



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

# 2016 年报

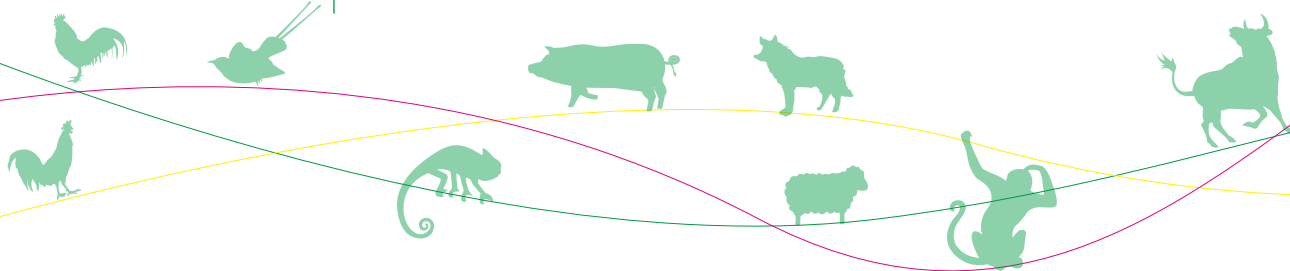
## ANNUAL REPORT



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

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## 主任致辞

2016年是“十三五”规划的开局之年，也是五年一度的实验室评估之年。遗传资源与进化国家重点实验室在各级主管部门的领导与关怀下，立足于我国西南和东南亚丰富的生物多样性遗传资源，面向战略生物资源的国家需求和世界科技前沿，继续团结奋进、协力创新，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。

在科研项目方面，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96项，包括国家自然科学基金重大研究计划1项，国家自然科学基金委国际(地区)合作与交流项目2项，中国科学院境外机构建设项目2项，中科院前沿重点研究项目1项。目前在研省部级项目229项，国际合作项目14项，横向协作项目28项。年度到位科研经费8046万元。在致力于基础研究的同时，实验室也积极面向国家和地区的战略与发展需求，加强技术的创新与推广应用，例如建立了中科院西南家猪育种基地，将生命条形码技术应用于战略生物资源鉴定与保护、食品溯源等。

在科研成果方面，实验室在科研项目的支持下，围绕三大研究方向，继续在遗传资源收集保护、家养动物的起源与驯化、动植物重要经济性状功能基因挖掘、动物适应性进化机制等方面开展持续深入、系统的研究。2016年发表SCI论文155篇(JCR一区论文95篇)，以第一作者或通讯作者(含并列)发表SCI论文110篇，包括发表在*Nature Genetics*(2篇)，*Systematic Biology*，*PNAS*，*Molecular Biology and Evolution*，*Nature Communication*等 $IF_{5\text{-year}} > 9$ 的国际著名期刊论文16篇。另授权发明专利11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。2人入选国家“万人计划”领军人才；1人荣获国家自然科学基金“优秀青年基金”资助；国家自然科学基金创新研究群体获得延续资助；此外，新引进青年博士5名。研究生培养方面，为国家输送博士18名，硕士10名。1人荣获中科院院长奖学金特别奖。此外，实验室还成功举办2016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。举办国际会议“家犬基因组学术峰会”，进一步推动世界范围的大型国际合作计划“万犬基因组计划”项目；举办第一届进化遗传青年科学家论坛，促进国内进化遗传领域青年科学家交流合作；协办了第八届世界两栖爬行动物学大会，产生了重要的国际影响。此外，邀请27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。

实验室认真准备并参加了科技部组织的对生命科学领域国家重点实验室的五年一次的评估，向评估专家组全面地汇报了过去五年的工作与取得的成绩。

潮平岸阔催人进，风正扬帆正当时！新的五年评估周期已经开始，实验室将在过去的工作基础上，继续团结一致、砥砺前行！力争为我国“十三五”发展中做出更大的贡献。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！

张亚平



## Director's Report

The “State Key Laboratory of Genetic Resources and Evolution” made considerable progress in 2016, with regards to grant awards, scientific research output, talent recruitment and scientific exchange.

**Grant awards.** - The Lab was awarded 96 new grants in 2016, including one Major Research Plan and two International (Regional) Cooperation and Exchanges Programs funded by National Natural Science Foundation, two International Institutions Construction Projects, and one Frontier Key Program of Chinese Academy of Sciences. Currently the Lab holds 229 ministerial and provincial projects, 14 international cooperation projects and 28 horizontal collaboration projects. The grant funds of the Lab totaled 80.46 million RMB. In addition to basic research, the Lab also promoted applied researches including established a Southwest pig breeding base of Chinese Academy of Sciences, and application of DNA-barcoding technology in protection of strategic biological resources and tracing of food sources.

**Publications and Awards.** - The Lab also made systematic progress in genetic resources collection, adaptive evolution, the mining of important phenotypic genes of economical plants and animals, and animals adaptive evolutionary mechanism in 2016. The Lab published in total 155 papers in SCI journals (95 of them are in Q1), including 16 papers in top journals ( $IF_{5\text{-year}} > 9$ ) such as *Nat Genet*, *Syst Biol*, *Mol. Biol. Evol.*, *PNAS*, *Nat. Commun* etc. Besides, eleven invention patents were authorized.

**Talent recruitment.** - In 2016, Prof. Peng Shi and Qingpeng Kong were selected into Ten Thousand Talent Program. Prof. Jing Che was funded by NSFC Excellent Youth Science Foundation. And the Creative Research Groups headed by Prof. Wen Wang was renewed by NSFC. Five young doctors were recruited. Eighteen Ph.D. and 10 M.Sc. students graduated from the Lab in 2016. Mingshan Wang won the Chinese Academy of Sciences Dean Scholarship Special Award. In addition, the “Evolutionary Biology” Summer School was successfully held in July, attracting many young people to join the Lab. The Lab also successfully held 10 series of the “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 2016, the Lab continued to follow the principle of “promoting communication for cooperation” to promote academic exchanges and cooperation at home and abroad. We held “The Academic Summit of Dog Genomes” to promote the World Wide-Scale International Cooperation Program “DOG 10K” project, held the first Young Scientists Forum on Evolutionary Genetic, and co-organized the 8th World Congress of Herpetology (WCH8). Twenty-seven scholars were invited to visit the Lab and to give lectures this year for scientific exchange and co-operation. In 2016, the Lab also funded 15 “open projects” to promote cooperation with scholars in related fields.

In 2016, the Lab participated in the assessment of the State Key Laboratories in the field of life science organized by MOST. The new five-year assessment period has already begun, and 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!

Yaping Zhang



## 实验室概况 Laboratory Overview

### 一、第二届学术委员会 (The Second Academic Committee)

#### 主任 (Director):

朱作言 院士, 北京大学  
Academician Zuoyan Zhu, Peking University

#### 副主任 (Deputy director):

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

#### 委员 (Members, 按姓氏笔画排序):

文建凡 研究员, 中国科学院昆明动物研究所  
Prof. Jianfan Wen, Kunming Institute of Zoology, Chinese Academy of Sciences  
朱有勇 院士, 云南农业大学  
Academician Youyong Zhu, Yunnan Agricultural University  
李德铤 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  
张亚平 院士, 中国科学院  
Academician Yaping Zhang, Kunming Institute of Zoology, 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  
康 乐 院士, 中国科学院动物研究所  
Academician Le Kang, Institute of Zoology, Chinese Academy of Sciences  
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  
黄路生 院士, 江西农业大学  
Academician Lusheng Huang, Jiangxi Agricultural University  
黄京飞 研究员, 中国科学院昆明动物研究所  
Prof. Jingfei Huang, Kunming Institute of Zoology, Chinese Academy of Sciences

### 二、现任实验室领导 (Leader of the Lab.)

#### 主任 (Director):

张亚平 院士 Academician Yaping Zhang

#### 常务副主任 (Executive Deputy director)

施 鹏 研究员 Prof. Peng Shi

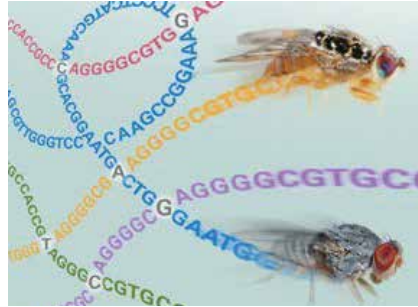
**副主任 (Deputy director):**

文建凡 研究员 Prof. Jianfan Wen  
毛炳宇 研究员 Prof. Bingyu Mao

**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

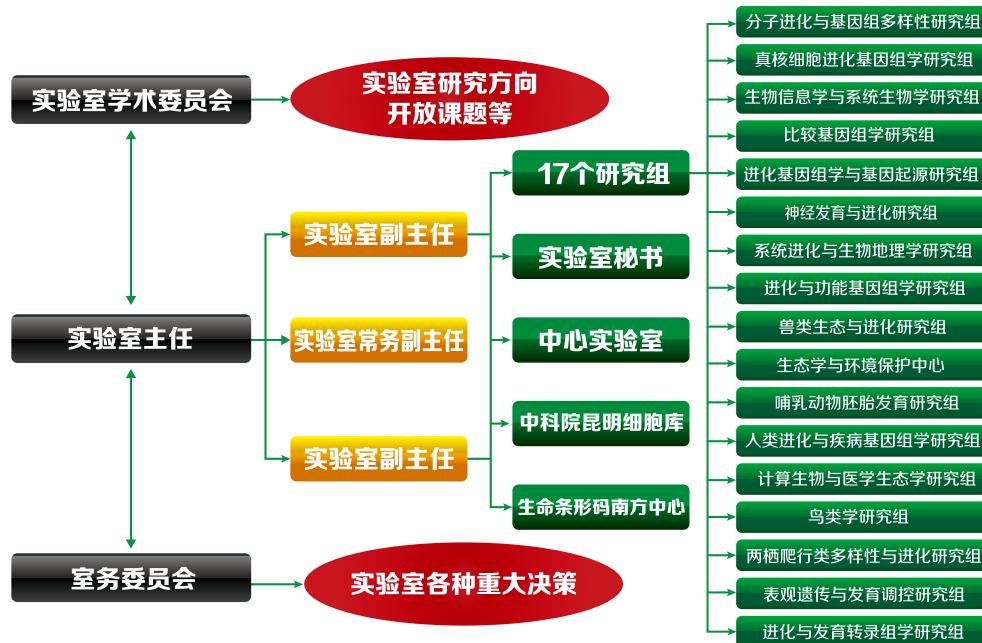


遗传发育与进化  
Genetics, development and evolution

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

实验室有研究组 17 个，支撑部门 3 个，现有固定人员 119 人，其中博士 67 人，平均年龄 35 岁。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，国家“万人计划”领军人才 3 人，青年千人计划 1 人，中科院“百人计划”7 人，云南省“高端人才”5 人。

There are 17 research groups and 3 facility centers in the key lab. Among the 119 staff members, 67 of them hold Ph.D. degrees. The average age of the team is 35 years old. 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 “Ten Thousand Talent Program”, 1 holder of “Thousand Talent Program for Young Outstanding Scientists”, 7 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

蛙属生物地理和物种分化研究中取得新进展

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 DOI:10.1093/sysbio/syw005  
 Advance Access publication June 10, 2016

Spatiotemporal Diversification of the True Frogs (Genus *Rana*): A Historical Framework for a Widely Studied Group of Model Organisms

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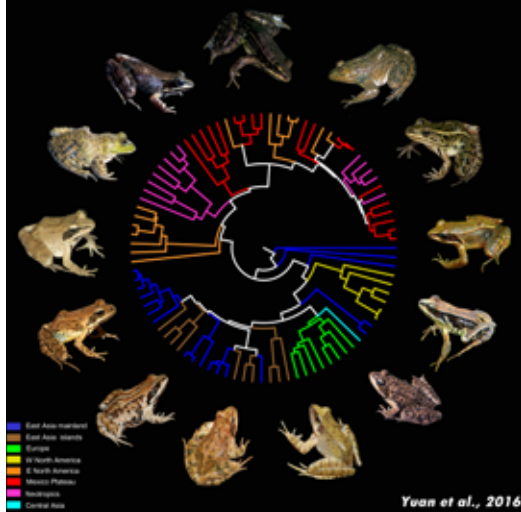
The first three authors share equal first authorship.

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 Associate Editor: Richard Glor

**Abstract.**—True frogs of the genus *Rana* are widely used as model organisms in studies of development, genetics, physiology, ecology, behavior, and evolution. Comparative studies among the more than 100 species of *Rana* rely on an understanding of the evolutionary history and patterns of diversification of the group. We estimate a well-resolved, time-calibrated phylogeny from sequences of six nuclear and three mitochondrial loci sampled from most species of *Rana*, and use that phylogeny to clarify the group's diversification and global biogeography. Our analyses consistently support an "Out of Asia" pattern with two independent dispersals of *Rana* from East Asia to North America via Beringian land bridges. The more species-rich lineage of New World *Rana* appears to have experienced a rapid radiation following its colonization of the New World, especially with its expansion into montane and tropical areas of Mexico, Central America, and South America. In contrast, Old World *Rana* exhibit different trajectories of diversification; diversification in the Old World began very slowly and later underwent a distinct increase in speciation rate around 29–18 Ma. Net diversification is associated with environmental changes and especially intensive tectonic movements along the Asian margin from the Oligocene to early Miocene. Our phylogeny further suggests that previous classifications were misled by morphological homoplasy and plesiomorphic color patterns, as well as a reliance primarily on mitochondrial genes. We provide a phylogenetic taxonomy based on analyses of multiple nuclear and mitochondrial gene loci. [Amphibians; biogeography; diversification rate; Holarctic; transcontinental dispersal.]

SPATIOTEMPORAL DIVERSIFICATION OF THE TRUE FROGS

Systematic Biology  
 Advance Access  
 published June 10, 2016



分子系统学的一个发展方向是完整地重建一些世界广布的重要类群的进化关系。蛙属 *Rana* 是广泛分布于亚洲、欧洲和美洲并倍受关注的模式类群。车静研究组牵头联合多个国家、地区十余位学者，通过合作研究，第一次在全球尺度上完整构建了蛙属物种的系统演化历史。研究发现该类群起源于中国西南地区，从东亚经白令海峡两次独立进入北美，其中一支后迁入中、南美地区。后期，从东亚经中亚，进入欧洲地区。新、旧大陆在蛙属物种多样性分化方面存在较大差异。该研究通过多物种类群的比较研究支持两爬物种北半球洲际扩散的普通模式——“跨白令海峡陆桥”假说，同时发现与森林植物研究类似，“走出亚洲”模式在两爬物种中较为普遍。该研究成果目前发表在 *Systematic Biology*。

研究方向一：遗传资源多样性的演化与保护

代表性成果二

群体遗传学模型分析得出脊椎动物近期快速群体数量下降

## Large numbers of vertebrates began rapid population decline in the late 19th century

Haipeng Li<sup>a,h,1</sup>, Jinggong Xiang-Yu<sup>h,1</sup>, Guangyi Dai<sup>b</sup>, Zhili Gu<sup>b</sup>, Chen Ming<sup>b,c</sup>, Zongfeng Yang<sup>b,c</sup>, Oliver A. Ryder<sup>d</sup>, Wen-Hsiung Li<sup>a,e,2</sup>, Yun-Xin Fu<sup>b,h,2</sup>, and Ya-Ping Zhang<sup>a,c,9,2</sup>

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Contributed by Wen-Hsiung Li, October 12, 2016 (sent for review July 22, 2016; reviewed by William J. Murphy and Jianzhi Zhang)

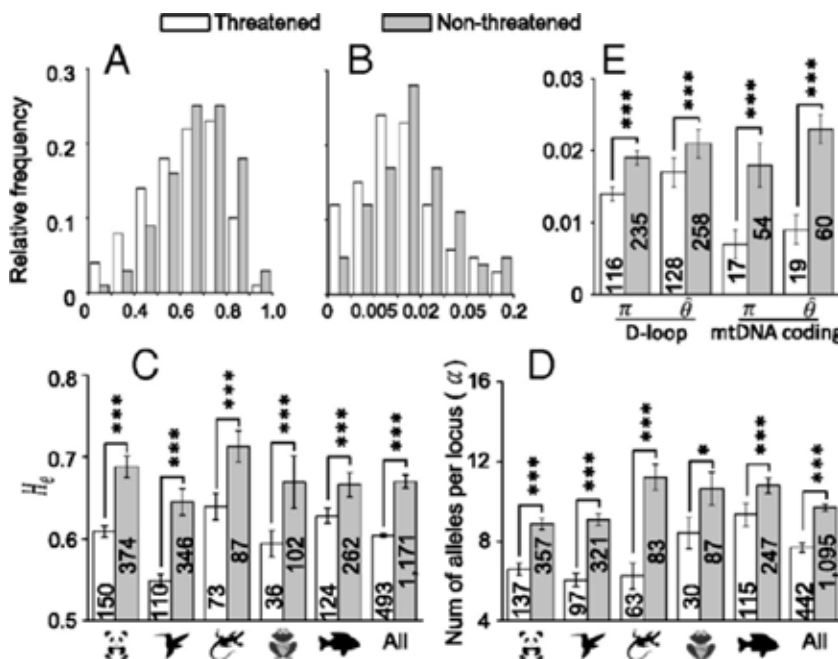
Accelerated losses of biodiversity are a hallmark of the current era. Large declines of population size have been widely observed and currently 22,176 species are threatened by extinction. The time at which a threatened species began rapid population decline (RPD) and the rate of RPD provide important clues about the driving forces of population decline and anticipated extinction time. However, these parameters remain unknown for the vast majority of threatened species. Here we analyzed the genetic diversity data of nuclear and mitochondrial loci of 2,764 vertebrate species and found that the mean genetic diversity is lower in threatened species than in related nonthreatened species. Our coalescence-based modeling suggests that in many threatened species the RPD began ~123 y ago (a 95% confidence interval of 20–260 y). This estimated date coincides with widespread industrialization and a profound change in global living ecosystems over the past two centuries. On average the population size declined by ~25% every 10 y in a threatened species, and the population size was reduced to ~5% of its ancestral size. Moreover, the ancestral size of threatened species was, on average, ~22% smaller than that of nonthreatened species. Because the time period of RPD is short, the cumulative effect of RPD on genetic diversity is still not strong, so that the smaller ancestral size of threatened species may be the major cause of their reduced genetic diversity; RPD explains 24.1–37.5% of the difference in genetic diversity between threatened and nonthreatened species.

a significant depletion of available habitats and resources. Consequently, we were able to draw conclusions based on present-day polymorphism data from a large number of threatened species and their nonthreatened relatives. Our method is depicted in Fig. 1. Here we studied RPD in vertebrates, because vertebrates have been more extensively investigated in the past. However, our conclusions should have some generality because vertebrate species live in a wide range of ecosystems. Moreover, the proposed method is also suitable for studying nonvertebrate species.

**Results and Discussion**

**Data Collected.** We reviewed more than 10,000 peer-reviewed papers published in the last two and half decades, among which ~2,500 papers in 164 scientific journals were found to have surveyed the genetic diversity of at least one vertebrate species. The level of genetic diversity was measured with one of the following summary statistics (9): the expected and observed heterozygosity ( $H_e$  and  $H_o$ ), the number of alleles per locus ( $a$ ) at the microsatellite loci, Watterson's  $\theta_w$  (10), and the mean number of nucleotide differences per nucleotide site between two mitochondrial sequences ( $\alpha$ ). The collected dataset includes 2,764 vertebrate species belonging to 1,466 genera and 465 families (Fig. 2). Then, we used the International Union for Conservation of Nature (IUCN) Red List categories (3)

PNAS | December 6, 2016 | vol. 113 | no. 49 | 14079–14084



全球许多物种的群体数量正在大幅下降，甚至有许多物种在野外乃至地球上就已经消失了。这一群体数量的快速下降是什么时候开始的？这对于解答物种濒危的原因极为重要。张亚平组使用原创的群体遗传学模型，分析了2,764种脊椎动物的遗传多样性数据，发现濒危脊椎动物的群体数量的快速下降始于19世纪末期，为19世纪工业化扩张导致的物种数量大幅减少和群体数量快速下降等全球范围的生态环境恶化提供了遗传学方面的证据。被PNAS选为当期亮点推荐，Washington Post等对此做了专题报道。



## 研究方向一：遗传资源多样性的演化与保护

## 代表性成果三

## 揭示家鸡视觉退化的无意识选择作用机制

ORIGINAL ARTICLE

Cell Research (2016) :1-18.

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## Positive selection rather than relaxation of functional constraint drives the evolution of vision during chicken domestication

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As noted by Darwin, chickens have the greatest phenotypic diversity of all birds, but an interesting evolutionary difference between domesticated chickens and their wild ancestor, the Red Junglefowl, is their comparatively weaker vision. Existing theories suggest that diminished visual prowess among domestic chickens reflect changes driven by the relaxation of functional constraints on vision, but the evidence identifying the underlying genetic mechanisms responsible for this change has not been definitively characterized. Here, a genome-wide analysis of the domestic chicken and Red Junglefowl genomes showed significant enrichment for positively selected genes involved in the development of vision. There were significant differences between domestic chickens and their wild ancestors regarding the level of mRNA expression for these genes in the retina. Numerous additional genes involved in the development of vision also showed significant differences in mRNA expression between domestic chickens and their wild ancestors, particularly for genes associated with phototransduction and photoreceptor development, such as *RHO* (rhodopsin), *GUCY1A1*, *PDE6B* and *NR2E3*. Finally, we characterized the potential role of the *VIT* gene in vision, which experienced positive selection and downregulated expression in the retina of the village chicken. Overall, our results suggest that positive selection, rather than relaxation of purifying selection, contributed to the evolution of vision in domestic chickens. The progenitors of domestic chickens harboring weaker vision may have showed a reduced fear response and vigilance, making them easier to be unconsciously selected and/or domesticated.

