
19	杨晓君	范闯，田天祺，黎思涵，何书航，陈逸林，袁兴海，JACINTA MURINGI MURIITHI，GLADYS NYAKERU KUNG'U	卢光义，单鹏飞，王继山，王洁	
20	吴东东	任小蝶	李明莉， ADEOLA OLUWAKEMI AYOOLA	郭兴

毕业研究生一览表（Students Graduated）

序号	姓名	专业	学位	导师姓名
1	张凯	动物学	博士	Douglas w Yu
2	刘家倩	遗传学	博士	黄京飞
3	陈中正	动物学	博士	蒋学龙
4	李肇天	动物学	博士	蒋学龙
5	张斌	动物学	博士	蒋学龙
6	Narayan Prasad KoJu	动物学	博士	蒋学龙
7	王晓雄	遗传学	博士	孔庆鹏
8	王晓磊	细胞生物学	博士	毛炳宇
9	刘晓亮	细胞生物学	博士	毛炳宇
10	许东明	遗传学	博士	施鹏
11	沈文菁	遗传学	博士	王文
12	刘力源	遗传学	博士	王文
13	李毓劲	细胞生物学	博士	文建凡
14	张煦	遗传学	博士	宿兵
15	林强	遗传学	博士	宿兵
16	刘杰伟	遗传学	博士	宿兵
17	王荣兴	动物学	博士	杨晓君
18	王明山	遗传学	博士	张亚平
19	吴宏	遗传学	硕士	张亚平
20	叶凌群	遗传学	硕士	张亚平
21	王鑫轶	细胞生物学	硕士	郑萍
22	李朝晖	细胞生物学	硕士	郑萍
23	郭琨	细胞生物学	硕士	郑萍
24	安三奇	遗传学	硕士	黄京飞
25	李文兴	生物学	硕士	黄京飞
26	杜宜青	动物学	硕士	蒋学龙
27	程峰	生物学	硕士	蒋学龙
28	冯旭	细胞生物学	硕士	焦保卫
29	樊萌萌	遗传学	硕士	马占山
30	王娅丽	遗传学	硕士	马占山

31	杜加诚	细胞生物学	硕士	毛炳宇
32	郭雨龙	遗传学	硕士	施鹏
33	张佳	遗传学	硕士	施鹏
34	罗天逊	动物学	硕士	王瑞武
35	生承晔	生物工程	硕士	王文
36	朱亚楠	遗传学	硕士	王文
37	黄海波	细胞生物学	硕士	文建凡
38	李敏	生物工程	硕士	宿兵
39	郑秋旸	动物学	硕士	杨君兴
40	芦方茹	生物工程	硕士	张亚平
41	宋娇娇	生物学	硕士	张亚平
42	班文赞	细胞生物学	硕士	郑萍

研究生优秀论文奖
（Outstanding Paper Awards for Graduate Students）

一等奖（6篇，影响因子≥9）：

The First prize (6, IF≥9)

李朝晖 Chaohui Li (Cell Research, IF12.393)

王鑫轶 Xinyi Wang (Genome Research, IF14.331)

曾 琳 Ling Zeng (Molecular Biology and Evolution, IF14.558)

曾 琳 Ling Zeng (Molecular Biology and Evolution, IF14.558)

Newton O.Otecko (Molecular Biology and Evolution, IF14.558，并列一作)

张伟道 Weidao Zhang (Cell Research, IF14.331，并列一作)

二等奖（1篇，6≤影响因子<9）：

The Second prize(1, 6≤IF<9)

和耀喜 Yaoxi He (Molecular Biology and Evolution, IF14.558，排名第三并列一作)

三等奖（7篇，4≤影响因子<6）：

The third prize(7, 4≤IF<6)

江建军 Jianjun Jiang (Epigenetics & Chromatin, IF4.464)

王晓雄 Xiaoxiong Wang(Oncotarget, IF5.415)

刘晓亮 Xiaoliang Liu(The Journal of Biological Chemistry, IF 4.403)

和耀喜 Yaoxi He (Molecular Biology and Evolution, IF14.558，排名第三并列一作)

余 琴 Qing Yu (Oncotarget, IF5.168，并列一作)

叶青青 Qingqing Ye (Scientific Reports, IF4.847)

和耀喜 Yaoxi He (American Journal of Hematology, IF5.275，并列一作)

说明：按申请先后顺序排列，影响因子按申请时公布的期刊五年平均影响因子为准

Note: Ordered by application date. The impact factors of the journalsare the journal's five-year average impact factor at the timeof application.