**Keywords:** chicken domestication; unconscious selection; genome evolution; evolution of vision

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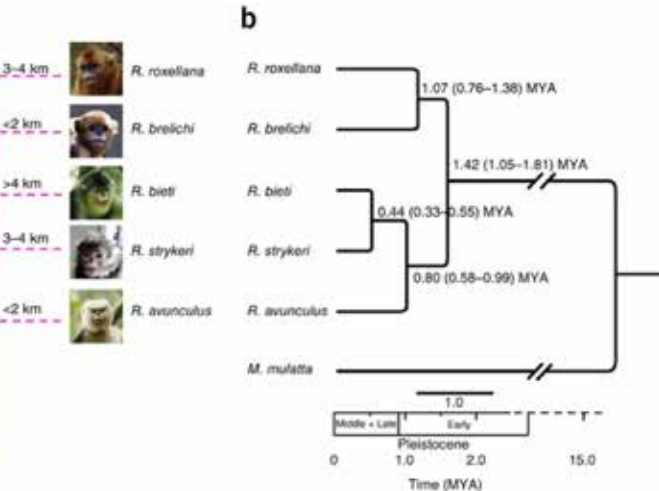
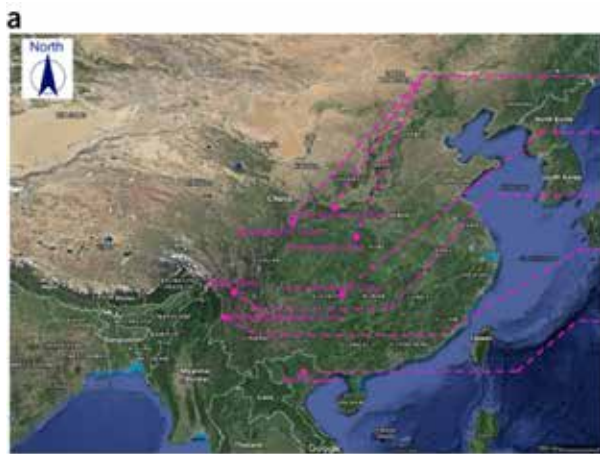
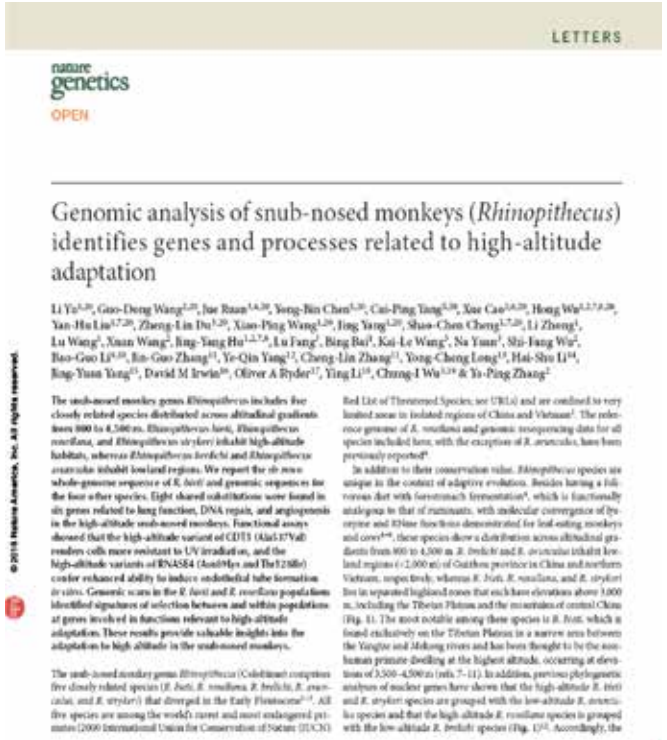
经过长期的驯化和人工选择作用，家鸡的视觉功能显著退化，但是其遗传机制并不清楚。我们基于家鸡和红原鸡的基因组和转录组数据，分析发现正选择而非选择压力放松促使家鸡视觉退化，正选择可能通过影响视网膜中基因的表达来影响家鸡视觉的退化。研究人员推测早期人们对家鸡的视觉的选择是种无意识的选择，视觉退化的鸡更加有利于驯化和饲养管理。此研究成果为无意识选择在家养动物驯化中的重要作用提供了一个有趣的范例。另外，该项工作也发现了一个新的视觉相关基因 *VIT*，为视觉相关进化、疾病的研究提供新的靶点。成果发表于 Cell Research。



研究方向二：基因与基因组进化

代表性成果一

基因组研究揭示金丝猴属物种高海拔适应遗传机制



张亚平组和云南大学于黎课题组，中科院昆明动物研究所陈勇斌课题组、芝加哥大学吴仲义教授课题组和北京基因组所强强联合，成立联合攻关团队，对金丝猴属物种高海拔环境适应遗传机制开展研究。

本研究基于多层次研究，包括种上和群体的基因组序列分析，转录组和功能实验，发现与金丝猴物种适应高海拔环境相关的遗传机制。以非人灵长类为研究模型，为高海拔适应这一复杂性状提供一个新的和更全面的揭示。研究结果发表在 Nature Genetics。

研究方向二：基因与基因组进化

代表性成果二

在家犬起源迁徙研究中取得进展

Open  
ORIGINAL ARTICLE

Cell Research (2016) 26:21-33  
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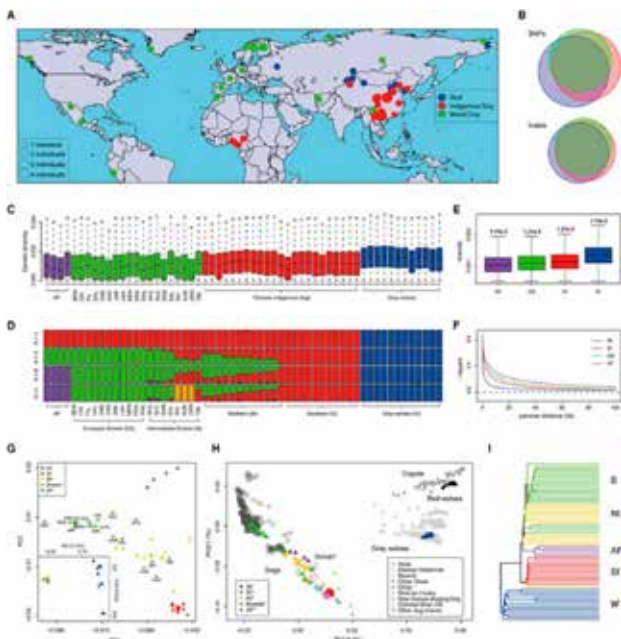
Out of southern East Asia: the natural history of domestic dogs across the world

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The origin and evolution of the domestic dog remains a controversial question for the scientific community, with basic aspects such as the place and date of origin, and the number of times dogs were domesticated, open to dispute. Using whole genome sequences from a total of 58 canids (12 gray wolves, 27 primitive dogs from Asia and Africa, and a collection of 19 diverse breeds from across the world), we find that dogs from southern East Asia have significantly higher genetic diversity compared to other populations, and are the most basal group relating to gray wolves, indicating an ancient origin of domestic dogs in southern East Asia 33 000 years ago. Around 15 000 years ago, a subset of ancestral dogs started migrating to the Middle East, Africa and Europe, arriving in Europe at about 10 000 years ago. One of the out of Asia lineages also migrated back to the east, creating a series of admixed populations with the endemic Asian lineages in northern China before migrating to the New World. For the first time, our study unravels an extraordinary journey that the domestic dog has traveled on earth.

**Keywords:** dog domestication; demography; Chinese indigenous dog; gene flow; artificial selection  
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灰狼是在何时何地、经过何种方式被人类所驯化，这些问题一直是科学家们研究的热点问题，也是领域内许多科学家们争论的焦点问题。张亚平院士课题组利用二代测序技术，对采自世界各地的 12 只灰狼、27 只土狗和 19 只不同品种犬进行了全基因组测序，利用群体遗传学的各种手段对家犬的遗传多样性、群体结构和群体历史等进行了深入研究。根据对这些结果的分析研究人员推断，家犬是在 3 万 3 千年前左右开始在东亚的南部地区逐渐被人类驯化。家犬在这一地区与人类共同生活了几千年后，于 1 万 5 千年前开始向中东、非洲和欧洲等地迁徙扩散，并在 1 万年前左右到达欧洲地区。其后，这些迁徙出亚洲的家犬群体中的一个支系又向东迁徙，在东亚北部与当地家犬群体杂交形成了一系列混合群体。并在其后随人类迁往美洲地区。这一工作采用极为丰富的家犬基因组测序数据，首次揭示了家犬扩散到世界各地的迁徙路线。由于人类与家犬间绝无仅有的跨物种的密切关系，这一家犬群体历史的研究也为人们了解人类过去的社会活动和迁徙历史提供了参考材料。 研究结果发表在 Cell Research。



研究方向二：基因与基因组进化

代表性成果三

发现了动物适应性进化的第二套基因组学机制

Current Biology  
Report



Convergent Evolution of Rumen Microbiomes in High-Altitude Mammals

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<http://dx.doi.org/10.1016/j.cub.2016.05.012>

**SUMMARY**  
 Studies of genetic adaptation, a central focus of evolutionary biology, most often focus on the host's genome and only rarely on its co-evolved microbiome. The Qinghai-Tibetan Plateau (QTP) offers one of the most extreme environments for the survival of human and other mammalian species. Yaks (*Bos grunniens*) and Tibetan sheep (*Ovis montanus*) have adaptations for living in this harsh high-altitude environment, where nomadic Tibetan people keep them primarily for food and livelihood [1]. Adaptive evolution affects energy-metabolism-related genes in a way that helps these ruminants live at high altitude [2, 3]. Herein, we report convergent evolution of rumen microbiomes for energy harvesting persistence in two typical high-altitude ruminants, yaks and T-sheep. Both ruminants yield significantly lower levels of methane and higher yields of volatile fatty acids (VFAs) than their low-altitude relatives, cattle (*Bos taurus*) and ordinary sheep (*Ovis aries*). Ultra-deep metagenomic sequencing reveals significant enrichment in VFA-yielding pathways of rumen microbial genes in high-altitude ruminants, whereas methanogenesis pathways show enrichment in the cattle metagenome. Analyses of RNA transcriptomes reveal significant upregulation in 36 genes associated with VFA transport and absorption in the ruminal epithelium of high-altitude ruminants. Our study provides novel insights into the contributions of microbiomes to adaptive evolution in mammals and sheds light on the biological control of greenhouse gas emissions from livestock enteric fermentation.

**RESULTS AND DISCUSSION**  
**Low-Methane and High-VFA Production in High-Altitude Ruminants**  
 We hypothesized that adaptive evolution occurs in cohabiting microbiomes of high-altitude mammals, especially in ruminants, because they extend host metabolic repertoire [4–6]. For instance, volatile fatty acids (VFAs; primarily acetic, propionic, and butyric acids) supplied by rumen microbes lead to energy gain [7]. By contrast, methane, a byproduct of rumen fermentation by methanogenic archaea, causes energy loss [1]. To test this hypothesis, we first measured methane emissions and VFA production, both of which are largely produced by rumen microbes. Using controlled *in vitro* gas production experiments [12] with the same amount of oat hay (*Avena sativa*) as the fermentation substrate, we compared methane emissions and VFA production from yaks and cattle (Figure 1A and 1B). Yaks produce significantly ( $p < 0.04$ ) 1.1-fold more total VFAs (TVFAs) than cattle, especially for acetate ( $p < 0.01$ ), propionate ( $p < 0.05$ ), and butyrate ( $p < 0.001$ ) (Figure 1C). Independent *in vitro* experiments involving 72 hr incubation validate these observations (study 2). After 12 hr incubation, cattle produce significantly ( $p < 0.001$ ) 1.1-fold more methane than yaks, although the increase in rate of methane emission slows after 48 hr (Figure 2A). Similarly, yaks produce significantly ( $p < 0.001$ ) 1.1-fold more VFAs after 72 hr incubation than cattle (Figure 2B). These results coincide with previous *in vivo* observations [13, 14]. Compared with other similar studies from different cattle strains, yaks produce less methane and more TVFAs (Figure 2C), suggesting that an observable production of both low methane and high VFAs has been found in yaks after they split from the common ancestor of cattle.  
 To determine whether our observations for the yak are typical of high-altitude ruminants, we repeated 48 hr *in vitro* experiments using Tibetan sheep (T-sheep) at 3,500 m and ordinary sheep

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施鹏组与北京生命科学研究院以及兰州大学的相关研究人员组成联合研究团队在动物适应性进化领域取得重大突破。该联合团队发现了动物适应高原极端环境过程中宿主和微生物组的协同进化,是同域哺乳动物适应进化的必然选择之一。另外,发现的低甲烷排放的高海拔哺乳动物,为进一步通过生物调控策略缓解其他动物排放甲烷引起的温室效应具有重要的现实意义。2016年7月,相关研究成果发表在学科顶级杂志 Current Biology 上,并入选2016年《中国科学:生命科学》的亮点研究工作。

研究方向三：遗传、发育与进化

代表性成果一

利用树鼩精原干细胞获得世界首只转基因树鼩，成功建立转基因树鼩技术平台

ORIGINAL ARTICLE

Cell Research (2017) 27:241-252.  
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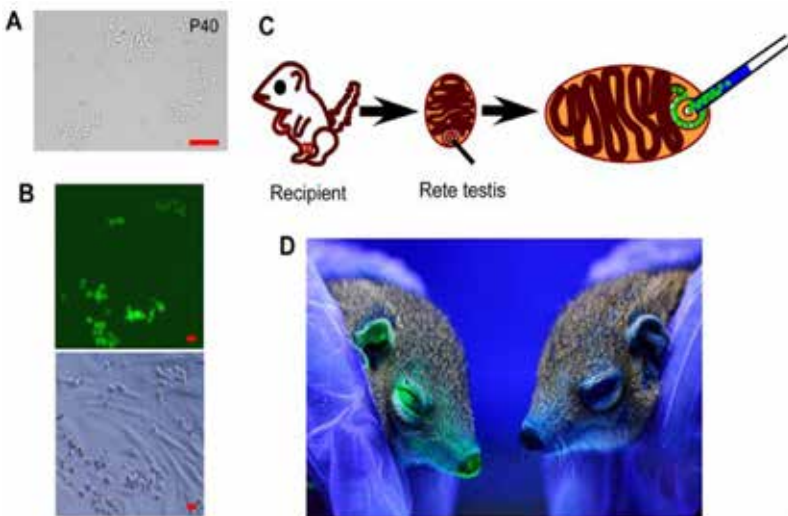
Long-term propagation of tree shrew spermatogonial stem cells in culture and successful generation of transgenic offspring

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Tree shrews have a close relationship to primates and have many advantages over rodents in biomedical research. However, the lack of gene manipulation methods has hindered the wider use of this animal. Spermatogonial stem cells (SSCs) have been successfully expanded in culture to permit sophisticated gene editing in the mouse and rat. Here, we describe a culture system for the long-term expansion of tree shrew SSCs without the loss of stem cell properties. In our study, thymus cell antigen 1 was used to enrich tree shrew SSCs. RNA-sequencing analysis revealed that the Wnt $\beta$ -catenin signaling pathway was active in undifferentiated SSCs, but was downregulated upon the initiation of SSC differentiation. Exposure of tree shrew primary SSCs to recombinant Wnt3a protein during the initial passages of culture enhanced the survival of SSCs. Use of tree shrew Sertoli cells, but not mouse embryonic fibroblasts, as feeder was found to be necessary for tree shrew SSC proliferation, leading to a robust cell expansion and long-term culture. The expanded tree shrew SSCs were transfected with enhanced green fluorescent protein (EGFP)-expressing lentiviral vectors. After transplantation into sterilized adult male tree shrew's testes, the EGFP-tagged SSCs were able to restore spermatogenesis and successfully generate transgenic offspring. Moreover, these SSCs were suitable for the CRISPR/Cas9-mediated gene modification. The development of a culture system to expand tree shrew SSCs in combination with a gene editing approach paves the way for precise genome manipulation using the tree shrew.

**Keywords:** tree shrew; spermatogonial stem cells; Wnt $\beta$ -catenin signaling; Sertoli cells; gene editing  
Cell Research (2017) 27:241-252. doi: 10.1038/cr.2016.156, published online 23 December 2016



树鼩是一种具有重要潜在应用价值的实验动物。然而，缺乏遗传操作手段严重制约了树鼩作为实验动物的广泛应用和推广。由于树鼩早期胚胎收集和胚胎移植技术的难题目前均未解决，通过树鼩精原干细胞进行遗传修饰，可为树鼩遗传操作另辟蹊径。

郑萍组成功筛选到用于富集树鼩睾丸中的精原干细胞的表面标记分子 Thy1。通过优化培养体系，建立了多株可长期稳定传代培养的树鼩精原干细胞系。经基因修饰后的树鼩精原干细胞移植到雄性受体树鼩睾丸内，可以产生基因修饰精子，通过自然交配可获得基因修饰子代树鼩。该工作解决了树鼩研究

中缺乏基因操作技术的瓶颈难题，为树鼩作为新型实验动物的广泛应用打下良好基础。研究结果发表在 Cell Research。

## 研究方向三：遗传、发育与进化

## 代表性成果二

## 揭示人和灵长类大脑在进化过程中的甲基化模式

Mol. Biol. Evol. 33(11):2947–2959

## Comparative Methylome Analyses Identify Epigenetic Regulatory Loci of Human Brain Evolution

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The Gene Expression Omnibus accession numbers for the data reported in this paper are GSE77124 and GSE85868 for WGBS and targeted validation data, respectively.

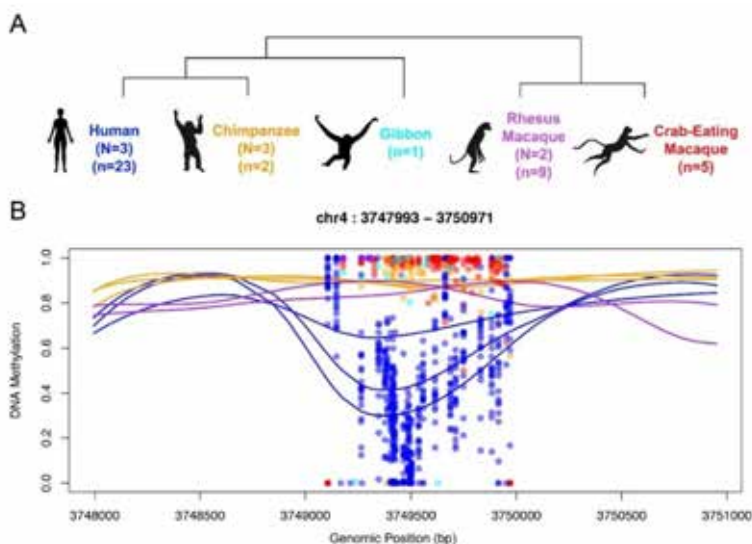
## Abstract

How do epigenetic modifications change across species and how do these modifications affect evolution? These are fundamental questions at the forefront of our evolutionary epigenomic understanding. Our previous work investigated human and chimpanzee brain methylomes, but it was limited by the lack of outgroup data which is critical for comparative (epi)genomic studies. Here, we compared whole genome DNA methylation maps from brains of humans, chimpanzees and also rhesus macaques (outgroup) to elucidate DNA methylation changes during human brain evolution. Moreover, we validated that our approach is highly robust by further examining 38 human-specific DMRs using targeted deep genomic and bisulfite sequencing in an independent panel of 37 individuals from five primate species. Our unbiased genome-scan identified human brain differentially methylated regions (DMRs), irrespective of their associations with annotated genes. Remarkably, over half of the newly identified DMRs locate in intergenic regions or gene bodies. Nevertheless, their regulatory potential is on par with those of promoter DMRs. An intriguing observation is that DMRs are enriched in active chromatin loops, suggesting human-specific evolutionary remodeling at a higher-order chromatin structure. These findings indicate that there is substantial reprogramming of epigenomic landscapes during human brain evolution involving noncoding regions.

**Key words:** DNA methylation, human brain evolution, transcriptional divergence, differentially methylated regions, epigenomes.

Downloaded from <http://dx.doi.org/10.1093/molbev/msw014> at Kunming Institute of Zoology, Chinese Academy of Sciences on August 10, 2016

Article



变化在人类大脑功能演化过程中发挥着重要的生物学功能。研究结果发表在 Molecular Biology and Evolution。

表观遗传修饰的重要性越来越被人所认识，但是表观遗传的变化如何对表型的进化产生影响，特别是表观遗传调控在人类大脑进化中的作用仍然不是很清楚。为了揭示人类特异的甲基化模式在全基因组水平的变化模式。宿兵组与美国 Soojin V. Yi 教授合作对人类、黑猩猩和猕猴 3 个物种的大脑前额叶进行了全基因组甲基化测序，发现了 85 个人类特异的甲基化变化区域 (DMR)。进一步的重测序与基因表达验证发现，大部分 DMR 集中在基因间区域，而这些区域基本上都是 H3K4me3 标识的转录活跃区域；这些区域可能通过影响一些神经特异转录因子的结合参与神经发育调控过程。研究结果提示表观遗传



## 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: 生物多样性考察监测及评价、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 and 保育; 湿地生态系统的恢复研究。本年度共有在研课题 33 项, 其中新申请批准的项目 14 项。发表论文 14 篇, 其中 SCI 论文 9 篇, 获授权国家发明专利 1 项。

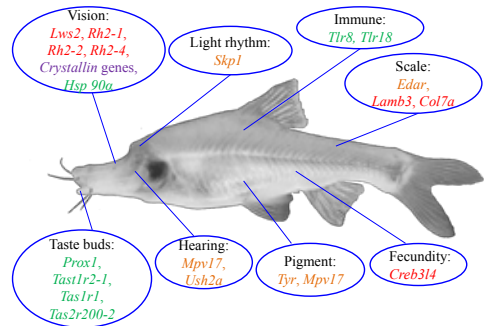
### 重要成果 (Highlights)

#### 论著 (Publications)

1. **Yang JX\***, Chen XL, Bai J, Fang DM, Qiu Y, **Jiang WS\***, ..., Shi Q. 2016. The *Sinocyclocheilus* cavefish genome provides insights into cave adaptation. *BMC Biology*, 14(1):1-13.
2. **Zheng LP**, Chen XY\*, **Yang JX\***. 2016. Molecular systematics of the Labeonini inhabiting the karst regions in southwest China (Teleostei, Cypriniformes). *ZooKeys*, 612: 133-148.
3. **Zheng LP**, **Yang JX\***, Chen XY\*. 2016. Molecular phylogeny and systematics of the Barbiniae (Teleostei: Cyprinidae) in China inferred from mitochondrial DNA sequences. *Biochemical Systematics and Ecology*, 68: 250-259.
4. **Zheng LP**, **Yang JX**, Chen XY\*. 2016. *Garra incisorbis*, a new species of labeonine from Pearl River basin in Guangxi, China (Teleostei: Cyprinidae). *Ichthyological Exploration of Freshwaters*, 26: 299-303.
5. **Liu SW**, **Yang JX**, Chen XY\*. 2016. *Paralepidocephalus translucens* (Teleostei: Cobitidae), a new cave species of loach from Eastern Yunnan, China. *Ichthyological Exploration of Freshwaters*, 27(1): 61-66.
6. **Yang KF**, **Jiang WS\***, Chen XY, Zhou W, **Yang JX**. 2016. An integrative approach to reappraising species validity in *Pseudoxostoma* (Teleostei: Sisoridae). *Zootaxa*, 4158 (3): 352-366.
7. 潘晓赋, 宋玉竹, 张远旭, 杨君兴, 刘锐, 刘倩. 滇池金线鲃胱抑素基因及其应用, 专利号: ZL 201410335924.7. (2016.4.20 授权)

### 1. 洞穴金线鲃基因组研究及其适应性

我们第一次开展了中国洞穴金线鲃属的全基因组研究, 通过比较研究发现了洞穴种类许多重要的遗传变化, 例如: 基因丢失 (如视蛋白基因)、假基因化 (如晶状体蛋白基因)、突变 (如色素相关基因)、片段缺失 (如鳞片相关的基因) 以及基因表达量下调 (如节律通路基因等) 可能是其典型退化性性状 (如眼睛退化、皮肤白化、鳞片退化、节律丢失等) 的重要原因。而有一些味觉相关基因拷贝数发生了增加, 这可能是其补偿性进化性状的一种反应。这不仅为了解洞穴适应的遗传机制提供了思路, 同时也为将来更好地了解洞穴生物学提供了基础资源。



### 2. 野鲮亚科和鲃亚科鱼类系统发育研究取得新进展

通过广泛的采样, 从分子水平重建了野鲮亚科喀斯特类群和中国鲃亚科鱼类的系统发育关系。阐明了野鲮亚科各新属、新种的系统地位, 建立了一个新属并发现了一些分类学问题。对鲃亚科的研究, 阐明了中国鲃亚科各属之间的关系, 发现多个属不是单系, 且一些种的属级归类有待修订。这些研究结果为后续研究奠定了重要基础。系统发育研究共发表 SCI 论文 2 篇。

### 3. 墨头鱼属、细头鳅属、拟鲃属等鱼类分类取得综合进展

本年度课题组成员对墨头鱼属、细头鳅属、拟鲃属等鱼类进行了分类学研究, 发现了 2 新种, 分别是缺刻墨头鱼和透明尖头鳅。综合各种研究方法重新评估了拟鲃属鱼类的物种有效性。分类学研究共发表 SCI 论文 3 篇。

### 4. 云南珍稀特有鱼类的人工繁殖、养殖推广和野外种群复壮

2016 年繁殖滇池金线鲃鱼苗 100 余万尾, 抚仙金线鲃鱼苗 2 万余尾。突破杞麓鲤和异口新光唇鱼的人工繁殖, 繁殖杞麓鲤 1 万余尾, 异口新光唇鱼 5000 余尾。繁殖西畴金线鲃 2 万余尾, 繁殖鱈鱼良白鱼 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 30 万余尾 (其中昆明 1000 余尾, 会泽 30 万余尾)。目前, 珍稀鱼类保育基地饲养有土著鱼类 50 余种, 40 万余尾, 无重大鱼病出现。单位养殖水体的养殖密度逐年提高。对西畴、曲靖、会泽、香格里拉、保山、德泽鱼类增殖放流站等养殖基地定期进行技术指导。

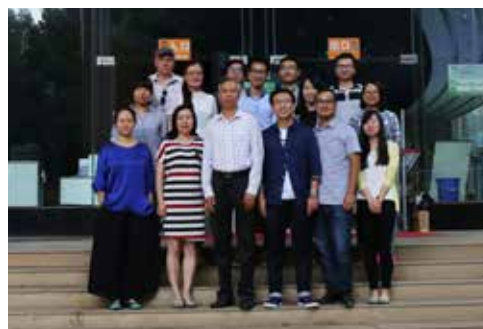
2016 年度在昆明晋宁古滇艺码头放流滇池金线鲃 9.7 万余尾。支持西畴、会泽三个水产公司滇池金线鲃鱼苗 30 万余尾, 裂腹鱼、光唇鱼等种鱼 200 余千克。9 月 21 日在德泽水库放流 6 万余尾滇池金线。



## 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 2016, total 33 research programs have been implementing with 14 programs newly approved. A total of 14 papers have been published which 9 of them are SCI papers. One national invention patent licensing.

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### 1. The *Sinocyclocheilus* cavefish genome provides insights into cave adaptation

As the first time, we carried out comparative analyses of cavefish genomes among distinct species in *Sinocyclocheilus*. We found that many genetic changes, such as gene loss (e.g. opsin genes), pseudogenes (e.g. crystallin genes), mutations (e.g. melanogenesis-related genes), deletions (e.g. scale-related genes) and down-regulation (e.g. circadian rhythm pathway genes), are possibly associated with the regressive features (such as eye degeneration, albinism, rudimentary scales and lack of circadian rhythms), and that some gene expansion (e.g. taste-related transcription factor gene) may point to the constructive features (such as enhanced taste buds) which evolved in these cave fishes. Our work provides not only insights into genetic mechanisms of cave adaptation, but also represents a fundamental resource for a better understanding of cavefish biology.

### 2. The phylogeny of Labeoninae and Barbinae

The phylogeny of Labeoninae and Barbinae (Cypriniformes) was respectively reconstructed based on an extensive samples. The relationships of the species of Labeoninae inhabiting in the karst regions were demonstrated, and a new genus was erected. The monophyly of several genera of Barbinae was not supported, and the generic allocations of some species need to be revised.

### 3. The taxonomy of *Garra*, *Paralepidocephalus*, and *Pseudexostoma*

In this year, we described two new species (*Paralepidocephalus translucens* and *Garra incisorbis*) from Yunnan and Guangxi province. In addition, we adopted an integrative approach combining both morphology-based (traditional measurements, truss-based and geometric morphometrics, fin skeleton examination and X-ray photography) and molecular approaches (genetic distances, haplotype network, phylogenetic relationships) to reappraise species validity in *Pseudexostoma*.

### 4. 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*, *S. tingi*, *S. xichouensis*, *Anabarrilius grahami*, *Neolissochilus benasi* and *Schizothorax wangchiachii*. More than 1 million individuals were expanded to cultivated in other fish farms which in Huize County and Xichou County, and more than 0.5 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  
Dec. 2016

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张源伟 Yuanwei Zhang 2013

郑秋旻 Qiuyang Zheng 2014

Marco Endrueit 2014

牛诚祎 Chengyi Niu 2015

杜丽娜 Lina Du 2016



## 兽类生态与进化



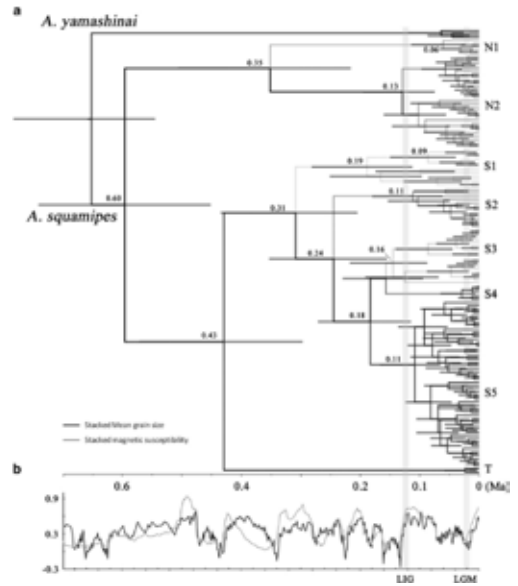
蒋学龙, 博士, 研究员。立足于东喜马拉雅-横断山地区开展哺乳动物生态与进化研究, 主要研究内容包括哺乳动物分类、系统演化与生物地理, 灵长类动物的生态行为, 兽类资源与保护, 以揭示横断山地区哺乳动物多样性的形成机制及在特殊生态条件下的适应性进化与保护。近年来, 主要以东喜马拉雅-横断山地区特有与常见小型哺乳动物、灵长类、偶蹄类动物、亚洲象为研究对象, 重点探讨横断山区哺乳动物多样性形成、西黑冠长臂猿的生态行为与适应性、麝类及其他偶蹄类动物资源与保护的现状及致危因素分析、剖析人与象冲突的行为生态原因并探讨冲突防范和缓解对策。

### 重要成果 (Highlights) 论著 (Publications)

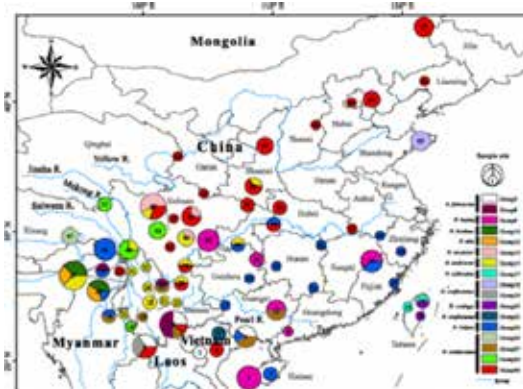
1. He K, Hu NQ, Chen X, Li JT, Jiang XL. Interglacial refugia preserved high genetic diversity of the Chinese mole shrew in the mountains of southwest China. *Heredity*, 2016, 116: 23-32.
2. Koju NP, He K, Chalise MK, ..., Jiang XL. Multilocus approaches reveal underestimated species diversity and inter-specific gene flow in pikas (*Ochotona*) from southwestern China. *Molecular Phylogenetics and Evolution*, 2016, 107: 239-245
3. Li XY, Bleisch WV, Jiang XL. Effects of Ethnic Settlements and Land Management Status on Species Distribution Patterns: A Case Study of Endangered Musk Deer (*Moschus* spp.) in Northwest Yunnan, China[J]. *Plos One*, 2016, 11(5):e0155042.
4. Li ZT, Peng YQ, Wen XL, Jandér KC. Selective resource allocation may promote a sex ratio in pollinator fig wasps more beneficial for the host tree[J]. *Sci Rep*, 2016, 6(x):35159.
5. Orkin JD, Yang YM, Yang CY, ..., Jiang XL. Cost-effective scat-detection dogs: unleashing a powerful new tool for international mammalian conservation biology[J]. *Scientific Reports*, 2016, 6:34758.
6. Zhang B, Kai H, Tao W, ..., Jiang XL. Multi-locus phylogeny using topotype specimens sheds light on the systematics of *Niviventer* (Rodentia, Muridae) in China[J]. *Bmc Evolutionary Biology*, 2016, 16(1):261.

### 1. 中国西南山地间冰期避难所

中国西南山地因其复杂的地形地貌、地质历史、气候变化与环境孕育着丰富的生物多样性, 探索其形成与维持机制一直是重要的科学问题。通过对区域内微尾鼯进行广泛取样, 利用多基因遗传标记, 探讨地貌和气候变化在区域物种遗传多样性和物种分化中的作用。结果表明: 西南山地南部具有显著较高的遗传多样性, 但地形地貌对该物种的地理遗传结构影响较小, 相反气候波动对物种的分布、扩散与种群动态的影响深刻。由于巨大的气候季节性变化, 微尾鼯在末次间冰期扩散受限, 并被隔离在南部的一些微避难所中, 而在末次冰期快速扩散。研究首次为中国西南山地更新世间冰期物种避难所及其纬度效应提供了证据。



### 2. 白腹鼠属系统发育



为解决白腹鼠属系统发育关系、厘定其分类系统、评估其物种多样性, 通过大量文献回溯, 并在中国广泛采样 (白腹鼠属各物种、亚种和同物异名的地模标本) 及收集邻近地区的样品, 使用分子系统学方法对标本和样品进行比较分析。

结果表明, 白腹鼠属可以分为 4 个主要分支, 各分支之间的系统发育关系得到了很好的解决; 分子物种界定分析表明白腹鼠属物种多样性被低估, 在中国范围内至少存在 11 个种, 包括 3 个隐存种, 同时多个物种的分类地位需要重新评估, 包括亚种。尽管目前的数据尚不能完全地解决白腹鼠属系统发育关系以及物种多样性问题, 但提示从基因组学方面解决问题的可能性。



# 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 endangered species-based investigations of ecology, behavior and conservation of black crested gibbon, musk deer and other large mammals.

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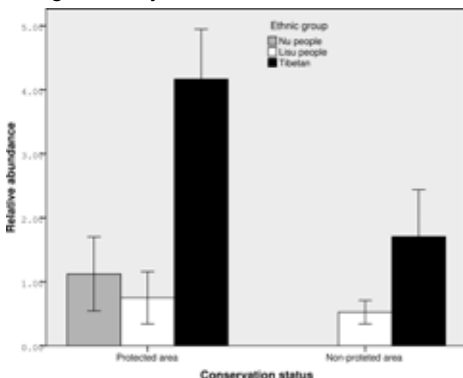
## 1. Cost-effective scat-detection dogs: unleashing a powerful new tool for international mammalian conservation biology

Recently, detection dogs have been utilized to collect fecal samples from cryptic and rare mammals. Despite the great promise of this technique for conservation biology, its broader application has been limited by the high cost (tens to hundreds of thousands of dollars) and logistical challenges of employing a scat-detection dog team while conducting international, collaborative research. Through an international collaboration of primatologists and the Chinese Ministry of Public Security, we trained and used a detection dog to find scat from three species of unhabituated, free-ranging primates, for less than \$3,000. We collected 137 non-human primate fecal samples that we confirmed by sequencing taxonomically informative genetic markers. Our detection dog team had a 92% accuracy rate, significantly outperforming our human-only team. Our results demonstrate that detection dogs can locate fecal samples from unhabituated primates with variable diets, locomotion, and grouping patterns, despite challenging field conditions. We provide a model for in-country training, while also building local capacity for conservation and genetic monitoring. Unlike previous efforts, our approach will allow for the wide adoption of scat-detection dogs in international conservation biology.



## 2. Effects of Ethnic Settlements and Land Management Status on Species Distribution Patterns: A Case Study of Endangered Musk Deer (*Moschus* spp.) in Northwest Yunnan, China

We developed models for endangered musk deer (*Moschus* spp.) abundance indices in and around protected areas inhabited by different ethnic groups in northwest Yunnan China to address different anthropogenic and management-related questions. We found that prediction of relative abundance of musk deer was best accomplished using ethnicity of settlements, conservation status and poaching pressure in an area.



Musk deer were around 5 times more abundant in Tibetan regions relative to Lisu regions.

We found no significant negative correlates of gathering and transhumance activities on musk deer abundance. Hunting pressure showed no significant differences between protected and non-protected areas, but showed significant differences among ethnic groups. Hunting pressures in areas adjacent to Lisu settlements was 7.1 times more than in areas adjacent to Tibetan settlements. Our findings indicate protected areas in southwest China are not fully effective in deterring human disturbance caused by traditional practices.

protected areas in southwest China are not fully effective in deterring human disturbance caused by traditional practices.

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- Laxman Khanal, 2014
- 杜宜清 Du Yiqing, 2014
- 程 峰 Cheng feng, 2014
- 牛晓炜 Niu xiaowei, 2015
- 甘 霖 Gan lin, 2015
- Kenneth Otieno Onditi, 2015
- 宋文宇 Song Wenyu, 2016
- 于秋鹏 Yu Qiupeng, 2016



## 鸟类学

杨晓君, 研究员, 主要从事西南地区鸟类分类区系、系统演化、生物地理、群落生态学及珍稀鸟类的行为生态学和保护生物学研究。近年来更关注青藏高原旗舰物种—黑颈鹤的保护及鸟类系统演化研究。目前已出版执行主编和副主编专著 8 部, 发表论文 100 余篇

### 重要成果 (Highlights) 论著 (Publications)

1. **Hu WZ, Wu F, Gao JY, Yan D, Liu LM, Yang XJ\***. Influences of interpolation of species ranges on elevational species richness gradients. *Ecography*. 2016, doi: 10.1111/ecog.02534.
2. **Li XL, Dong F, Lei FM, Alström P, Zhang RY, Ödeen A, Fjeldså J, Ericson PGP, Zou FS and Yang XJ\*** 2016. Shaped by uneven Pleistocene climate: phylogeographic pattern and population history of White Wagtail *Motacilla alba* (Aves: Passeriformes). *J Avian Biol.* 2016 47(2): 263-274.
3. **Dong HY, Lu GY, Zhong XY, Yang XJ\***. Winter diet and food selection of the Black-necked Crane *Grus nigricollis* in Dashanbao, Yunnan, China. *PeerJ.* 2016, 4:e1968.
4. **Wang RX, Wu F, Chang YY, Yang XJ\***. Waterbirds and their habitat utilization of artificial wetlands at Dianchi Lake: Implication for waterbird conservation in Yunnan-Guizhou Plateau lakes. *Wetlands*. 2016, 36:1087-1095.
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 Conserv Int.* 2016, doi:10.1017/S0959270916000058.
6. **王荣兴, 吴飞, 杨晓君\***. 云南昆明发现印度池鹭. *动物学杂志*. 2016, 51(4): 716.

### 1. 在中国西南山区的鸟类保护

山区通常被认为是生物多样性热点区域, 然而, 大多数山地森林由非原始林组成。了解非原始林对山地生物多样性的保护价值至关重要。在本研究中, 主要运用网捕法和样点法比较云南哀牢山山脊上的原始森林与附近低海拔地区次生林, 薪炭林和人工松林的鸟类群落。我们用这两种方法都发现不同栖息地间鸟类群落组成的周转非常快。虽然原始林森林内部鸟类和食虫鸟类的比例高于非原始林, 但非原始林依然记录了对较高比例的森林内部鸟类和食虫鸟类。更为重要的是许多鸟类物种、森林内部物种、食虫鸟类和画眉亚科鸟类仅仅在非原始林记录到。

我们的研究表明, 原始林对维持山区鸟类多样性具有重要作用。不过, 考虑到原始林仅仅局限于高海拔区域, 低海拔地区次生林, 薪炭林和人工松林通过增加景观多样性, 部分抵消低海拔带原始森林消失的影响, 在保护山区鸟类中同样扮演了重要的角色。因此, 我们呼吁除了保护原始林, 在中国西南部山区的保护工作也应该关注低海拔非原始林的保护。



### 2. 湿地鸟类

水鸟与环境的关系具有地域性。近年来, 沿海湿地与水鸟的关系有了较为深入的研究, 但鲜有关于云贵高原水鸟年组成以及其对人工湿地利用方面的报道。本研究对滇池水禽组成进行了 36 次调查, 对湖滨带池塘型、泥滩型、高挺水植被型、低挺水植被型、高浮水植被型、低浮水植被型和混合植被型人工湿地的水鸟多样性进行了对比分析。结果表明: (1) 在记录到的 74 种水鸟中, 繁殖鸟、旅鸟、冬候鸟和偶见鸟的种类和比例分别为 16 种 (21.6%), 27 种 (36.5%), 29 种 (39.2%) 和 2 种 (2.7%); 一年中物种多度 (Abundance) 在冬季表现出明显的优势, 丰度 (Species richness) 表现出 3 个峰值, 分别在迁徙高峰 5 月和 9 月和越冬中期 1 月。这说明滇池不仅是水鸟的越冬地, 也是繁殖地和迁徙中途停歇地。(2) 混合植被型、低挺水植被型以及泥滩型人工湿地较其他 4 种类型人工湿地水鸟多样性更高。本研究暗示: (1) 云贵高原的湖泊管理应该考虑不同居留型的水鸟需求; (2) 保留和维持混合植被型、低挺水植被型以及泥滩型人工湿地对云贵高原的水鸟保护非常重要。



## 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 over 100 papers have been published.

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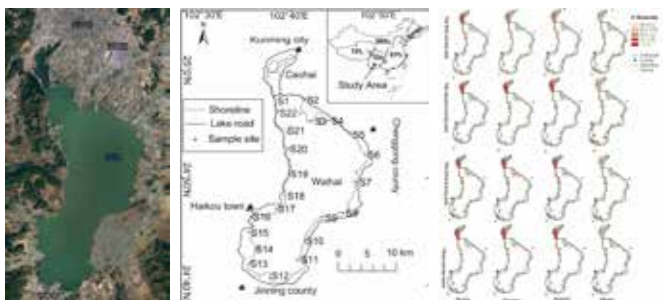


### 1. Birds' Conservation in mountainous regions in south-west China

Mountain systems are often recognized as biodiversity hotspots; however, most montane forests are human-modified. Understanding the conservation value of human-modified forests is essential to mountain biodiversity conservation. In this study, mist-nets and point-counts were used to compare the bird communities of primary forests on ridges in the Ailao Mountains of Yunnan, China, and secondary forests, firewood forests, and pine plantations in nearby lower elevation zones. We found that community turnover among habitats was very high using both methods. Although the percentage of forest interior species and insectivores in each habitat was higher in the primary forests than in the human-modified forests, relatively high percentages of forest interior species and insectivores were recorded in the human-modified forests. Moreover, many bird species, forest interior species, insectivores and babblers were only recorded in the human-modified forests. Our study indicated that the primary forests are important for sustaining mountain bird diversity. However, given that primary forests are restricted to ridges, secondary forests, firewood forests, and pine plantations at lower elevations also play important roles in bird conservation in mountainous regions by increasing landscape diversity and partially offsetting species loss from primary forests. Therefore, conservation efforts should also be concentrated on human-modified forests at lower elevations in mountainous regions in south-west China.

### 2. Birds in Wetlands

The effects of coastal artificial wetlands on waterbirds have been studied more extensively in China, but the annual composition of waterbirds and their utilization of constructed wetlands in Yunnan–Guizhou Plateau lakes are poorly understood. We conducted 36 waterbird surveys over a year at Dianchi Lake, and found that it supports diverse habitats for breeders (16 species), migrants (27 species) and winter visitors (29 species). Among artificial wetland types, we found that mixed vegetation, low emerging plant and mudflat wetlands supported higher species richness and density than the other wetland types. Our findings had the following implications: management of Yunnan–Guizhou Plateau lakes should take the requirements of different waterbirds into consideration; and maintenance of low emerging plants and mixed vegetation, as well as mudflats, is crucial to accommodate the diverse habitat requirements of waterbirds.