大事记 Major Events

（1）2017 年 1 月 12 日，由实验室蒋学龙研究员带领的研究团队与合作单位一起在昆明动物博物馆联合举办“命名白眉长臂猿新种 —— 高黎贡白眉长臂猿”的新闻发布会。

On Jan 12, 2017, the research team led by Prof. Xuelong Jiang and the co-agencies held a press conference entitled “Name a new White-Browed Gibbon, Skywalker hoolock gibbon" at the Kunming Museum of Zoology.

（2）2017 年 2 月 13 日，实验室参加生物和医学领域国家重点实验室评估综合评议，并最终获得“良好”。

On Feb 13, 2017, the Lab participated in the comprehensive evaluation of the state key laboratories in the fields of biology and medicine and finally got "good".

（3）2017 年 5 月 20 日，为贯彻落实习近平主席提出“科技创新、科学普及是实现创新发展的两翼，要把科学普及放在与科技创新同等重要位置”的重要指示，实验室在中科院昆明动物研究所“第十三届公众开放日”当天举办了科研成果海报展，用二十多个主题的海报及知识问答方式向市民们科普了实验室的科研成果。科普展活动也通过“央视新闻”网络平台进行了直播。

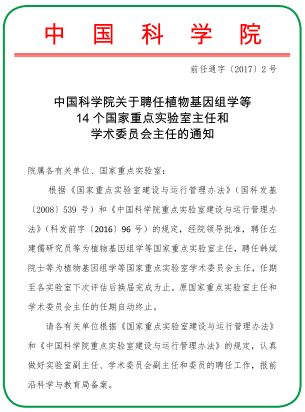
On May 20, 2017, in order to implement President Xi Jinping’s important directive on “science and technology innovation and popularization of science are the two wings of realization of innovation and development, putting the importance of science popularization as scientific and technological innovation, we held a popular science exhibition with more than 20 scientific research achievement posters on the day of “the Thirteenth Public Open Day”of the Kunming Institute of Zoology(KIZ), the Chinese Academy of Sciences(CAS). The exhibition was also broadcast live online through network platform of CCTV.

（4）继 2016 年成功举办 10 期青年学者论坛后，2017 年 5 月 26 日，重点实验室举行 2017 年“纳瑞杯”遗传资源与进化青年学者论坛第一场报告会，之后，每月 1 期，共计 10 期的论坛极大地促进了实验室内外的学术交流与合作。

After the success of holding 10 youth scholars forums in 2016, the key lab held the first forum of the 2017 ‘NARI Cup’ youth scholars forums about Genetic Resources and Evolution on May 26, 2017. Then, a total of 10 forums were held once a month a time, greatly promoting academic exchanges and cooperation both inside and outside the key lab.

（5）2017 年 6 月 12 日，实验室召开 2017 年战略研讨会。
The strategic meeting of the key lab was held on June. 12, 2017.

（6）2017 年 7 月 21 日，经研究所推荐，主管部门中国科学院聘任张亚平院士担任实验室新一届学术委员会主任，聘任施鹏研究员担任实验室主任。之后，由研究所聘任并组建了实验室第三届学术委员会及新一届领导班子。
On July 21, 2017, as recommended by KIZ, the CAS appointed Academician Yaping Zhang as the director of the new Academic Committee of the key lab, and appointed Prof. Peng Shi as the key lab's director. Then KIZ appointed and set up the third academic committee and the new leader team of the key lab.