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## 生态学与环境保护中心

**Douglas W. Yu**, 博士, 研究员。生态学与环境保护中心负责人, 首批云南省高端人才项目引进人才。主要关注两个方面的研究内容: 生物多样性快速评估方法和互利共生研究。目前已发表超过 90 篇论文于国际期刊 Nature, Science, PNAS, PLoS Biology, Ecology Letters, Ecological Monographs, Ecology, American Naturalist, Evolution 等上。

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### 重要成果 (Highlights) 论著 (Publications)

1. Hua FY., Wang XY, Zheng XL, Fisher B., Wang L, Zhu JG, Tang Y, Yu D.W.\*, & Wilcove D.S.\* Opportunities for biodiversity gains under the world's largest reforestation programme. *Nature Communications*. 2016, 7: 12717. doi: 10.1038/ncomms12717.
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3. Zhang K, Lin SL, Ji YQ, Yang CX, Wang XY, Yang CY, Wang H, Jiang HS, Harrison R.D.\* & Yu, D.W.\* Plant diversity accurately predicts insect diversity in two tropical landscapes. *Molecular Ecology*. 2016, 25(17):4407-4419. doi:10.1111/mec.13770.
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### 1. 真菌生物多样性影响朽木分解速率研究

每年, 全球的朽木在分解过程中所产生的 CO<sub>2</sub> 与燃烧化石能源所排放的量相当。如何控制和减缓化石能源燃料所排放的 CO<sub>2</sub> 一直是社会广泛关注的问题, 因为这对于缓解全球变暖和温室效应等具有非常重要的意义。然而, 人们对于控制朽木分解速率的因素了解的还不够深入。温度和湿度, 虽然影响着朽木分解的速率, 但它们并不能很好的解释: 为何在同样温度和湿度下的朽木分解速率也会有很大差异? Douglas Yu 研究组和西双版纳热带植物园的 Douglas Schaefer 合作在 Scientific Reports 上发表了真菌生物多样性影响朽木分解速率的相关研究成果。文章分析了在哀牢山样地中倒木样本的真菌多样性与其分解速率的关系, 研究结果显示, 如果朽木里真菌的生物多样性越高, 其分解的速率会更慢。进一步的群落组成分析同样支持真菌的多样性影响 (‘purediversity’ effect), 研究人员分析这可能与真菌之间的干扰竞争有关。我们利用高通量测序技术, 直接分析了在自然环境中朽木样本中的真菌多样性。基于研究成果团队提出了一项科学假设: 在全球尺度, 真菌多样性因维持朽木的小生境, 降低朽木分解向大气排放 CO<sub>2</sub> 的速率, 从而具有非常重要的生态服务功能。



### 2. 基于 DNA 高通量条形码研究中国两个热带山地景观中植物多样性与昆虫多样性的关系

Douglas 课题组与原西双版纳热带植物园的 Rhett D. Harrison 研究员、华南师范大学的江海声教授合作, 在中国海南和西双版纳的两个热带山地景观中利用样方调查植物多样性和昆虫多样性。植物多样性采用形态学鉴定, 昆虫多样性使用马氏网 (Malaise trap) 采集并采用宏条形码技术 (metabarcoding) 鉴定。我们使用常用的皮尔森相关分析和 Basset et al. (2012) 的“植物模型”分析物种丰富度间的关系 ( $\alpha$  多样性), 使用 Procrustes 分析检验群落组成间的关系 ( $\beta$  多样性)。结果表明 (1) 植物模型与非参数估计 (nonparametric estimator) 得出的昆虫物种丰富度非常接近, 但是常用的皮尔森相关分析发现样方水平上植物物种丰富度和昆虫物种丰富度的相关性较低; (2) Procrustes 分析发现植物和昆虫的群落组成高度相关。以上结果均在两个景观、两个季节旱季、雨季、昆虫的不同目间一致。我们采用的高通量方法使在大尺度上检验热带的超高多样性的不同假说成为可能, 为改进全球节肢动物物种多样性的预测提供进一步的理论基础。





## 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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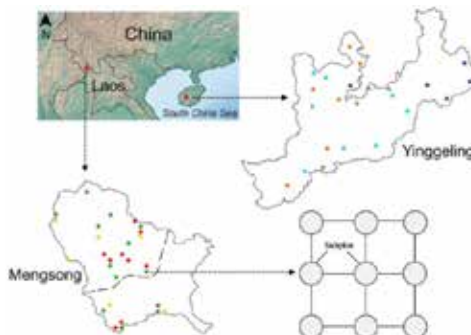


### 1. Higher fungal diversity is correlated with lower CO<sub>2</sub> emissions from dead wood in a natural forest

Wood decomposition releases almost as much CO<sub>2</sub> to the atmosphere as does fossil-fuel combustion, so the factors regulating wood decomposition can affect global carbon cycling. We used metabarcoding to estimate the fungal species diversities of naturally colonized decomposing wood in subtropical China and, for the first time, compared them to concurrent measures of CO<sub>2</sub> emissions. Wood hosting more diverse fungal communities emitted less CO<sub>2</sub>, with Shannon diversity explaining 26 to 44% of emissions variation. Community analysis supports a 'pure diversity' effect of fungi on decomposition rates and thus suggests that interference competition is an underlying mechanism. Our findings extend the results of published experiments using low-diversity, laboratory-inoculated wood to a high-diversity, natural system. We hypothesize that high levels of saprotrophic fungal biodiversity could be providing globally important ecosystem services by maintaining dead-wood habitats and by slowing the atmospheric contribution of CO<sub>2</sub> from the world's stock of decomposing wood. However, large-scale surveys and controlled experimental tests in natural settings will be needed to test this hypothesis.

### 2. Plant diversity accurately predicts insect diversity in two tropical landscapes

Plant diversity surely determines arthropod diversity, but only moderate correlations between arthropod and plant species richness had been observed until Basset et al. (Science, 338, 2012 and 1481) finally undertook an unprecedentedly comprehensive sampling of a tropical forest and demonstrated that plant species richness could indeed accurately predict arthropod species richness. We now require a high-throughput pipeline to operationalize this result so that we can (i) test competing explanations for tropical arthropod megadiversity, (ii) improve estimates of global eukaryotic species diversity, and (iii) use plant and arthropod communities as efficient proxies for each other, thus improving the efficiency of conservation planning and of detecting forest degradation and recovery. We therefore applied metabarcoding to Malaise-trap samples across two tropical landscapes in China. We demonstrate that plant species richness can accurately predict arthropod (mostly insect) species richness and that plant and insect community compositions are highly correlated, even in landscapes that are large, heterogeneous and anthropogenically modified. Finally, we review how metabarcoding makes feasible highly replicated tests of the major competing explanations for tropical megadiversity.



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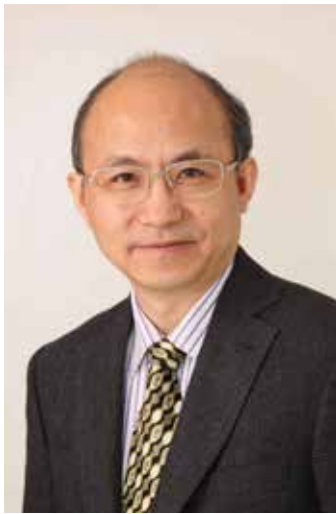
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## 分子进化与基因组多样性研究

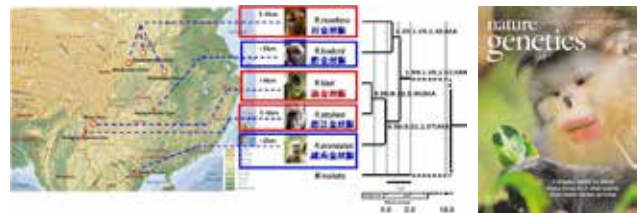
张亚平, 博士, 研究员, 中国科学院院士, 中国科学院副院长, 遗传资源与进化国家重点实验室主任。主要从事基因组多样性研究, 近几年重点开展家养动物起源驯化机制与人工选择的基因组进化机制和动物高原适应的分子机制方面的研究, 基因组研究揭示了金丝猴属物种高海拔适应的遗传机制, 以及远缘杂交的异源四倍体鲫鱼品系在多倍化初期的基因组变化特征; 阐明了家鸡驯化过程中视觉退化和体型大小的进化机制; 揭示了家犬由东亚扩散到世界各地的迁徙路线, 不支持家犬中亚起源的假说; 甄别出藏猪和藏鸡中嗅觉受体的丢失并不是高原适应选择作用所导致的结果, 提示对基因家族相关研究时需排除基因组缺陷带来的误差; 而欧洲人群中 *ADH1B* 基因的伪选择信号提示需对群体遗传结构加以考虑。大数据分析发现濒危脊椎动物群体数量的快速下降起始于 19 世纪末期, 为 19 世纪工业化扩张导致的全球范围生态环境恶化提供了有力的证据。2016 年在 *Nat Genet* (2), *Cell Res*(2), *PNAS*(3) 等国际刊物发表 SCI 文章 27 篇。

### 重要成果 (Highlights) 论著 (Publications)

1. Yu L<sup>\*</sup>, Wang GD<sup>1</sup>, Ruan J<sup>1</sup>, Chen YB<sup>1</sup>, Yang CP<sup>1</sup>, Cao X<sup>1</sup>, Wu H<sup>1</sup>, Liu YH<sup>1</sup>, Du ZL<sup>1</sup>, Wang XP<sup>1</sup>, Yang J<sup>1</sup>, Cheng SC<sup>1</sup>, Zhong L, Wang L, Wang X, Hu JY, Fang L, Bai B, Wang KL, Yuan N, Wu SF, Li BG, Zhang JG, Yang YQ, Zhang CL, Long YC, Li HS, Yang JY, Irwin DM, Ryder OA, Li Y, Wu CI<sup>\*</sup>, Zhang YP<sup>\*</sup>. Genomic analysis of snub-nosed monkeys (*Rhinopithecus*) identifies genes and processes related to high-altitude adaptation. *Nat Genet.* 2016, 48:947.
2. Li HP, Xiang-Yu JG, Dai GY, Gu ZL, Ming C, Yang ZF, Ryder OA, Li WH<sup>\*</sup>, Fu YX<sup>\*</sup>, Zhang YP<sup>\*</sup>. Large numbers of vertebrates began rapid population decline in the late 19th century. *PNAS.* 2016, 113:14079-14084.
3. Shen QK, Sulaiman X, Yao YG, Peng MS<sup>\*</sup>, Zhang YP<sup>\*</sup>. Was *ADH1B* under Selection in European Populations? *Am J Hum Genet.* 2016, 99:1217-1219.
4. Wang GD, Zhai WW, Yang HC, Wang L, Zhong L, Liu YH, Fan RX, Yin TT, Zhu CL, Poyarkov AD, Irwin DM, Hytonen MK, Lohi H, Wu CI, Savolainen P, and Zhang YP<sup>\*</sup>. Out of southern East Asia: the natural history of domestic dogs across the world. *Cell Res.* 2016, 26:21-33.
5. Wang GD, Peng MS, Yang HC, Savolainen P, Zhang YP<sup>\*</sup>. Questioning the evidence for a Central Asian domestication origin of dogs. *PNAS.* 2016, 113:E2554-E2555.
6. Wang MS, Zhang RW, Su LY, Li Y, Peng MS, Liu HQ, Zeng L, Irwin DM, Du JL, Yao YG, Wu DD<sup>\*</sup>, Zhang YP<sup>\*</sup>. Positive selection rather than relaxation of functional constraint drives the evolution of vision during chicken domestication. *Cell Res.* 2016, 26: 556-573.
7. Wang MS, Huo YX, Li Y, Otecko NO, Su LY, Xu HB, Wu SF, Peng MS, Liu HQ, Zeng L, Irwin DM, Yao YG, Wu DD<sup>\*</sup>, Zhang YP<sup>\*</sup>. Comparative population genomics reveals genetic basis underlying body size of domestic chickens. *J Mol Cell Biol.* 2016, 8(6):542-552.

### 1. 基因组研究揭示金丝猴属物种高海拔适应遗传机制

金丝猴属五个近缘物种占据了从低海拔到高海拔的生境类型 (800-4500m), 是研究哺乳动物高原适应的理想模型。采用基因组学、转录组学和功能验证等多角度的研究, 成功解密了



【Yu L et al. 2016 Nature Genetics, IF=32.197, 封面文章】

金丝猴适应高海拔生存能力背后的遗传学因素, 发现与 DNA 修复, 心脏和血管发育, 缺氧反应, 能量代谢和血管生成相关的基因可能与金丝猴高海拔适应相关。该成果是以非人类灵长目动物为研究模型揭示高原适应复杂性状的突破性成果, 有助于促进人类高原反应和相关疾病的机理研究。Nat Genet 对此配发了同期评述报道, Faculty of 1000 Biology 对此做了专题报道。

### 2. 脊椎动物近期快速的群体数量下降

全球许多物种的群体数量正在大幅下降, 甚至有许多物种在野外乃至地球上就已经消失了。这一群体数量的快速下降是什么时候开始的? 这对于解答物种濒危的原因极为重要。我们使用原创的群体遗传学模型, 分析了 2,764 种脊椎动物的遗传多样性数据, 发现濒危脊椎动物的群体数量的快速下降始于 19 世纪末期, 为 19 世纪工业化扩张导致的物种数量大幅减少和群体数量快速下降等全球范围的生态环境恶化提供了遗传学方面的证据。被 PNAS 选为当期亮点推荐, Washington Post 等对此做了专题报道。【Li HP et al. 2016 PNAS, IF=10.285】

### 3. 家鸡视觉退化及体型大小的进化机制

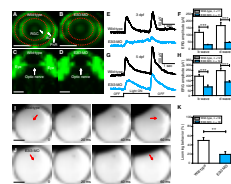


图 1. VIT 抑制表达导致斑马鱼视觉行为显著受损

经过长期的驯化和人工选择作用, 家鸡的视觉功能显著退化, 但是其遗传机制并不清楚。我们基于家鸡和红原鸡的基因组和转录组数据, 分析发现正选择而非选择压力放松促使家鸡视觉退化, 正选择可能通过影响视网膜中基因的表达来影响家鸡视觉的退化。研究人员推测早期人们对家鸡的视觉的选择是种无意识的选择, 视觉退化的鸡更加有利于驯化和饲养管理。此研究成果为无意识选择在家养动物驯化中的重要作用提供了一个有趣的范例。另外, 该项工作也发现了一个新的视觉相关基因 VIT (图 1), 为视觉相关进化、疾病的研究提供新的靶点。【Wang MS et al. 2016 Cell Res, IF=12.393】

体型是家鸡在日常生产和育种中最主要的经济性状之一。比较群体基因组学分析发现 BMP10 基因所在的区域在以小体型著称的元宝鸡中表现出很强的选择信号。该基因在元宝鸡心脏的表达量显著上调, 相关性分析表明 BMP10 与家鸡体重变异显著相关, 可以解释元宝鸡体型 22.41% 变异。在斑马鱼中过表达 BMP10 可导致生长受阻。本研究表明 BMP10 是决定元宝鸡体型小的重要基因, 为今后的育种提供重要的靶点。【Wang MS et al. 2016 JMCB, IF=6.983, 封面文章】

# 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 *Anim Genet*. This year we focused on genomic evolution of artificial selection and molecular mechanism of the high-altitude adaptation in animals. We revealed evolutionary mechanism of high-altitude adaptation in snub-nosed monkeys, and vision reduce & body size of domesticated chickens. We also unravelled rapid population decline in vertebrates began in the late 19th century, which coincides with the widespread industrialization and profound change of global living ecosystems. Within 2016, the above research progresses were published in 27 SCI papers, including *Nat Genet* (2), *Cell Res* (2), *PNAS*(3), *AJHG*(1).

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## 1. Genomic analysis of snub-nosed monkeys (*Rhinopithecus*) identifies genes and processes related to high-altitude adaptation

The snub-nosed monkey genus *Rhinopithecus* includes five closely related species distributed across altitudinal gradients from 800 to 4,500 m. On the basis of a multilevel survey, the genomic analyses from both the species level and population level, as well as the transcriptomic analyses and functional assays, we identified genes involved in DNA repair, heart and vascular development, hypoxia response, energy metabolism, and angiogenesis, which are adaptive signatures that may reflect molecular adaptations consistent with the high-altitude environments of three snub-nosed monkey species. This study has been published on "*Nature Genetics*" as a cover paper, and recommended by Faculty of 1000 Biology.

## 2. Rapid population decline in vertebrates

The rate and the initiation date of rapid population decline can provide important clues about the driving forces of population decline in threatened species, but are generally unknown. Our novel population genetics modeling was applied for analyzing the genetic diversity data in 2,764 vertebrate species. We found that in many threatened vertebrate species the rapid population decline began in the late 19th century (Fig. 1), the mean current size of threatened vertebrates is only 5% of their ancestral size. We estimated ~25% population decline every 10 years in threatened vertebrate species. This estimated date coincides with the widespread industrialization and profound change of global living ecosystems over the past two centuries.

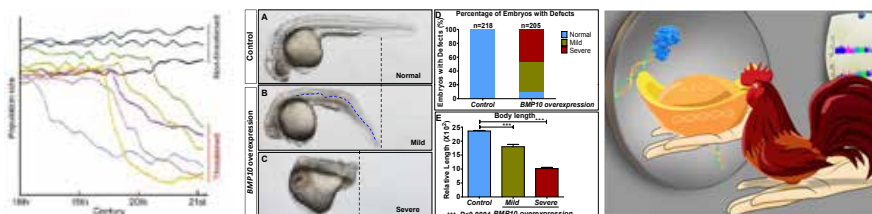


Fig. 1 Dynamics of population sizes of many vertebrates.

Fig. 2 Over-expression of BMP10 in zebrafish induced a significant decrease in its body length.

## 3. Evolutionary mechanism of vision reduce and body size of domesticated chickens

We analyzed genomic and transcriptome data from domestic chicken and Red junglefowl, and discovered that positive selection, rather than relaxation of purifying selection as previous postulated, had contributed to the reduce of vision in domestic chickens. We deduced that the progenitors of domestic chickens harboring weaker vision may have showed a reduced fear response and vigilance, making them easier to be unconsciously selected and/or domesticated. It raised the appreciation of unconscious selection in the characterization of the evolution of domestic animals. In addition, we also characterized the function of a novel gene, *VIT*, that showed an integral role in vision regulation. This provides an important target for future evolutionary and medical research.

Body size is the most important economic trait for animal production and breeding. Comparative population genomics revealed that the most significant selection signal for a small body sized chicken breed - Yuanbao was mapped to the *BMP10* gene. The expression of *BMP10* was remarkably up-regulated in Yuanbao chicken. Overall, *BMP10* showed a significant association with body size, explaining up to 22.41% of the total weight variance in Yuanbao chicken. Additionally, over-expression of *BMP10* induced a significant decrease in body length by inhibiting angiogenic vessel development in zebrafish (Fig. 2).

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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, 其中 SCI 论文 37 篇。

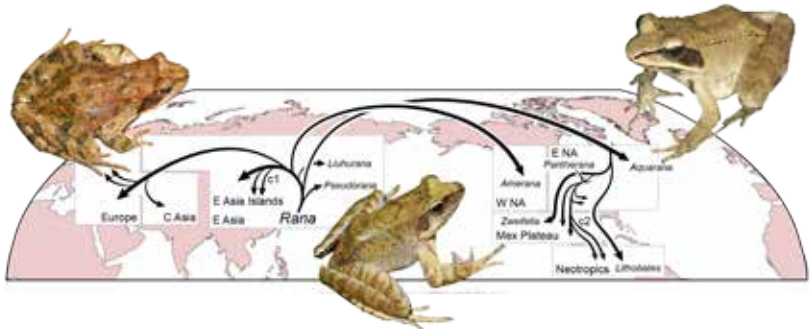
### 重要成果 (Highlights)

#### 论著 (Publications)

1. Yuan ZY<sup>#</sup>, Zhou WW<sup>#</sup>, Chen X<sup>#</sup>, Poyarkov NA, Chen HM, Jang-Liaw NH, Chou WH, Matzke NJ, Iizuka K, Min MS, Kuzmin SL, Zhang YP\*, Cannatella DC\*, Hillis DM\*, Che J\*. Spatio-temporal diversification of the true frogs (*Genus Rana*) across Eurasia and the Americas. *Systematic Biology*. 2016, doi:10.1093/sysbio/syw055.
2. Yuan ZY, Zhang BL, Wu YK, Che J\*. A new species of the genus *Pachytriton* (Caudata: Salamandridae) from Hunan and Guangxi, southeastern China. *Zootaxa*. 2016, 4085, 219–232.
3. Suwannapoom C<sup>#</sup>, Yuan ZY<sup>#</sup>, Chomdej S, Chen JM, Hou M, Zhao HP, Wang LJ, Nguyen SN, Nguyen TT, Fei L, Murphy RM, Che J\*. Taxonomic revision of the Chinese *Limnodynastes* (Anura, Dicroglossidae) with the description of a new species from China and Myanmar. *Zootaxa*. 2016, 4093, 181–200.
4. Yuan ZY, Suwannapoom C, Yan F, Poyarkov JRNA, Nguyen NS, Chen HM, Chomdej S, Murphy WR, Che J\*. Red River barrier and Pleistocene climatic fluctuations shaped the genetic structure of *Microhyla fissipes* complex (Anura: Microhylidae) in southern China and Indochina. *Current Zoology*. 2016, 1–13.
5. Jiang K<sup>#</sup>, Yan F<sup>#</sup>, Wang K, Zou DH, Li C, Che J\*. A new genus and species of tree frog from Medog, southeastern Tibet, China (Anura, Rhacophoridae). *Zoological Research*. 2016, 37(1): 15–20.
6. Jiang K, Wang K, Zhou DH, Yan F, Li PP, Che J\*. A new species of the genus *Scutiger* (Anura: Megophryidae) from Medog of southeastern Tibet, China. *Zoological Research*. 2016, 37(1): 21–30.
7. Jiang K, Wang K, Yan F, Xie J, Zou DH, Jiang JP, Li C, Che J\*. A new species of the genus *Amolops* (Amphibia: Ranidae) from southeastern Tibet, China. *Zoological Research*. 2016, 37(1): 31–40.
8. Suwannapoom C, Yuan ZY, Poyarkov Jr AN, Yan F, Kamtaeja S, Osathanukul M, Murphy WR, Che J\*. A new species of genus *Fejervarya* (Anura: Dicroglossidae) from northern Thailand. *Zoological Research*. 2016, 37(6):1–11.

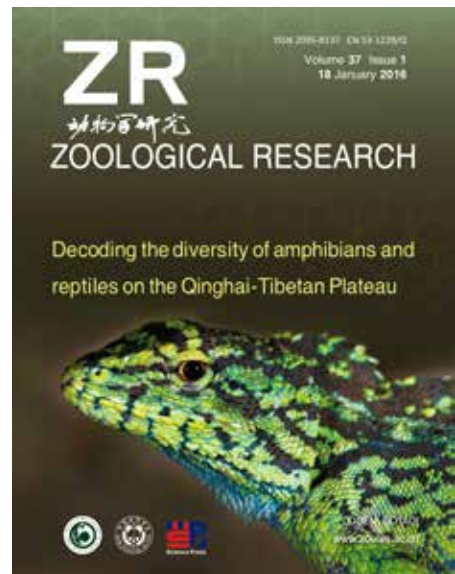
### 1. 蛙属在新、旧大陆的生物地理演化及多样性分化研究

蛙属 *Rana* 是广泛分布于亚洲、欧洲和美洲并倍受关注的重要类群。联合来自美洲、欧洲和亚洲的十余位学者, 第一次在全球尺度上完整构建了蛙属物种的系统演化历史 (Yuan et al. 2016. *Syst Biol*)。该类群起源于中国西南地区, 从东亚经白令海峡两次独立进入北美, 其中一支后迁入中、南美地区。后期, 从东亚经中亚, 进入欧洲地区。新、旧大陆在蛙属物种多样性分化方面存在较大差异: 例如, 东亚地区物种在分化过程中经历了明显的物种形成速率的增高变动, 与东亚岛屿的剧烈构造运动和气候波动所偶联的海平面变化相关; 而美洲物种整体经历了一个“适应辐射”的过程, 成种速率呈逐渐降低趋势。通过对 16 个物种类群的比较研究支持两爬物种北半球洲际扩散的普通模式——“跨白令海峡陆桥”假说 (13 个类群), 同时发现与森林植物研究 (Donohue and Smith, 2004) 类似, “走出亚洲”模式在两爬物种种较为普遍 (10/13 个类群)。



### 2. 青藏高原及横断山区两栖爬行动物物种分类及多样性研究

2016 年 1 月《*Zoological Research*》专刊报道了研究组在西藏及其东部横断山区的阶段性研究成果, 其中确定了中国、缅甸及泰国科级新纪录 - 亚洲角蛙科 *Ceratobatrachidae*, 这是我国两栖类的第十三个科, 也是近 10 年来再次增加的中国两栖爬行动物新纪录科; 还命名了中国两栖类一独特新属 - 棱鼻树蛙属 *Nasutixalus*。此外命名了 5 个新种。该研究提示, 两栖爬行动物多样性被低估, 新的技术手段, 例如 DNA 条形码技术的加入有助于我们更快速和高效的了解区域多样性。



# 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.

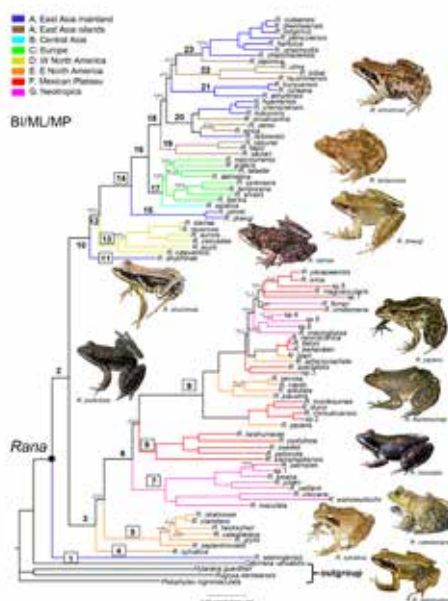
Email: [chej@mail.kiz.ac.cn](mailto:chej@mail.kiz.ac.cn)



## 1. Spatiotemporal diversification of the true frogs (Genus *Rana*): A historical framework for a widely studied group of model organisms

The genus *Rana* crosses Eurasia and the Americas are widely used as model organisms in studies of development, genetics, ecology, behavior, etc. However, the evolutionary history and diversification of this group is still not clear.

Based on a well-resolved, time-calibrated phylogeny of *Rana*, Yuan et al. (2016) revealed an “Out of Asia” pattern with two independent dispersals of *Rana* from East Asia to North America via Beringian land bridges. Trans-Beringian dispersal was also identified to be a common pattern in amphibians and reptiles after summarized the previous studies. Further, different processes of diversification were identified within the New World and Old World *Rana*. The lineage of New World *Rana* appears to have experienced a rapid radiation following its colonization of the New World. In contrast, diversification in the Old World began very slowly and later underwent a distinct increase in speciation rate, which associated with intensive tectonic movements along the Asian margin from the Oligocene to early Miocene.



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张宝林 Baolin Zhang 2015  
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  
徐 伟 Wei Xu 2016  
徐 凯 Kai Xu 2016

## 联合培养

陈进民 Jinmin Chen 2015  
杨春华 Yang Chun 2016

## 2. Biodiversity Research of Amphibians and Reptiles

As one of the active laboratories for herpetofaunal diversity research in China, we take an integrative approach to biodiversity research, incorporating morphology, ecology, and phylogenetic methods such as DNA barcoding. Recently, Zoological Research published a special issue on the results of Che lab's projects on herpetofaunal diversity of Tibet and the Hengduan Mountain Region of China, highlighting the discoveries of a new record of anuran family Ceratobatrachidae in China, a new genus of treefrog, three new species of amphibians, and two new species of reptiles.



## 进化基因组学与基因起源

王文, 中国科学院昆明动物研究所, 研究员、博士生导师, 进化基因组学与基因起源学科负责人, 遗传资源与进化国家重点实验室学术委员会副主任。长期以来一直进行进化基因组学研究, 有丰富的基因组大数据处理经验。目前已经在 Science、Nature、PNAS 及 PLoS Genetics 等重要学术杂志上发表论文 100 余篇, 论文被各类 SCI 刊物累计引用 6590 余次, H 指数 36。973 项目首席科学家, 国家基金委创新群体项目负责人, 中科院战略性先导专项 (B) 两个首席科学家之一, 2012 年获得“国家自然科学二等奖”(第一完成人)。

实验室主页: [http://159.226.149.45/wangw2013/WenWang\\_Labweb\\_2013-3-22.htm](http://159.226.149.45/wangw2013/WenWang_Labweb_2013-3-22.htm)

### 重要成果 (Highlights)

#### 论著 (Publications)

1. Liu LY<sup>#</sup>, Wang JH<sup>#</sup>, Duan SC<sup>#</sup>, Chen L, Xiang H<sup>#</sup>, Dong Y<sup>#</sup>, Wang W<sup>#</sup>. Systematic evaluation of sericin protein as a substitute for fetal bovine serum in cell culture. *Sci Rep*. 2016, 6:31516
2. Liu H<sup>#</sup>, Ma X<sup>#</sup>, Yu HQ<sup>#</sup>, Fang DH, Li YQ, Wang X, Wang W, Dong Y<sup>#</sup>, and Xiao BG<sup>#</sup>. Genomes and virulence difference between two physiological races of *Phytophthora nicotianae*. *Gigascience*. 2016, 5:3
3. Li XW<sup>#</sup>, Kui L<sup>#</sup>, Zhang J, Xie YP, Wang LP, Yan Y, Wang N, Xu JD, Li CY, Wang W, van Nocker S, Dong Y<sup>#</sup>, Ma FW<sup>#</sup>, Guan QM<sup>#</sup>. Improved hybrid de novo genome assembly of domesticated apple (*Malus x domestica*). *Gigascience*. 2016, 5(1):35
4. Li HH<sup>#</sup>, Wang G<sup>#</sup>, Hao ZQ<sup>#</sup>, Zhang GZ, Qing YB, Liu SH, Qing LL, Pan WR, Chen L, Liu GC, Zhao RP, Jia BY, Zeng LY, Guo JX, Zhao LX, Zhao H, Lv CX, Xu KX, Cheng WM, Li HS, Zhao HY<sup>#</sup>, Wang W<sup>#</sup>, Wei HJ<sup>#</sup>. Generation of biallelic knock-out sheep via gene-editing and somatic cell nuclear transfer. *Sci Rep*. 2016, 6:33675
5. Li CC, Wang X, Cai HM, Fu YH, Luan Y, Wang W, Xiang H<sup>#</sup>, Li CC<sup>#</sup>. Molecular microevolution and epigenetic patterns of the long non-coding gene H19 show its potential function in pig domestication and breed divergence. *Bmc Evol Biol*. 2016, 16:87
6. Okpeku M<sup>#</sup>, Esmailzadeh A<sup>#</sup>, Adeola AC<sup>#</sup>, Shu LP, Zhang YS, Wang YZ, Sanni TM, Imumorin IG, Peters SO, Zhang JJ, Dong Y, Wang W<sup>#</sup>. Genetic Variation of Goat Interferon Regulatory Factor 3 Gene and Its Implication in Goat Evolution. *Plos One*. 2016, 11(9):e0161962
7. Hou YJ<sup>#</sup>, Ma X<sup>#</sup>, Wan WT, Long N, Zhang J, Tan YT, Duan SC, Zeng Y<sup>#</sup>, Dong Y<sup>#</sup>. Comparative Genomics of Pathogens Causing Brown Spot Disease of Tobacco: *Alternaria longipes* and *Alternaria alternata*. *Plos One*. 2016, 11(5):e0155258
8. Zhang J<sup>#</sup>, Tian Y<sup>#</sup>, Yan L<sup>#</sup>, Zhang GH<sup>#</sup>, Wang X, Zeng Y, Zhang JJ, Ma X, Tan YT, Long N, Wang YZ, Ma YJ, Xue Y, Hao SM, Yang SC, Wang W, Zhang LS<sup>#</sup>, Dong Y<sup>#</sup>, Chen W<sup>#</sup>, Sheng J<sup>#</sup>. Genome of octoploid plant maca (*Lepidium meyenii*) illuminates genomic basis for high altitude adaptation in the central Andes. *Mol Plant*. 2016, 9(7):1066-77.

### 1. 系统评估细胞培养中丝胶蛋白替代血清

血清作为常规细胞培养基的组分, 严重制约了动物细胞的细胞培养。开发无血清培养基能够提高细胞培养的安全性, 降低成本并且提高市场竞争力。无血清培养基中, 来自家蚕的丝胶蛋白就是一种替代血清的有效成分。然而, 丝胶蛋白替代血清的系统评估试验的缺乏极大地阻碍了无血清培养基的广泛接受和应用。

我们从细胞形态学、细胞生理学和转录组水平对三类广泛使用的哺乳动物细胞系在丝胶蛋白替代血清的培养条件下进行了评估。结果表明, 三类细胞系与对照组相比, 在丝胶蛋白替代血清培养条件下, 都具有相似的细胞形态、细胞代谢活力和更快的细胞分裂速率。其次, 在丝胶蛋白替代的条件下, 三种细胞的细胞群体倍增时间变短, S 和 G2 期的细胞百分比增大, G2 期和 G1 期细胞的 DNA 量比值没有变化, 这些结果说明了该培养条件不仅具有增加细胞增殖的潜力, 而且没有造成遗传物质的畸变。再次, 丝胶蛋白替代和血清培养条件下相比较, 三种细胞内的差异表达基因都主要富集在与细胞生长和细胞增殖过程。综上结果都表明, 丝胶替代血清维持动物细胞的生长和繁殖的效果与血清培养基相当或更好。

### 2. 黑胫病菌致病机制差异研究取得重要进展

黑胫病菌是我国农业重要的危害菌, 感染柑橘、烟草等多种茄科作物, 病发后植物出现茎部变黑、叶片枯萎等症状, 黑胫病菌在分布上又可以分为不同的生理小种, 不同生理小种间的致病性变异较大, 给防治工作带来了很大困难。我们在与云南烟科院合作下, 完成了中国危害最严重的两个黑胫病菌生理小种的基因组解析, 揭示了黑胫病菌生理小种间致病性差异的遗传机制, 对于防治黑胫病菌有着重要的应用意义。文章于 2016 年 1 月发表于 GigaScience 杂志, 当年影响因子 7.463, 第一作者刘晖博士为王文研究员的博士研究生, 通讯作者为云南烟科院肖炳光博士。

### 3. 取得高质量的苹果参考基因组

苹果世界上享有盛名的水果之一, 高质量的参考基因组对这一物种的品种选育和分子育种具有非常重要的意义。然而, 目前现有的苹果参考基因组质量较低, 远不能满足目前研究的需求。

为了组装高质量的苹果参考基因组, 中科院昆明动物研究所基因起源与进化课题组和西北农林科技大学园艺学院果树逆境生物学实验室全面合作, 选择苹果中的优良品种——金冠苹果为研究对象, 采用三代测序技术 (Pac Bio RS II 平台) 和二代测序技术 (Illumina Hiseq4000 平台) 对其进行基因组测序, 最终组装出的基因组大小为 632.4G, 基因组完整度为 90% 以上。成果于 2016 年 5 月发表于 GigaScience, 由基因起源与进化课题组博士研究生奎玲和逆境生物学实验室的李雪薇共同负责本项目的具体工作, 共同贡献, 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 6590 times with a H-index of 36. 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 the second prize in China's National Natural Science Award.

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## 1. Systematic evaluation of sericin protein as a substitute for fetal bovine serum in cell culture

Sericin protein derived from the silkworm cocoon has become increasingly popular due to its diverse and beneficial cell culture characteristics. However, systematic evaluation of sericin as a substitute for FBS in cell culture medium remains limited. In this study, we conducted cellular morphological, physiological, and transcriptomic evaluation on three widely used mammalian cells. Compared with cells cultured in the control, those cultured in sericin substitute medium showed similar cellular morphology, similar or higher cellular overall survival, lower population doubling time (PDT), and a higher percentage of S-phase with similar G2/G1 ratio, indicating comparable or better cell growth and proliferation. At the transcriptomic level, differentially expressed genes between cells in the two media were mainly enriched in function and biological processes related to cell growth and proliferation, reflecting that genes were activated to facilitate cell growth and proliferation. The results of this study suggest that cells cultured in sericin-substituted medium perform as well as, or even better than, those cultured in FBS-containing medium.

## 2. Genomes and virulence difference between two physiological races of *Phytophthora Nicotianae*

Black shank is a severe plant disease caused by the soil-borne pathogen *Phytophthora nicotianae*. Two physiological races of *P. nicotianae*, races 0 and 1, are predominantly observed in cultivated tobacco fields around the world. The molecular mechanisms underlying the difference in virulence between race 0 and 1 remain elusive. We assembled and annotated the genomes of *P. nicotianae* races 0 and 1, which were obtained by a combination of PacBio single-molecular real-time sequencing and second-generation sequencing (both HiSeq and MiSeq platforms). Gene family analysis revealed a highly expanded ATP-binding cassette transporter gene family in *P. nicotianae*. Specifically, more RxLR effector genes were found in the genome of race 0 than in that of race 1. In addition, RxLR effector genes were found to be mainly distributed in gene-sparse, repeat-rich regions of the *P. nicotianae* genome. These results provide not only high quality reference genomes of *P. nicotianae*, but also insights into the infection mechanisms of *P. nicotianae* and its co-evolution with the host plant.

## 3. Improved hybrid de novo genome assembly of domesticated apple (*Malus x domestica*)

Domesticated apple (*Malus x domestica* Borkh) is a popular temperate fruit with high nutrient levels and diverse flavors. A high-quality apple genome assembly is crucial for the selection and breeding of new cultivars. Currently, a single reference genome is available for apple, assembled from 16.9 × genome coverage short reads via Sanger and 454 sequencing technologies. Although a useful resource, this assembly covers only ~89 % of the non-repetitive portion of the genome, and has a relatively short (16.7 kb) contig N50 length. These downsides make it difficult to apply this reference in transcriptive or whole-genome re-sequencing analyses. Here we present an improved hybrid de novo genomic assembly of apple (Golden Delicious), which was obtained from 76 Gb (~102 × genome coverage) Illumina HiSeq data and 21.7 Gb (~29 × genome coverage) PacBio data. The new apple genome assembly will serve as a valuable resource for investigating complex apple traits at the genomic level. It is not only suitable for genome editing and gene cloning, but also for RNA-seq and whole-genome re-sequencing studies.

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## 比较基因组学

宿兵, 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、国家自然科学基金杰出青年基金获得者、“新世纪百万人才工程”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)

- Li, M., Luo, X.J., Landen, M., Bergen, S.E., ... (36 authors), Swedish Bipolar Study, G., Rietschel, M., Liu, C., Kleinman, J.E., Hyde, T.M., Weinberger, D.R. & **Su, B.\*** Impact of a cis-associated gene expression SNP on chromosome 20q11.22 on bipolar disorder susceptibility, hippocampal structure and cognitive performance. *British Journal of Psychiatry* 208, 128-37 (2016).
- Mendizabal, I.#, Shi, L.#, Keller, T.E., Konopka, G., Preuss, T.M., Hsieh, T.F., Hu, E., Zhang, Z., **Su, B.\*** & Yi, S.V.\* Comparative Methylome Analyses Identify Epigenetic Regulatory Loci of Human Brain Evolution. *Mol Biol Evol* 33, 2947-2959 (2016).
- Shi, L., Zhang, Z. & **Su, B.\*** Sex Biased Gene Expression Profiling of Human Brains at Major Developmental Stages. *Sci Rep* 6, 21181 (2016).
- Yang, Z., Zhong, H., Chen, J., Zhang, X., Zhang, H., Luo, X., Xu, S., Chen, H., Lu, D., Han, Y., Li, J., Fu, L., Qi, X., Peng, Y., Xiang, K., Lin, Q., Guo, Y., Li, M., Cao, X., Zhang, Y., Liao, S., Peng, Y., Zhang, L., Guo, X., Dong, S., Liang, F., Wang, J., Willden, A., Seang Aun, H., Serey, B., Sovannary, T., Bunnath, L., Samnom, H., Mardon, G., Li, Q., Meng, A., Shi, H. & **Su, B.\*** A Genetic Mechanism for Convergent Skin Lightening during Recent Human Evolution. *Mol Biol Evol* 33, 1177-87 (2016).
- Zhang, X., Zhang, Q. & **Su, B.\*** Emergence and evolution of inter-specific segregating retrocopies in cynomolgus monkey (*Macaca fascicularis*) and rhesus macaque (*Macaca mulatta*). *Sci Rep* 6, 32598 (2016).
- Shi, L., Hu, E., Wang, Z., 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* doi:10.1007/s00439-016-1748-5 (2016)

### 1. 揭示人和灵长类大脑在进化过程中的甲基化模式:

揭示人和灵长类大脑在进化过程中的甲基化模式: 表观遗传修饰的重要性越来越被人所认识, 但是表观遗传的变化如何对表型的进化产生影响, 特别是表观遗传调控在人类大脑进化中的作用仍然不是很清楚。为了揭示 DNA 甲基化在灵长类大脑功能演化中的变化模式, 我们对 4 个大脑容量调控关键基因 *ASPM*、*CDK5RAP2*、*CENPJ* 和 *MCPH1* 上游非翻译区 (5'-UTR) 的甲基化模式进行了系统的分析。发现 *CENPJ* 基因在人类大脑中是低甲基化的, 同时我们在人的大脑中检测到比非人灵长类高得多的 *CENPJ* 的表达。在人类大脑中 *CENPJ* 的低甲基化和高表达提示这一人类特异的表观遗传变化可能是伴随人类起源而发生的。由于 *CENPJ* 是神经发育调控的重要参与者, 所以我们推测 *CENPJ* 的高表达可能造成人类神经前体细胞数量的增加, 从而最终导致人类大脑容量的增加和认知能力的提高。研究结果发表在分子进化领域重要期刊 *Shi L et al. Mol Biol Evol* 31: 594-604 (2014)。该基因反映了在人类大脑中存在人类特异的低甲基化变化模式, 但这种人类特异的甲基化模式在全基因组水平的变化模式仍然不清楚。我们与 Soojin V. Yi 教授合作对人类、黑猩猩和猕猴 3 个物种的大脑前额叶进行了全基因组甲基化测序, 发现了 85 个人类特异的甲基化变化区域 (DMR)。进一步的重测序与基因表达验证发现, 大部分 DMR 集中在基因间区域, 而这些区域基本上都是 H3K4me3 标识的转录活跃区域; 这些区域可能通过影响一些神经特异转录因子的结合参与神经发育调控过程。研究结果提示表观遗传变化在人类大脑功能演化过程中发挥着重要的生物学功能。研究结果发表在分子进化领域重要期刊 *Mendizabal I., Shi L. et al. Mol Biol Evol.* 33(11):2947-2959。

### 2. 脑容量调控基因 *CASC5* 在现代人类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, 是现代人类特有的变异位点。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* (Published online 26 Nov 2016)。

### 3. 揭示东亚人群肤色变浅的分子机制

现代人类从起源地非洲向世界其它地区迁徙过程中, 会面临各种环境压力, 这些环境压力作为一种自然选择推动力促使人类的生理机能会发生一些适应性的进化。例如, 皮肤颜色的变化是人类进化历程中的重要事件, 我们的非洲祖先为了适应靠近赤道的高紫外线辐射环境而进化出很深的肤色, 而生活在高纬度地区人群的肤色较浅 (如下图), 这体现了人群对环境紫外线辐射强度变化的适应。前人的研究提出欧洲和东亚人群的肤色变浅可能是独立的进化事件。目前对欧洲人群的肤色变浅机制已有非常系统的研究, 并发现了一系列导致肤色、眼睛颜色和头发颜色变化的基因, 但是, 对东亚人群肤色变浅的遗传机制尚不清楚。东亚地区幅员辽阔, 纬度跨度很大, 常年紫外线的照射量随着纬度的不同有所差异, 是研究肤色变浅机制的理想地区。我们利用全基因组芯片技术系统分析近千份东亚人群的全基因组数据与肤色表型数据, 发现了具有深肤色的南亚语系人群与具有浅肤色的中国北方汉族人群之间遗传差异最大的色素基因——*OCA2*。该基因在东亚人群中受到了强烈的达尔文正向选择, 第 615 位的一个氨基酸突变 (rs1800414, His615Arg) 在东亚人群中广泛分布, 而欧洲和非洲人群中则没有这个突变。肤色表型相关性分析及体外和体内功能验证实验均证明了该突变会明显影响黑色素的合成和成熟, 最终导致东亚人群肤色的变浅。研究成果首次阐明了东亚人群肤色变浅的内在机制, 对深入理解趋同进化和表型适应性进化的遗传机制具有重要科学价值。研究结果发表在分子进化领域重要期刊 *Yang ZH et al. Mol Biol Evol* 33, 1177-1187 (2016)。

## 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. Comparative Methylome Analyses Identify Epigenetic Regulatory Loci of Human Brain Evolution

How do epigenetic modifications change across species and how do these modifications affect evolution? These are fundamental questions at the forefront of our evolutionary epigenomic understanding. Our previous work investigated human and chimpanzee brain methylomes, but it was limited by the lack of outgroup data which is critical for comparative (epi)genomic studies. Here, we compared whole genome DNA methylation maps from brains of humans, chimpanzees and also rhesus macaques (outgroup) to elucidate DNA methylation changes during human brain evolution. Moreover, we validated that our approach is highly robust by further examining 38 human-specific DMRs using targeted deep genomic and bisulfite sequencing in an independent panel of 37 individuals from five primate species. Our unbiased genome-scan identified human brain differentially methylated regions (DMRs), irrespective of their associations with annotated genes. Remarkably, over half of the newly identified DMRs locate in intergenic regions or gene bodies. Nevertheless, their regulatory potential is on par with those of promoter DMRs. An intriguing observation is that DMRs are enriched in active chromatin loops, suggesting human-specific evolutionary remodeling at a higher-order chromatin structure. These findings indicate that there is substantial reprogramming of epigenomic landscapes during human brain evolution involving noncoding regions. Mendizabal, I.#, Shi, L.#, et al *Mol Biol Evol* 33, 2947-2959 (2016).