中 国 科 学 院

前任通字（2017）2 号

中国科学院关于聘任植物基因组学等
14 个国家重点实验室主任和
学术委员会主任的通知

院属各有关单位、国家重点实验室：

根据《国家重点实验室建设与运行管理办法》（国科发基〔2008〕539 号）和《中国科学院重点实验室建设与运行管理办法》（科发前字〔2016〕96 号）的规定，经院领导批准，聘任左建儒研究员等为植物基因组学等国家重点实验室主任，聘任韩斌院士等为植物基因组学等国家重点实验室学术委员会主任，任期至各实验室下次评估后换届完成为止。原国家重点实验室主任和学术委员会主任的任期自动终止。

请各有关单位根据《国家重点实验室建设与运行管理办法》和《中国科学院重点实验室建设与运行管理办法》的规定，认真做好实验室副主任、学术委员会副主任和委员的聘任工作，报前沿科学与教育局备案。

张亚平院士
Academician Yaping Zhang

施鹏研究员
Prof. Peng Shi

（7）2017 年 7 月 17-7 月 22 日，实验室与所研究生部在昆明联合举办 “2017 年进化生物学暑期班 ”。
On July 17-22, 2017, the Evolutionary Biology Summer Course was held in Kunming organized by the key lab and the Office of Postgraduate Affairs of KIZ.

（8）2017 年 6 月 -9 月，实验室组织了由 4 个研究组参与的考察团队参加了中国科学院第二次青藏高原综合科学考察。
From June to September 2017, the key lab actively organized a team of four research groups to participate in the second comprehensive scientific investigation of the Tibetan Plateau organized by CAS.

（9）2017 年 10 月 26-29 日，由实验室主要承办的中国动物学会两栖爬行动物学分会 2017 年学术研讨会在昆明圆满举行。
On Oct 26 -29, 2017, the 2017 Symposium of Chinese Herpetological Society hosted by the key lab was successfully held in Kunming.

（10）2017 年 12 月 2 日，由盛能印研究员负责的“神经突触机制与功能研究组”加入实验室。
The research group called“Synaptic Function and Mechanism group” leading by Prof. Nengying Sheng joined the key lab on Dec 2, 2017.

（11）2017 年 12 月，由张国捷研究员负责的“生物多样性基因组学研究组”作为客座研究组加入实验室。
The Guest research group called“Biodiversity Genomics group” leading by Prof. Guojie Zhang joined the key lab in December, 2017.

工作人员名单 （Staff）

（按姓氏笔画排序）

研究组长 (PI)

Douglas W Yu	马占山	孔庆鹏	文建凡	毛炳宇	王 文
车 静	张亚平	张国捷	吴东东	杨君兴	杨晓君
佴文惠	郑 萍	施 鹏	宿 兵	黄京飞	盛能印
焦保卫	蒋学龙				

其他工作人员

丁 果	万 韬	卫小娟	马鹏程	王 林	王林（郑萍组）
王 洁	王 慧	王文智	王运宇	王国栋	王明山
王金焕	王洪娇	王荣兴	王晓爱	石 磊	代绍兴
田航宇	叶雅馨	朱建国	朱春玲	伍和启	刘 振
刘 倩	刘 衡	刘贵春	刘淑伟	刘鹤群	许东明
祁学斌	许绍斌	孙艳波	苏伟婷	李玉春	李功华
李学友	李学燕	李宗煦	李桂梅	李朝翠	李春梅
李毓劲	李兴统	汪嘉欣	杨 钦	杨 晖	杨双娟
杨滨宇	杨利琴	杨春燕	杨敏敏	肖富辉	时晓菲
吴 飞	吴世芳	吴春莹	何 锴	何水旺	何永捍
余 蕊	余国华	邹 丽	闵 锐	张 慧	张业胜
张志刚	张 洋	张洪磊	张栋儒	张晓明	张浩淼
陈 兵	陈小琼	陈中正	陈宏满	邵 永	邵静茹
岩 道	季吟秋	金洁琼	周中银	周炜帏	郑兰平
赵 博	赵亚鹏	赵 洁	赵若苹	赵士萍	郝军军
饶定齐	高 云	高建云	徐 沙	郭 琨	郭 彦
唐 嘉	浦绍艳	常云艳	彭 云	彭 忆	彭旻晟
黄岩淦	董 锋	董志巍	蒋万胜	韩徐曼	程乐华
舒树森	谢海兵	廖爱文	熊子军	潘晓赋	

2017 ANNUAL REPORT

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遗传资源与进化国家重点实验室

State Key Laboratory of Genetic Resources and Evolution

2017年报

遗传资源与进化国家重点实验室

中国科学院昆明动物研究所

云南省昆明市教场东路32号

邮编：650223

实验室主页：http://www.kiz.cas.cn/gre/

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