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

Human evolution is marked by a continued enlargement of the brain. Previous studies on human brain evolution focused on identifying sequence divergences of brain size regulating genes between humans and nonhuman primates. However, the evolutionary pattern of the brain size regulating genes during recent human evolution is largely unknown. We conducted a comprehensive analysis of the brain size regulating gene *CASC5* and found that in recent human evolution, *CASC5* has accumulated many modern human specific amino acid changes, including two fixed changes and six polymorphic changes. Among human populations, 4 of the 6 amino acid polymorphic sites have 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 by regional Darwinian positive selection in East Asians. Further analysis of brain image data of Han Chinese showed significant associations of the amino acid polymorphic sites with gray matter volume. Hence, *CASC5* may contribute to the morphological and structural changes of the human brain during recent evolution. The observed between-population divergence of *CASC5* variants was driven by natural selection that tends to favor a larger gray matter volume in East Asians. **Shi L. et al. *Human Genetics* doi:10.1007/s00439-016-1748-5 (2016)**

### 3. A Genetic Mechanism for Convergent Skin Lightening during Recent Human Evolution

Skin lightening among Eurasians is thought to have been a convergence occurring independently in Europe and East Asia as an adaptation to high latitude environments. Among Europeans, several genes responsible for such lightening have been found, but the information available for East Asians is much more limited. Here, a genome-wide comparison between dark-skinned Africans and Austro-Asiatic speaking aborigines and light-skinned northern Han Chinese identified the pigmentation gene *OCA2*, showing unusually deep allelic divergence between these groups. An amino acid substitution (His615Arg) of *OCA2* prevalent in most East Asian populations—but absent in Africans and Europeans—was significantly associated with skin lightening among northern Han Chinese. Further transgenic and targeted gene modification analyses of zebrafish and mouse both exhibited the phenotypic effect of the *OCA2* variant manifesting decreased melanin production. These results indicate that *OCA2* plays an important role in the convergent skin lightening of East Asians during recent human evolution. Yang, Z. et al. *Mol Biol Evol* 33, 1177-87 (2016).

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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, 遗传资源与进化国家重点实验室学术委员会委员。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。已培养博士、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. Zhao Y, Wang Y, Zou L, **Huang J-F**<sup>\*</sup>. Reconstruction and applications of consensus yeast metabolic network based on RNA sequencing. *FEBS Open Bio*, 2016, 6(4): 264-75.
2. Li W-X, Li W, Cao J-Q, Yan H-Y, Sun Y-Y, Hong Z, Zhang Q, Tang L, Wang M-M, **Huang J-F**<sup>\*</sup>. Folate Deficiency Was Associated with Increased Alanine Aminotransferase and Glutamyl Transpeptidase Concentrations in a Chinese Hypertensive Population: A Cross-Sectional Study. *Journal of Nutritional Science and Vitaminology*, 2016, 62(4): 265-71.
3. Li W-X<sup>#</sup>, Dai S-X<sup>#</sup>, Wang Q, Guo Y-C, Hong Y, Zheng J-J, Liu J-Q, Liu D-H, Li G-H, **Huang J-F**<sup>\*</sup>. Integrated analysis of ischemic stroke datasets revealed sex and age difference in anti-stroke targets. *PeerJ*, 2016, 4: e2470.
4. Li W-X<sup>#</sup>, Dai S-X<sup>#</sup>, Liu J-Q, Wang Q, Li G-H, **Huang J-F**<sup>\*</sup>. Integrated analysis of Alzheimer's disease and schizophrenia dataset revealed different expression pattern in learning and memory. *Journal of Alzheimer's Disease*, 2016, 51(2): 417-25.
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### 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着许多限制和缺点。因此, 我们需要不断地研发新的、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。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 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。上述结果发表在 *Scientific Reports*。

### 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。上述结果发表在 *PeerJ*。



## 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, 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. Chen B, Shao JR, Zhuang HF, Wen JF\*. Evolutionary dynamics of triosephosphate isomerase gene intron location pattern in Metazoa: A new perspective on intron evolution in animals. 2016. *Gene*. Doi: 10.1016/j.gene.2016.11.027.
2. Ding KJ, Yang JZ, Reynolds GP, Chen, Shao JR, Liu RX, Qian QJ, Liu H, Yang RX, Wen JF\* & Kang CY\*. 2016. DAT1 methylation is associated with methylphenidate response on oppositional and hyperactive-impulsive symptoms in children and adolescents with ADHD. *World J Biol Psychiatry*.

### 1. 寄生原虫能量代谢途径的比较基因组学研究

寄生原虫是引起常见、甚至恶性的几种寄生虫病的病原体。它们之所以能十分成功地寄生于人类等宿主, 重要的原因就在于它们较之自由生活的近亲种类发生了显著的适应各自寄生生活的适应性进化, 其中能量代谢途径就是它们发生这种进化的重要方面。我研究组利用比较基因组学的手段对: 1) 亲缘关系较远但寄生在相似的低氧腔道环境的几种常见寄生原虫, 2) 同属顶复类但寄生环境不同的几种原虫, 分别进行了能量代谢途径系统的比较分析研究, 得到了以下结果与结论:

1) 蓝氏贾第虫、痢疾阿米巴、阴道毛滴虫和微小隐孢子虫的三羧酸循环、脂的氧化分解和氧化呼吸链的所有基因基本都发生了丢失, 却都存在丙酮酸 (Pyruvate) 代谢途径。对酶的调查进一步发现, 这些原虫中大量关键调控酶如 PEPCK, PFK 和 PFO 等都催化一样的反应, 行使相似的功能, 但这些酶的来源却不同。分子系统分析发现它们丙酮酸代谢途径中的如 MAL, PPK, ADHE 和 ACS 等基因都是通过不同的水平基因转移而来的。最重要的是, 我们发现这些原虫均是通过丙酮酸代谢途径与氧的“偶联”, 产生了一种随氧浓度不同而将丙酮酸代谢成不同终产物的“弹性”代谢机制以适应环境氧气的动态变化, 从而全面解除氧的有害作用。

2) 选取寄生部位不同的四种顶复类寄生原虫: 刚地弓形虫、恶性疟原虫、鼠隐孢子虫和微小隐孢子虫为研究对象, 并以它们的两种自由生活的近亲: 第四双小核草履虫和嗜热四膜虫为对照, 通过对 KEGG 数据库和这些原虫的全基因组数据进行调查, 并结合文献数据, 系统鉴定了相关代谢途径的基因/酶, 并进而重建了它们各自的能量代谢途径。研究结果表明顶复类寄生原虫的相关代谢基因在自由生活的近亲中基本都存在, 但相反, 在顶复门从自由生活的物种中分化出来后, 寄生原虫各自发生了相关基因的不同丢失或者改造。结合它们的寄生环境分析, 我们认为: 氧作为一种关键因子, 因其浓度在不同寄生环境中的不同而导致了这些原虫能量代谢的适应性辐射。

### 2. 内含子分布模式与后生动物的进化

内含子的进化, 包括其随着真核生物的进化过渡和多样化而发生的动态改变, 仍然悬而未决。由于数据缺乏造成的类群抽样不足, 不甚清楚的类群间系统演化关系, 以及研究外群的不当应用, 都可能是影响因素。除此之外, 一个基因中所有内含子的完整性, 在以往的研究中也往往被忽视。我们利用古老且保守的磷酸丙糖异构酶 (tim) 基因, 动物中相对清晰的系统演化关系, 且以领鞭毛虫为外群, 详细调查了动物界中内含子分布模式 (ILP) 的动态改变。从 10 个动物门类的 133 个物种中, 共计鉴定出 30 种 ILP 类型。最常见的一种, 包含最大数量的 6 个内含子位点, 在超过一半的调查物种中存在, 并出现在 6 个动物门类 (包括了动物界三大超群) 中, 并且, 高度相似的 ILP 在领鞭毛虫中也存在。该模式从而被推断为动物祖先中 tim 基因内含子分布的古老模式。该模式在原生动物的祖先中就已经形成, 且一直保留并传至每个后生动物门类的祖先类群; 在随后的动物分化过程中, 又出现不同的进化轨迹: 在后口动物类群中依然极其保守 (仅在少数快速进化的物种中发生细微的改变), 但在快速分化的原口动物类群中, 除了少量但十分显著的保守分布外, 更多的是发生了大规模的内含子丢失和相对较少的获得。因此, 本研究明确揭示出一个基因祖先型的外显子-内含子排列模式, 除了证实早期动物的基因中富含内含子这一观点外, 还揭示出基因结构的重排与物种/基因组的快速进化相关联, 而与动物的大生物进化事件 (如两侧对称体制、三胚层、脊索的出现等) 无关。本研究从一个新的视角探讨了内含子在动物界中的研究规律, 对内含子的进化研究有重要意义 (Gene. 2016)。



# 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. Comparative genomics of energy metabolism pathway in parasitic protists

1) *G. lamblia*, *E. histolytica*, *T. vaginalis* and *C. parvum* are several lumen parasitic protozoa, of energy metabolic pathways. In fact, the mitochondrion of these parasites have happened "degradation" or even "specialization" and have completely lost the oxidative phosphorylation function. These protozoa have all lost Krebs cycle, lipid oxidation decomposition and oxidative phosphorylation, their ATP generate are mainly rely on glycolysis. And we also find they all have a similar Pyruvate metabolic pathway. Further, we investigated the enzymes of energy metabolism, and found that a lot of enzymes, such as PEPC, PFK and PFO catalyzed same reaction in these parasites, but these enzymes come from different sources. We further constructed phylogenetic tree of MAL, PPK, ADHE and ACEL genes, and found they are acquired by horizontal gene transfer from different donors.

2) We selected four apicomplexan parasites that live in different parts of human body: *T. gondii*, *P. falciparum*, *C. muris* and *C. parvum* and along with its two free-living cousins *Paramecium tetraurelia* and *Tetrahymena thermophila* as comparison, we thoroughly searched energy metabolic genes in KEGG database and genome data of these parasites, and combining with literature data, system identification and rebuild their respective energy metabolic pathways. To reconstruction of both cryptosporidium species energy metabolic pathway, we chose toxoplasma and plasmodium experiment data as reference. Our results suggest that many enzymes which previous thought only in parasites are generally exist in the free living relatives of apicomplexan. Our above results suggest that an obvious is adaptive radiation has occurred in energy metabolisms among the four parasites, and the key factor is the environment oxygen concentration difference.

## 2. Evolutionary dynamics of triosephosphate isomerase gene intron location pattern in Metazoa: A new perspective on intron evolution in animals

Intron evolution, including its dynamics in the evolutionary transitions and diversification of eukaryotes, remains elusive. Inadequate taxon sampling due to data shortage, unclear phylogenetic framework, and inappropriate outgroup application might be among the causes. Besides, the integrity of all the introns within a gene was often neglected previously. Taking advantage of the ancient conserved triosephosphate isomerase gene (*tim*), the relatively robust phylogeny of Metazoa, and choanoflagellates as outgroup, the evolutionary dynamics of *tim* intron location pattern (ILP) in Metazoa was investigated. From 133 representative species of ten phyla, 30 types of ILPs were identified. A most common one, which harbors the maximum six intron positions, is deduced to be the common ancestral *tim* ILP of Metazoa, which almost had formed in their protozoan ancestor and was surprisingly retained and passed down till to each ancestors of metazoan phyla. Therefore, a common ancestral exon-intron arrangement pattern of an animal gene is definitely discovered; besides the 'intron-rich view' of early animal genes being confirmed, the novel insight that high exonintron re-arrangements of genes seem to be associated with the relatively recently rapid evolution of lineages/species/genomes but have no correlation with the ancient major evolutionary transitions in animal evolution, is revealed.

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## 进化与功能基因组学



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### 重要成果 (Highlights)

#### 论著 (Publications)

1. Li YY<sup>#</sup>, Liu Z<sup>#</sup>, Qi FY, Zhou X, Shi P<sup>\*</sup>, Functional effects of a retained ancestral polymorphism in *prestin*. *Molecular Biology and Evolution*, 34(1):88-92, 2017/1, (5-Year IF=13.002)
2. Zhang ZG<sup>#</sup>, Xu DM<sup>#</sup>, Wang L<sup>#</sup>, Hao JJ, Wang JF, Zhou X, Wang WW, Qiu Q, Huang XiD, Zhou JW, Long RJ<sup>\*</sup>, Zhao FQ<sup>\*</sup>, Shi P<sup>\*</sup>, Convergent Evolution of Rumen Microbiomes in High-Altitude Mammals. *Current Biology*, 26(14):1873-9, 2016/7, (5-Year IF=9.733)
3. Li ZP<sup>#</sup>, Wright ADG, Si HZ, Wang XX, Qian WX<sup>\*</sup>, Zhang ZG<sup>#</sup> and Li GY<sup>\*</sup>, Changes in the rumen microbiome and metabolites reveal the effect of host genetics on hybrid crosses. *Environmental Microbiology Reports*, 8(6):1016-1023, 2016/10, (5-Year IF=3.517)

### 1. 发现了动物适应性进化的第二套基因组学机制

中国科学院昆明动物研究所和北京生命科学研究院以及兰州大学的相关研究人员组成联合研究团队在动物适应性进化领域取得重大突破。该联合团队发现了动物适应高原极端环境过程中宿主和微生物组的协同进化, 是同域哺乳动物适应进化的必然选择之一。另外, 发现的低甲烷排放的高海拔哺乳动物, 为进一步通过生物调控策略缓解其他动物排放甲烷引起的温室效应具有重要的现实意义。2016年7月, 相关研究成果发表在学科顶级杂志 *Current Biology* 上 (doi: 10.1016/j.cub.2016.05.012), 并入选2016年《中国科学: 生命科学》的亮点研究工作 (Sci Sin Vitae, doi: 10.1360/N052016-00247)。当前, 该研究成果除被 *Nature Index* 收录, 被《*Mol Biol Evol*》发表的研究论文引用一次。



### 2. 导致表型趋同进化的新机制

表型的趋同变化通常被认为是适应性进化的结果, 对其分子机制的研究不仅能够探索基因型和表型的相互关系提供新的思路, 而且能够探究基因在演化过程中的可预测性和可重复性。利用分子进化理论和实验分析, 我们发现, 回声定位相关基因 *prestin* 的功能在回声定位调频蝙蝠中表现出了相同的功能变化。导致该趋同变化趋势的位点并不是受到趋同或平行进化的位点, 而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。该研究结果不仅提示着哺乳动物趋同性状回声定位演化的分子机制可能比之前预想的更加复杂, 而且进一步拓宽了人们对趋同性状发生发展的分子机制的认识。此研究结果以 *Functional effects of a retained ancestral polymorphism in prestin* 为题在线发表于 *Molecular Biology and Evolution* (doi: 10.1093/molbev/msw222) 上。



## 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. Convergent Evolution of Rumen Microbiomes in High-Altitude Mammals

Studies of genetic adaptation, a central focus of evolutionary biology, most often focus on the host's genome and only rarely on its co-evolved microbiome. The Qinghai-Tibetan Plateau (QTP) offers one of the most extreme environments for the survival of human and other mammalian species. Yaks (*Bos grunniens*) and Tibetan sheep (T-sheep) (*Ovis aries*) have adaptations for living in this harsh high-altitude environment, where nomadic Tibetan people keep them primarily for food and livelihood. Adaptive evolution affects energy-metabolism-related genes in a way that helps these ruminants live at high altitude. Herein, we report convergent evolution of rumen microbiomes for energy harvesting persistence in two typical high-altitude ruminants, yaks and T-sheep. Both ruminants yield significantly lower levels of methane and higher yields of volatile fatty acids (VFAs) than their low-altitude relatives, cattle (*Bos taurus*) and ordinary sheep (*Ovis aries*). Ultra-deep metagenomic sequencing reveals significant enrichment in VFA-yielding pathways of rumen microbial genes in high-altitude ruminants, whereas methanogenesis pathways show enrichment in the cattle metagenome. Analyses of RNA transcriptomes reveal significant upregulation in 36 genes associated with VFA transport and absorption in the ruminal epithelium of high-altitude ruminants. Our study provides novel insights into the contributions of microbiomes to adaptive evolution in mammals and sheds light on the biological control of greenhouse gas emissions from livestock enteric fermentation.

### 2. Functional Effects of a Retained Ancestral Polymorphism in *Prestin*

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.

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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* 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 2,900 余次，H 指数 27。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。

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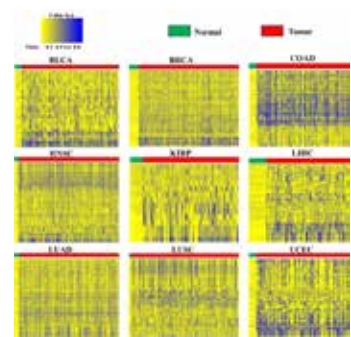
### 重要成果 (Highlights)

#### 论著 (Publications)

1. He YH<sup>#</sup>, Chen XQ<sup>#</sup>, Yan DJ, Xiao FH, Lin R, Liao XP, Liu YW, Pu SY, Yu Q, Sun HP, Jiang JJ, Cai WW\*, Kong QP\*. Familial longevity study reveals a significant association of mitochondrial DNA copy number between centenarians and their offspring. *Neurobiology of Aging*, 2016, 47: 218. e11-e18.
2. He YH, Pu SY, Xiao FH, Chen XQ, Yan DJ, Liu YW, Lin R, Liao XP, Yu Q, Yang LQ, Yang XL, Ge MX, Li Y, Jiang JJ, Cai WW\*, Kong QP\*. Improved lipids, diastolic pressure and kidney function are potential contributors to familial longevity: a study on 60 Chinese centenarian families. *Scientific Reports*, 2016, 6:10.1038.
3. Pu SY<sup>#</sup>, Yu Q<sup>#</sup>, 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*, 2016 (In press).
4. Jiang JJ, Cheng LH, Wu H, He YH\*, Kong QP\*. Insights into long noncoding RNAs of naked mole rat (*Heterocephalus glaber*) and their potential association with cancer resistance. *Epigenetics & Chromatin*, 2016, 9:51.
5. 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*, 2016 (In press).
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7. Li YC<sup>#</sup>, Huang W<sup>#</sup>, Tian JY, Kong QP\*. Exploring the maternal history of the Tai people. *Journal of Human Genetics*, 2016, 61(8): 721-729.
8. He YH, Lu X, Tian JY, Li YC, Ge MX, Yang XL, Chen XQ, Yu Q, W Huang, Cai WW\*, Kong QP\*. Mitochondrial DNA plays an equal role in influencing female and male longevity in Chinese centenarians. *Experimental Gerontology*, 2016, 83:94-96.

### 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。快速发展的肿瘤大数据积累，为从广义到狭义多方面深入理解肿瘤发生发展的分子机制提供了绝佳的契机。鉴于此，我们对 TCGA 数据库的 12 种肿瘤的 DNA 甲基化状态及其相应的基因表达谱进行整合分析，发现不同肿瘤钙信号通路均受高甲基化调控 (Wang et al. 2016 *Oncotarget*)。此外，我们还发现 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。不仅如此，ERCC6L 表达水平与患者的肿瘤分期高度相关，且该基因高表达可预示肿瘤患者的低生存率 (Pu and Yu et al. 2016 *Oncotarget*)。

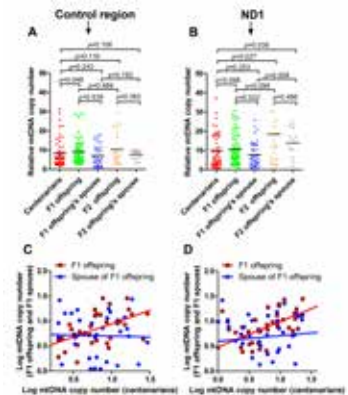


### 2. 长链非编码 RNA 与癌症的相关性研究

研究发现长链非编码 RNA (lncRNA) 不仅能精确调控发育和基因表达，还与诸多老年疾病的发生息息相关。我们分析 TCGA 数据库中 13 种肿瘤 RNA-seq 数据后发现一个 lncRNA (HILIC) 在人舌癌组织中显著高表达，通过功能实验证实了 HILIC 对舌鳞状细胞癌的迁移具有促进作用，且 HILIC 对肿瘤细胞的低氧应答具有重要调控作用 (未发表结果)。此外，从裸鼯鼠这一特殊的物种 (长寿且不患癌) 基因组中成功鉴定出 4,422 条高质量 lncRNA。通过共表达分析和功能预测发现大约 61.93% 的裸鼯鼠 lncRNA 与抑癌基因表达高度相关，进一步分析还发现裸鼯鼠的 lncRNA 与透明质酸相关基因存在较高的共表达关系，而透明质酸已被证实是裸鼯鼠具备抗癌特性的关键物质。这些结果表明裸鼯鼠的 lncRNA 可能通过调控透明质酸的生成，从而获得天然的抗癌特性 (Jiang et al. 2016 *Epigenetics & Chromatin*)。

### 3. 线粒体基因对家系长寿的影响研究

线粒体 DNA (mtDNA) 拷贝数对 ATP 产生和线粒体功能的维持具有重要作用。我们前期发现：衰老过程中 mtDNA 拷贝数呈下降趋势，而长寿老人的 mtDNA 拷贝数却显著高于普通老年人群。进一步发现该 mtDNA 拷贝数模式在长寿后代中也同样存在，提示 mtDNA 拷贝数的维持是家族长寿的重要原因；通过转录组测序和分析我们成功筛选到调控 mtDNA 拷贝数的关键基因 SSBP4 (He and Chen et al. 2016 *Neurobiology of Aging*)。由于女性寿命显著高于男性，且 mtDNA 遵循母系遗传规律，于是我们推测 mtDNA 可能对长寿的性别差异发挥作用，然而分析 402 例长寿老人和 458 例对照的



mtDNA 单倍型类群和遗传多样性，我们并未发现二者在男女之间存在差别 (He et al. 2016 *Experimental Gerontology*)，提示 mtDNA 对男女长寿可能具有相同的作用。

# 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*, with total citations over 2,900 times.

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## 1. Insights into the mechanism of tumorigenesis based on omics data

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. By analyzing the DNA methylation status and integrating the corresponding gene expression profile of 12 solid tumors, we showed that calcium signaling pathway is regulated by the hypermethylation across different tumor types (**Wang et al. 2016 Oncotarget**). 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. 2016 Oncotarget**).

## 2. Association between long noncoding RNAs and cancer

Long noncoding RNAs (lncRNAs) are a class of ubiquitous noncoding RNAs and have been found to act as tumor suppressors or oncogenes. By integrating bioinformatic analysis on RNA-seq data of 13 tumor types from TCGA database and a series of experimental research, we suggest that a long intergenic noncoding RNA, *HIL-INC*, was possibly involved in hypoxia response and tumorigenetic progress of head and neck squamous cell carcinomas (unpublished data). In addition, we developed a pipeline and identified a total of 4,422 lncRNAs in the genome of a seductive species, naked mole rat (NMR). Further correlation analysis indicated that some lncRNAs were intensively coexpressed with potential tumor-suppressor genes in NMR and four high-molecular-mass hyaluronan related genes which were previously identified to play key roles in cancer resistance of NMR. These results hint that lncRNAs may have effects on anti-cancer mechanism in NMR (**Jiang et al. 2016 Epigenetics & Chromatin**).

## 3. Effect of mitochondrial gene on familial longevity

Mitochondrial DNA (mtDNA) copy number is very important to ATP production and maintenance of mitochondrial function. We previously found that mtDNA copy number decreased during the aging process, which however exerted a higher level in longevity subjects than the general old subjects. Here, we showed evidence that this pattern of mtDNA copy number still exist in the offspring of the longevity subjects, indicating that the maintenance of mtDNA copy number is likely an important factor for familial longevity. Analyzing the transcriptome data from the same batch of longevity samples identified *SSBP4* gene to be the candidate regulator for mtDNA content (**He and Chen et al. 2016 Neurobiology of Aging**). In view of the gender dimorphism in human longevity as well as the maternal inheritance of mtDNA, we hypothesized that mtDNA may be involved in the gender dimorphism of longevity. However, analyses on mtDNA haplogroup and genetic diversity in longevity samples found no difference, indicating an equal role of mtDNA in determining male and female longevity in human (**He et al. 2016 Experimental Gerontology**).

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王昊天 Haotian Wang 2016

## 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; 以第一和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)

#### Highlights & Publications

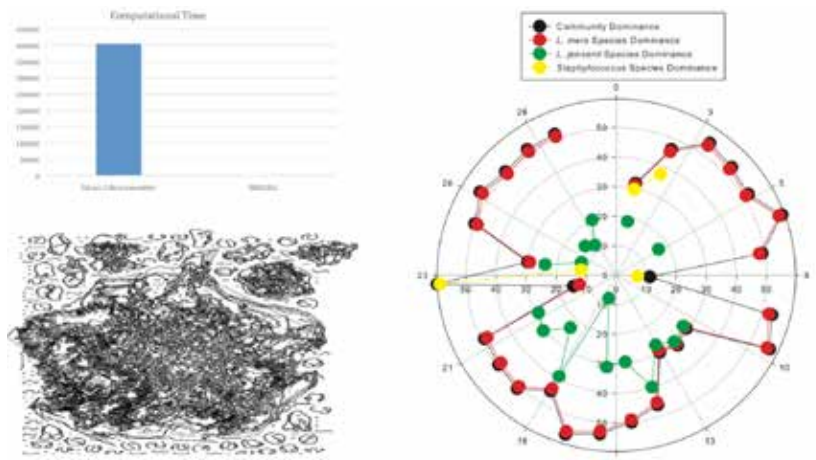
1. Ye CX & ZS Ma (2016) Sparc: a sparsity-based consensus algorithm for long erroneous sequencing reads. *PeerJ*. 4:e2016; DOI 10.7717/peerj.2016
  2. Ye CX, C Hill, J Ruan, ZS Ma (2016) DB-G2OLC: Efficient Assembly of Large Genomes Using Long Erroneous Reads of the Third Generation Sequencing Technologies. <http://www.nature.com/articles/srep31900>
  3. Li LW & ZS Ma (2016) Testing the Neutral Theory of Biodiversity with Human Microbiome Datasets. *Scientific Reports*. 6, Article No. 31448 <http://www.nature.com/articles/srep31448>
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  5. Ma ZS, LW Li, Wendy Li, J Li, HJ Chen (2016) Integrated network-diversity analyses suggest suppressive effect of Hodgkin's lymphoma and slightly relieving effect of chemotherapy on human milk microbiome. *Scientific Reports*, vol. 6, Article Number 28048,
  6. Ma ZS et al. (2016) A brief review on the ecological network analysis with applications in the emerging medical ecology. *Hydrocarbon and Lipid Microbiology Protocols*, Springer
- 7-12: 六项菌群生物信息学/医学生态学分析发明专利受理; 专利受理号如下:

201610584196.2  
201611126939.8  
201611127036.1  
201611126940.0  
201710066344.6  
201710063855.2  
201510084489.X

### 学科组重点研发领域简介

计算生物与医学生态学学科组成立之初(2011年)设定了两项主要研究目标:(1)基因组学软件开发;(2)微生物菌群宏基因组学。过去六年间,我们开发公布了三款大型基因组装软件:SPARC (2016: <https://sourceforge.net/projects/sparc-consensus/>)、DBG2OLC (2014: <http://sites.google.com/site/dbg2olc/>) 和 SparseAssembler (2012: <https://sites.google.com/site/sparseassembler/>)。其中前两款软件因分别解决了最新第三代基因测序超高错误率(15%-40%)以及超长计算时间和超大内存的技术难题【谷歌超级集群耗时达40万CPU小时:图(A)】,而处于行业国际领先水平。另外一款软件的核心算法 Sparse k-mers 发布后不久即为华大基因的旗舰软件 Soapdenovo-2 所采用,而成为目前二代基因测序最广泛使用的算法。在菌群宏基因组学领域,我们提出菌群“医学生态学”应该成为人体菌群宏基因组研究的核心理论之一,并为研发具有广泛应用前景的技术(特别是个性化精准医学)提供科学的分析方法。遵循这一研究目标,我们研发出了一系列医学生态学分析方法和软件,并加快积累相关的知识产权。仅2016年就有6项菌群医学生态学分析技术的专利受理。而一套涵盖生态建模分析、复杂网络分析,以及综合两类分析技术的大型软件工具包正在紧张的研发中,预计2018年前将对外发布。该软件包超越了目前微生物生态学和菌群宏基因组研究最广泛使用的大型软件包 QIIME 和 MOTHUR 的功能,并将重心放置在新方法和新技术功能的设计和实现,该软件包将定位于成为领域顶尖的软件工具之一。

事实上,医学生态学范畴不仅仅限于人类微生物菌群生态系统。虽然我们强调的生态学与医学交叉不应该像目前社会大众对“生态”一词的使用,但是现代医学的诸多领域确实需要生态学理论和研究方法。例如,癌细胞生态位理论显然来自于生态学,传统中医理论也饱含生态学思想。人体菌群具有非常显著的个体差异,也即高度的时空异质性,更加重要的是菌群失调(Dysbiosis)这一菌群相关疾病最重要的表征之一,事实上是一个生态平衡问题。因此,我们认为,医学生态学应该成为精准医学(特别是基于宏基因组大数据信息的精准医学)的核心理论之一。例如:图(B)显示我们首次提出的物种优势度(Species Dominance)与群落优势度(Community Dominance)的概念和模型以及在菌群相关疾病个性化诊断方面的应用(专利受理号:201710063855.2)。图(C)-(E)分别显示团队成员学科背景,我们对医学生态学的认知,以及正在开发软件的设计。



(A) 三代基因测序软件比较

(B) 统一的物种/群落优势度新概念

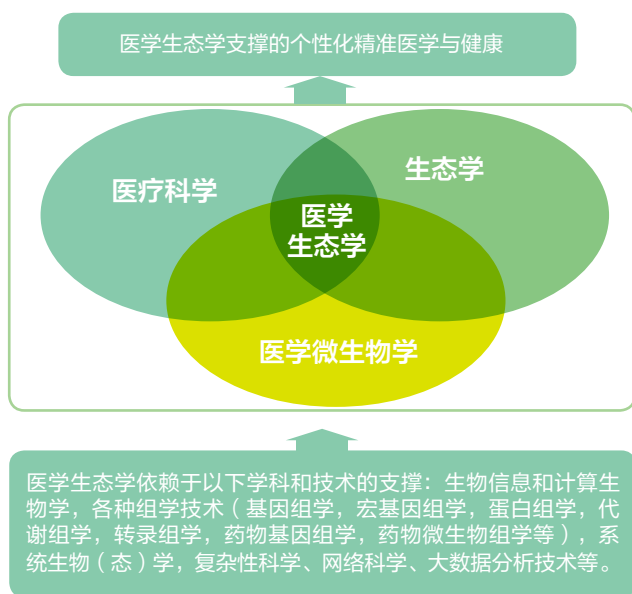
# Computational Biology and Medical Ecology

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

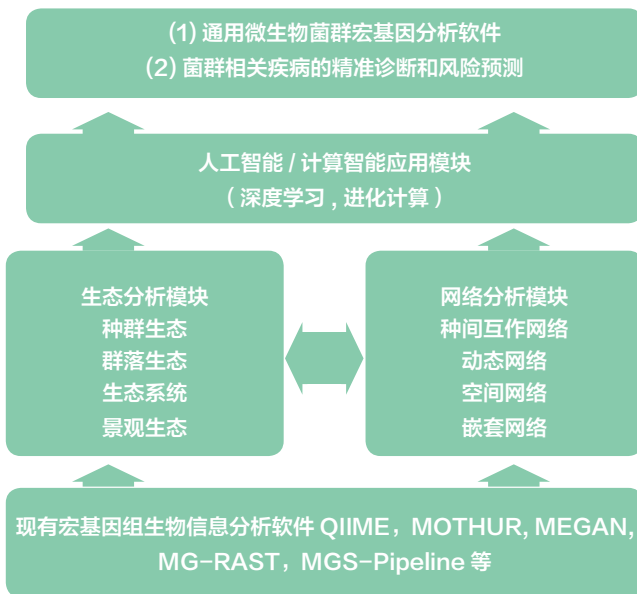


## (C) 团队成员背景简介

姓名	职位	背景	姓名	职位	背景
李连伟	助理研究员	生物信息学 (昆明理工与中科院联合培养)	夏尧	博士生	计算生物学, 公共卫生统计硕士 (中山大学)
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肖琬蒙	硕士生	生物信息学 (四川农业大学)	王慧敏	硕士生	数学 (昆明理工大学)
彭舒婷	硕士生	数理统计 (昆明理工大学)	寇贺丹	硕士生	数理统计 (昆明理工大学)
叶承曦	客座助理研究员	计算机科学 (美国马里兰大学博士)	邹权	客座教授	天津大学计算机科学教授



(D) 医学生态学概念 (Ma 2012, 2016)



(E) 菌群宏基因大数据分析软件系统





## 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 )

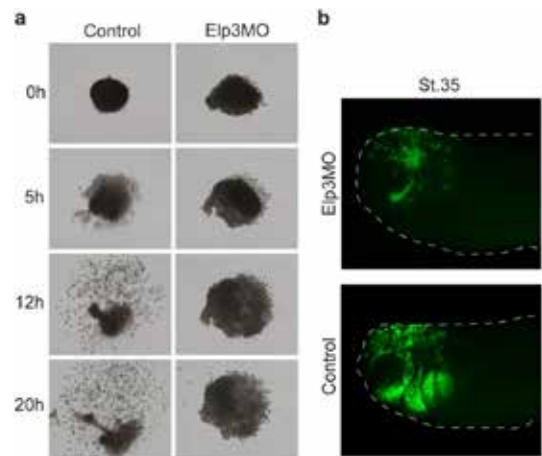
1. Yang X, Li J, Zeng W, Li C, **Mao B\***. Longator Protein 3 (Elp3) stabilizes Snail1 and regulates neural crest migration in *Xenopus*. *Scientific Reports*, 2016, 6:26238.
2. Wang X, Sun J, Li C, **Mao B\***. EphA7 modulates apical constriction of hindbrain neuroepithelium during neurulation in *Xenopus*. *Biochem Biophys Res Commun*. 2016, 479:759-765.
3. Liu X, Yang X, Li Y, Zhao S, Li C, Ma P\*, **Mao B\***. Trip12 is an E3 ubiquitin ligase for USP7/HAUSP involved in the DNA damage response. *FEBS letters*, 2016, 590:4213-4222
4. Yang K, Chen Y, Zhang Z, Ng P, Zhou W, Zhang Y, Liu M, Chen J, **Mao B\***, Tsui S\*. Transcriptome analysis of different developmental stages of amphioxus reveals dynamic changes of distinct classes of genes during development. *Scientific Reports*, 2016, 6:23195

### 1. Elp3 调控非洲爪蛙神经嵴细胞迁移

发现延伸因子复合物的第三亚基 Elp3 在非洲爪蛙神经嵴发育中具有重要作用。elp3 表达于非洲爪蛙胚胎迁移前和迁移中的神经嵴细胞中, 敲低 elp3 会抑制神经嵴细胞的迁移。而免疫共沉淀实验表明, Elp3 可以与调控神经嵴迁移的关键因子 Snail1 相互作用, 共表达 Elp3 降低可 Snail1 的泛素化水平并提高其蛋白稳定性。敲低 elp3 会造成神经嵴细胞粘附分子 N-cadherin 表达的下调, 而且共表达 mSnail1 或者 mN-cadherin 都可以挽救敲低 elp3 造成的神经嵴细胞迁移受损的表型。本项研究发现 Elp3 可能是通过稳定 Snail 蛋白, 激活 N-cadherin 的表达来调控非洲爪蛙神经嵴细胞迁移的功能发表在 *Scientific Reports*。

图 1 通过 Morpholino (MO) 敲低 Elp3 表达抑制非洲爪蛙神经嵴细胞迁移。

Fig.1 Knockdown of Elp3 by specific morpholino inhibits neural crest cell migration in *Xenopus*.



### 2. 文昌鱼早期发育的转录组分析

通过对文昌鱼不同发育时期混合样本的转录组分析, 获得了约 44166 个转录本, 通过数字化表达谱分析对基因表达 TAG 的高通量测序分析, 获得了 9000 多个基因在文昌鱼胚胎发育过程中的表达变化数据。与香港中文大学徐国荣教授课题组合作, 完成了转录组的拼装与数据分析。通过对不同发育时期胚胎进行了 SAGE 表达谱分析, 并与转录组数据进行了比对, 建立了文昌鱼早期发育基因表达的基本蓝图。通过共表达调控网络分析, 筛选了在不同发育时期差异表的基因, 鉴定了文昌鱼的母型-合子型转变 (MBT) 的时期和一批在 MBT 之前起始表达的基因, 可能在胚胎的早期发育中具有重要功能。上述结果为在基因组水平系统分析其早期胚胎发育的基因调控网络奠定了基础。论文发表于 *Scientific Reports*。

# 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. Elongator Protein 3 (Elp3) regulates neural crest migration in *Xenopus*

Elongator protein 3 (Elp3) is the enzymatic unit of the elongator protein complex, a histone acetyltransferase complex involved in transcriptional elongation. It has long been shown to play an important role in cell migration; however, the underlying mechanism is unknown. Here, we showed that Elp3 is expressed in pre-migrating and migrating neural crest cells in *Xenopus* embryos, and knock-down of Elp3 inhibited neural crest cell migration. Interestingly, Elp3 binds Snail1 through its zinc-finger domain and inhibits its ubiquitination by  $\beta$ -Trcp without interfering with the Snail1/Trcp interaction. We showed evidence that Elp3-mediated stabilization of Snail1 was likely involved in the activation of N-cadherin in neural crest cells to regulate their migratory ability. Our findings provide a new mechanism for the function of Elp3 in cell migration through stabilizing Snail1, a master regulator of cell motility.

## 2. Transcriptome analysis of different developmental stages of amphioxus

Amphioxus is widely used in evolutionary developmental biology research, such as on the basic patterning mechanisms involved in the chordate body plan and the origin of vertebrates. In this study, we applied high-throughput sequencing on the transcriptomes of 13 developmental stages of Chinese amphioxus to gain a comprehensive understanding of transcriptional processes occurring from the fertilized egg to the adult stage. The expression levels of 3,423 genes were significantly changed. All of these genes were included in a clustering analysis, and enrichment of biological functions associated with these clusters was determined. Significant changes were observed in several important processes, including the down-regulation of the cell cycle and the up-regulation of translation.

## 员工简介 (Lab Staff)

### 工作人员 (Staff)

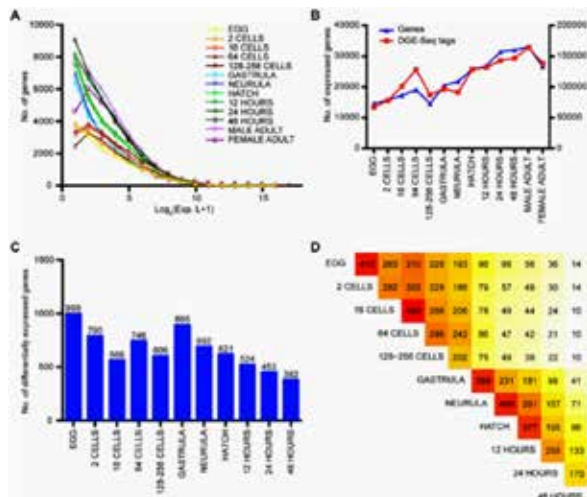
- 李朝翠 高级实验师  
Chaocui Li, Senior Technician
- 马鹏程 助理研究员  
Pengcheng Ma, Assistant Professor

### 研究生 (Graduate Students)

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- 刘晓亮 Xiaoliang Liu, 2011
- 李永鑫 Yongxin Li, 2013
- 杜加诚 Jiacheng Du, 2014
- 任碧玉 Biyu Ren, 2015
- 朱良 Liang Zhu, 2016

图 2. 文昌鱼早期发育的转录组分析

Figure 2. Expression profiles of transcripts across different developmental stages in amphioxus.





## 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) 早期胚胎如何有效维持遗传物质的稳定性。采用卵细胞、早期胚胎及胚胎干细胞等研究体系, 在小鼠、猕猴及人上系统研究早期胚胎维持遗传物质稳定性的调控机制; 2) 生殖干细胞的基础及应用研究。着重研究哺乳动物卵巢中是否存在雌性生殖干细胞及基于干细胞的卵细胞再生。并在树鼩及猴中研究精原干细胞调控自我更新及分化的机制, 并利用精原干细胞进行基因修饰, 建立树鼩及猴人类疾病动物模型。

### 重要成果 (Highlights)

#### 论著 (Publications)

1. Chao-Hui Li, Lan-Zhen Yan, Wen-Zan Ban, Qiu Tu<sup>4</sup>, Yong Wu, Lin Wang, Rui Bi, Shuang Ji, Yu-Hua Ma, Wen-Hui Nie, Long-Bao Lv, Yong-Gang Yao \*, Xu-Dong Zhao \*, and Ping Zheng \*. Long-term propagation of tree shrew spermatogonial stem cells in culture and successful generation of transgenic offspring. *Cell Res* (in press).
2. Xinyi Wang, Denghui Liu, Dajian He, Shengbao Suo, Xian Xia, Xiechao He, Jing-Dong J. Han#, Ping Zheng#. 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* (in press).
3. Yong-qing Lu, Xie-chao He, Ping Zheng\*, Decrease in expression of maternal effect gene *Mater* is associated with maternal ageing in mice. *Mol Hum Reprod*. 2016;22(4):252-60.
4. Guo K, Li CH, Wang XY, He DJ, Zheng P\*. Germ stem cells are active in postnatal mouse ovary under physiological conditions. *Mol Hum Reprod*. 2016;22(5):316-28

### 1. 胚胎干细胞应对 DNA 复制压力的分子机制研究

相对于分化细胞, 多能干细胞具有更强的 DNA 复制压力应对能力, 但具体机制尚不明确。我们首次鉴定出了多能干细胞特异表达蛋白 Filia 和 Floped 在调控复制压力反应方面的功能及机制。复制压力诱导 ATR 依赖的 Filia S151 位点磷酸化。p-Filia S151 与 Floped 蛋白形成复合体, 该复合体作为脚手架募集 E3 连接酶 Trim25, Trim25 进一步通过泛素化修饰募集解旋酶 Blm 到受阻的复制叉位点, 促进受阻复制叉的重启, 从而维持遗传物质稳定。该研究首次系统而深入地揭示了多能干细胞应对 DNA 复制压力的分子机制 (投稿中)。

### 2. 精原干细胞介导的转基因树鼩研究

树鼩作为新型实验动物在遗传及生理生化上接近于灵长类, 且繁殖周期短、生长快、价格适宜。然而, 缺乏遗传操作手段严重制约了树鼩的广泛应用。我们找到了用于分离和富集树鼩精原干细胞的表面分子标记, 并通过一系列的 RNA-seq 分析, 筛选到了调控树鼩精原干细胞自我更新的关键信号通路, 在此基础上逐步完善并最终建立了树鼩精原干细胞体外长期扩增培养体系, 建立了多株稳定的树鼩精原干细胞系, 并证明它们适用于 CRISPR-Cas9 介导的基因修饰。最后, 我们将携带 EGFP 的转基因精原干细胞移植到受体睾丸中, 将恢复生精功能的雄性受体和雌性树鼩交配, 获得了国际首批 EGFP 转基因树鼩。在出生的子代树鼩中, 约 6% 携带了转基因, 证明该方法的有效性和可行性。该工作解决了树鼩研究中缺乏基因操作技术的瓶颈难题, 为树鼩作为新型实验动物的广泛应用打下良好基础。论文于 2016 年 12 月 23 日在 *Cell Research* 上在线发表。

### 3. 猕猴早期胚胎发育

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。我们通过转录组分析, 绘制了首个详尽的猕猴着床前不同阶段胚胎发育基因表达图谱, 并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。通过系统比较和功能验证, 发现灵长类 (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, 其差异主要表现在 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, 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。论文已经被 *Genome Research* 接收。



# Mammalian Embryonic Development

**Prof. Ping Zheng**, Principal Investigator, joined in Kunming Institute of Zoology, Chinese Academy of Sciences in 2009. Our laboratory focuses on the regulation of genomic stability in early embryos, the biology of the germ 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

Embryonic stem cells (ESCs) encounter higher replication stress than differentiated cells, but the underlying mechanisms remain unclear. We report a ESCs specific Filia-Floped complex-dependent mechanism in maintaining their genomic stability by efficiently promoting the restart of stalled replication forks. ESC-specific Filia-Floped protein complex resides on replication forks. Upon replication stress, more Filia-Floped proteins are recruited to stalling forks and the serine 151 residue of Filia is phosphorylated in ATR-dependent manner. This phosphorylation modification enables Filia-Floped complex to act as a functional scaffold to recruit Trim25, an E3 ubiquitin ligase, to the stalled replication forks. Trim25 in turn ubiquitinates Blm to enhance its retention at stalled replication forks to promote their restart. The recruitment of the Trim25-Blm complex to replication forks in differentiated cells is less efficient due to lack of the PSC-specific Filia-Floped scaffold. Our study reveals a unique mechanism of promoting the stalled fork restart in PSCs.

## 2. Establishment of spermatogonial stem cell-based transgenic tree shrew

Tree shrews have a close relationship to primates and have many advantages over the use of rodents in biomedical research. However, a lack of gene manipulation methods has hindered the wider usage of this animal. Spermatogonial stem cells (SSCs) have been successfully expanded in culture to permit sophisticated gene editing in the mouse and rat. Here, we describe a culture system for the long-term expansion of tree shrew SSCs without the loss of stem cell properties. The expanded tree shrew SSCs were transfected with enhanced green fluorescent protein (EGFP)-expressing lentiviral vectors. After transplantation into sterilized adult male tree shrew testes, the EGFP-tagged SSCs were able to restore spermatogenesis and successfully generate transgenic offspring. Moreover, these SSCs were suitable for the CRISPR/Cas9-mediated gene modification. Thus, this study paves the way for precise genome manipulations using the tree shrew. *Cell Research* (in press).

## 3. Rhesus monkey early embryogenesis

The early embryo of the primate has more chromosome abnormality and higher rate of embryo wastage than in the rodent, but the mechanism is still unknown. Through the single-embryo transcriptome analyses, we report the genome-wide gene expression dynamics in rhesus monkey oocytes and pre-implantation embryos. We identified several classes of maternal and zygotic genes, whose expression peaks were highly correlated with the time frames of genome reprogramming, zygotic genome activation (ZGA) and cell fate commitment, respectively. Importantly, comparison of the ZGA-related network modules 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 provide insights for improved homologous recombination-mediated gene editing based on CRISPR/Cas9 in monkey. *Genome Research* (in press).

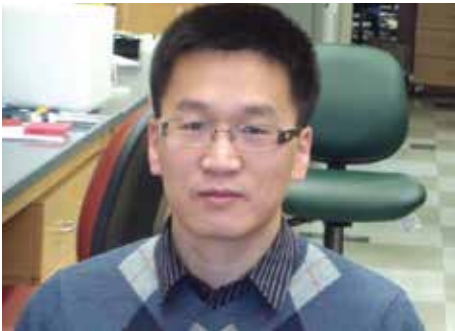
## 员工简介 (Lab Staff)

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赵博 副研究员  
王林 助理研究员

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何大健	He Dajian	2012
郭琨	Guo Kun	2012
张伟道	Zhang Weidao	2013
班文赞	Ban Wenzan	2013
李竞争	Li Jingzheng	2014
陈忠良	Chen Zhongliang	2015
孙春丽	Sun Chunli	2015
刘焱	Liu Yan	2015
李聪	Li Cong	2016
李秀峰	Li Xiufeng	2016



## 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. Ke H<sup>#</sup>, Zhao L<sup>#</sup>, Feng X, Xu H, Zou L, Yang Q, Su X, Peng L, Jiao B<sup>\*</sup>. NEAT1 is Required for Survival of Breast Cancer Cells Through FUS and miR-548. Gene Regulation and Systems Biology, 2016, 10(Suppl 1):11-7.
2. Wu Y<sup>#</sup>, Feng X<sup>#</sup>, Gao L<sup>\*</sup>, Jiao B<sup>\*</sup>. Imprinted genes: important regulators in development. Yi Chuan. 2016 Jun 20;38(6):508-522.

### 1. XCI 在发育中的作用

#### a. XCI 对于乳腺发育的表观遗传调控作用

近年来愈来愈多的证据表明乳腺的泌乳功能极大程度地被表观遗传机制控制: 如跨代遗传机制影响。我们的结论表明这一隔代现象与表观遗传中的另外一个重要表观遗传机制—XCI 有关。该部分将致力于分析 XCI 对于小鼠和其它模式动物的乳腺及其它营养器官发育的影响。

#### b. X 耦联基因在乳腺干细胞调控过程中的作用

乳腺干细胞属于成体干细胞的一种, 具有自我更新和分化为其他细胞群的能力。它对于乳腺发育具有至关重要的作用。我们初步数据显示 XCI 对于乳腺干细胞具有调控作用, 并将通过 X 耦联基因的功能研究分析和探讨 XCI 对乳腺干细胞的影响。

### 2. XCI 在遗传印迹进化中的角色分析

#### a. 乳腺泌乳性状在人工选择下的演化

遗传印迹是进化发育研究中的重要问题, 对于其起源及演化目前存在三种假说: 亲本冲突假说 (kinship conflict)、共适应假说 (coadaptation) 和性别冲突假说 (intra-locus sexual conflict)。我们在小鼠乳腺中的分析倾向于支持亲本冲突假说。除了自然选择, 人工选择筛选下乳腺性状对于亲本冲突的处理策略将是一个值得探讨的科学问题。我们将通过各种模式及家养哺乳动物乳腺和胎盘中 XCI 的状态, 分析 XCI 在成体组织和胚胎组织中功能的平衡及其进化意义。

#### b. XCI 在性染色体进化中的角色分析

不同的哺乳动物具有不同的 XCI 格局, 它们对于 XCI 中的重要分子和现象都呈现出极大的多样性。即使在小鼠和人这两个相近的物种, 人们也已发现极大的区别。对于这方面进行研究将丰富人们对于包括 X 染色体进化等现象的理解。在初步的探讨中, 我们将以我所优势动物模型树鼩和猕猴等为切入点, 通过分析对比小鼠 XCI, 为揭示 X 染色体进化规律提供支持论据。

### 3. 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。

### 4. 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:

#### The role of XCI in development

##### The epigenetic regulation of XCI in mammary gland development

Recently, more and more evidence shows that the mammary gland function of lactating is greatly regulated by epigenetic modification, such as inter-generational genetic. Our conclusions demonstrate that the phenomenon of inter-generational epigenetic is closely linked to another important epigenetic mechanism--XCI. We will focus on analyzing the impact of XCI in breast and other nutrients organ development for mice and other animals.

##### The role of X-linked genes on mammary stem cell

As one of adult stem cells, Mammary stem cells are capable of self-renewal and differentiation into other cell lines, which is crucial for breast development. Our preliminary data shows that XCI play a role in regulation of mammary stem cells; next, we will investigate the effects of XCI on mammary stem cells through analyzing the function of X-linked genes locus.

#### The role of XCI in the evolution of genetic imprinting

##### Evolution of lactating under artificial selection

Evolutionary developmental is an important issue on studying genetic imprinting, which exists three hypotheses: kinship conflict, co-adaptation and intra-locus sexual conflict. Our analysis in mouse mammary gland tends to support the hypothesis of kinship conflict. In addition to natural selection, artificial selection will be a wonderful strategy of exploring kinship conflict in screening breast traits. We will analyze the function of XCI in adult tissues and embryonic tissues development by studying the XCI status of breast and placenta in mouse and other model organism.

##### The role of XCI in sex chromosome evolution

Different mammals have their own pattern on XCI. Even between mouse and human, it shows a great difference, which will offer more comprehensive understanding on sex chromosome evolution. We will compare pattern of XCI among different animals, such as tree shrews and macaques, in order to reveal the law of the evolution on X chromosome.

#### 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.

### 员工简介 (Lab Staff)

#### 工作人员 (Staff)

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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学位论文, 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基金二等奖(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)

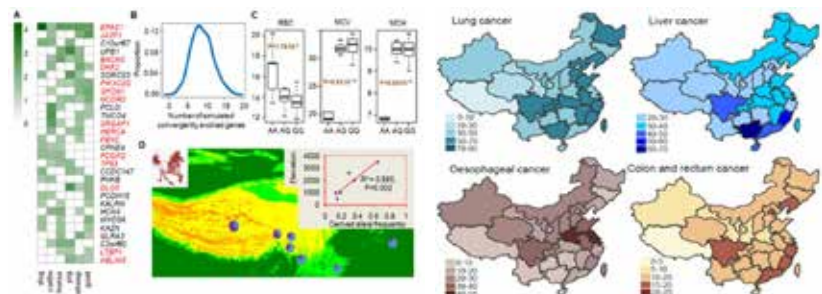
1. Wang MS, Yang HC, Otecko N, **Wu DD#**, Zhang YP#. Olfactory genes in Tibetan wild boar. *Nature Genetics* 2016 48(9):972-973. (SCI IF=31.616)
2. Li Y, Wang MS, Otecko N, Wang W, Shi P, **Wu DD#**, Zhang YP#. Hypoxia Potentially Promotes Tibetan Longevity. *Cell Research* 2016 doi: 10.1038/cr.2016.105 (SCI IF=14.812)
3. Wang MS, Su LY, Li Y, Peng MS, Liu HQ, Zeng L, Irwin DM, Yao YG, **Wu DD#**, Zhang YP#. Positive selection rather than relaxation of functional constraint drives the evolution of vision during chicken domestication. *Cell Research* 2016 26(5):556-573 (SCI IF=14.812)
4. Wang MS, Huo YX, Li Y, Otecko N, Su LY, Xu HB, Wu SF, Peng MS, Liu HQ, Zeng L, Irwin DM, Yao YG, **Wu DD#**, Zhang YP#. Comparative population genomics reveal genetic basis underlying body size of domestic chickens. *Journal of Molecular Cell Biology* 2016 (SCI IF= 6.459)
5. Wang MS\*, Li Y\*, Peng MS\*, Zhong L, Wang ZJ, Li QY, Tu XL, Dong Y, Zhu CL, Wang L, Yang MM, Wu SF, Miao YW, Liu JP, Irwin DM, Wang W, **Wu DD #**, Zhang YP#. Genomic Analyses Reveal Potential Independent Adaptation to High Altitude in Tibetan Chickens. *Molecular Biology and Evolution* 2015 32(7):1880-1889. (SCI IF=13.649)
6. **Wu DD\***, Ye LQ\*, Li Y\*, Sun YB, Shao Y, Chen C, Zhu Z, Zhong L, Wang L, Irwin DM, Zhang YE, Zhang YP. Integrative analyses of RNA-editing, alternative splicing and expression of young genes in human brain transcriptome by deep RNA-sequencing. *Journal of Molecular Cell Biology* 2015 7(4):314-325. (SCI IF= 6.459)
7. Li Y, **Wu DD #**, Boyko AR, Wang GD, Wu SF, Irwin DM, Zhang YP#. Population variation revealed high-altitude adaptation of Tibetan mastiffs. *Molecular Biology and Evolution* 2014 31(5):1200-1205. (SCI IF=13.649)

### 1. 青藏高原家养动物适应性状的解析

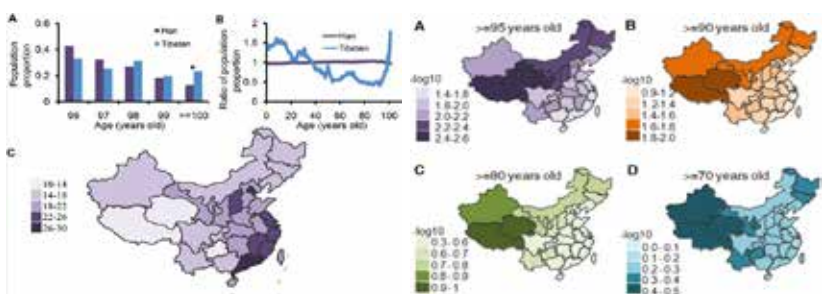
我们获得了超过 1000 个来自青藏高原和平原的家养动物(包括马、牛、狗、猪、山羊、绵羊、驴、鸡等)的基因组数据, 以期解析青藏高原家养动物高原适应的共性和个性特征。我们揭示了各个家养动物的高原适应的遗传基础。发现藏鸡有两个群体, 分别来自两个独立的世系, 钙离子通路在藏鸡高原适应中有着重要的作用。趋同进化在家养动物高原适应中普遍存在, 尤其是 *EPAS1* 基因在六个家养哺乳动物中均受到正选择作用 (Fig.1)。我们亦发现一个功能未知的基因在三个家养动物中发生快速进化, 进一步的细胞实验证明该基因很可能参与到低氧应激通路中, 在低氧适应中起到重要作用。

### 2. 低氧与健康

低氧是高原环境典型的特征, 亦是各种疾病尤其是肿瘤发生的重要因素。我们通过全基因组水平揭示了青藏高原各种动物的高原适应性遗传机制, 发现很多肿瘤发生相关基因发生快速进化。从这些发生快速进化的基因中, 我们亦研究揭示数个之前未报到与肿瘤发生相关的基因在肿瘤发生中起着重要作用。同时发现青藏高原人群癌症发生率较低 (Fig. 2), 间接揭示癌症发生的特征, 提示青藏高原适应的生物可能可以作为研究癌症发生的天然实验模型。



模式动物在实验室低氧条件下寿命会延长, 但是青藏高原人群的寿命却显著低于平原人群。我们基于中国人口普查数据分析显示, 藏族人群中的极端老年人群比例比平原人群高, 且老年人群相对死亡率低, 揭示藏族人群老年人可能更易长寿 (Fig. 3-4)。进一步群体遗传分析表明, 衰老相关的基因在藏族人群和西藏家养动物中受到正选择作用。我们的数据表明, 达尔文正选择作用可能促使自然界中低氧条件下人类的长寿。

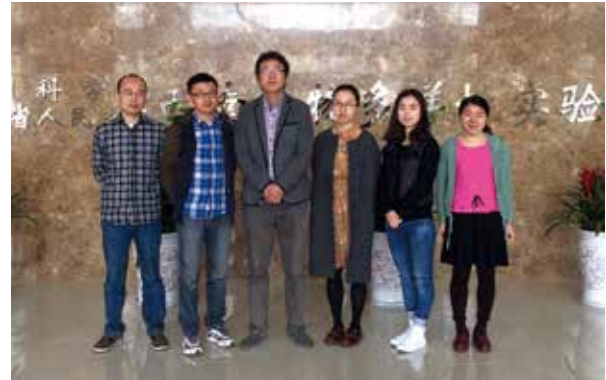


# Evolutionary and Developmental Transcriptomics

**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. High altitude adaptation of domestic animals

More than 1000 whole genome sequences of domestic animals including sheep, goats, cattle, dogs, pigs and horses from the Tibetan Plateau and lowland were obtained to reveal the generality and individuality of genetic mechanisms underlying high altitude adaptation. We found that the Tibetan chickens could broadly be placed into two groups, and revealed that candidate genes in the calcium-signaling pathway are possibly involved in adaptation to the hypoxia experienced by Tibetan chickens. Convergent evolution was commonly observed among domestic animals, particularly *EPAS1*, which evolved convergently under positive selection in six domestic mammals (Fig. 1). We also identified a novel gene that has a function in the response to hypoxia and has evolved convergently under positive selection in domesticated mammals.

## 2. Hypoxia and Diseases

Hypoxia naturally occurs at high-altitudes and commonly within pathological conditions (e.g. tumors). Both evolutionary and medical biologists have made great efforts to reveal the genetic mechanisms underlying adaptation to hypoxia, but they were not always supportive of each other on this landmark. Here, we used large-scale population genomes from horse, sheep, goat, cattle, pig and dog to investigate genetic mechanisms underlying hypoxia adaptation of domestic mammals. Interestingly, many genes involved in tumorigenesis were discovered to adaptively evolve (Fig.5), and some novel genes under positive selection were identified to be tumor associated. We further demonstrated that a novel positively selected gene, is highly expressed in cancerous tissues, and its depletion inhibits, whereas over-expression promotes, lung cancerous cell proliferation, migration and xenograft tumor in vivo. Our data will facilitate the pursuit of novel genes and potential therapeutic targets involved in hypoxic tumors.

Lifespan of a model animal can be extended under hypoxic conditions in the laboratory. Paradoxically, it has for a long time been believed that native Tibetan Plateau people, living under a natural hypobaric hypoxia, have much shorter lifespans relative to lower altitude populations. Interestingly, our secondary analysis of the Chinese census data revealed a greater proportion of older people among the Tibetans than lowlanders, possibly indicating longer lifespans among the Tibetans. Population genetic analysis revealed that aging associated genes evolved rapidly under positive selection in Tibetans and in domestic animals that were introduced into Tibet. Significant differential expression of genes associated with aging was found between animals living in Tibet and lowland areas, and the change in direction of the expression of these genes under hypoxia in animals and in humans was significantly negatively correlated. Our data suggests that positive natural selection might be a driving factor for human longevity under hypoxic conditions in nature.

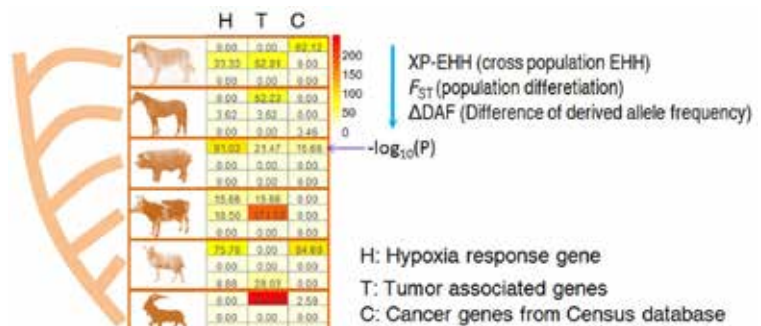


Fig.5

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- 李明莉 Mingli Li  
2015 级硕士研究生





## 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: RMB8.08 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: RMB2.395 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 vivo studies 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 6.589 million.

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：2014-2019；项目负责人：王文；金额：1125 万元。

Evolutionary Origins of New Genetic Structure in Genome and Animals' Adaptive Evolution. NSFC Science Fund for Creative Research Groups, Period, 2014-2019; Head of project, Wen Wang; Amount: RMB11.25 million.

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: RMB3.2 million.

灵长类大脑进化关键基因的功能研究，国家自然科学基金重点项目；执行年限：2012-2016；项目负责人：宿兵；金额：380 万。

Function of Key Genes in Primate Brain Evolution. Key project of National Science Foundation of China, Period: 2012-2016; Head of project, Bing Su; Amount: RMB 3.8 million.

藏族人群对高原低氧极端环境遗传适应的多基因互作机制研究，国家自然科学基金重大研究计划重点项目；执行年限：2013-2016；项目负责人：宿兵；金额：320 万。

Genetic Adaptation the Tibetan Population to High Altitude Hypoxia Extreme Environment. Major research plan of Na-



tional Science Foundation of China, Period, 2013-2016; Head of project, Bing Su; Amount: RMB3.20 million.

荒漠鼠适应荒漠极端生境的分子机制研究, 国家自然科学基金重大研究计划重点项目; 执行年限: 2013-2016; 项目负责人: 沈永义; 金额: 350 万。

Molecular Mechanisms of Desert Rodent to Adapt to the Desert Extreme Habitat. Major Research Plan of National Science Foundation of China, Period, 2013-2016; Head of project, Yongyi Shen; Amount: RMB3.50 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: RMB3.36 million.

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 Micro-evolution 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.

中国西南汉族群体中 ZNF804A 基因与精神分裂症的遗传易感性及功能分析, 国家自然科学基金 - 云南省联合基金; 执行年限: 2013-2016; 项目负责人: 宿兵; 金额: 200 万。

Genetic Susceptibility and Functional Analysis of ZNF804A Gene with Schizophrenia in the Han Population of Southwest China. NSFC Joint Funds of China-Yunnan Province; Period, 2013-2016; Head of project, Bing Su; Amount: RMB 2.0 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.



人类进化遗传学；国家自然科学基金委优秀青年科学基金；执行年限：2014-2016；项目负责人：孔庆鹏；金额：100 万元。

Human Evolutionary Genetics.NSFC Excellent Youth Science Foundation; Period, 2014-2016; Head of project, Qingpeng Kong; Amount: RMB 1.0 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. NSFC Excellent Youth Science Foundation; 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；中科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 Breeding 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 Breeding by Molecular Modules”, Period, 2013-2017; Head of project, Yun Gao; Amount:RMB12.0 million.

东非动物多样性格局，中科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，中科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 hound. International cooperation projects of Chinese Academy of Sciences. Period, 2015-2017; Head of project, Guodong Wang; Amount: RMB1.00 million.

西南家猪分子育种基地智能化系统，中科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.

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.

牦牛肠道微生物组高原适应的基因组学机制，云南省高端科技人才引进计划；执行年限：2013-2016；项目负责人：



施鹏；金额：200 万。

Genomics Mechanisms of Gut Microbiome in Yak to Adapt Plateau. Projects for Recruited Top Talent of Sciences and Technology of Yunnan Province, Period: 2013-2016; Head of project, Peng Shi; Amount: RMB 2.0 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.

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.

金沙江中游梨园水电站施工期水生生态监测，企业委托；执行年限：2012-2016；项目负责人：杨君兴；金额：200 万。

Aquatic Ecological Monitoring of the Jinsha River during the Construction Period of Liyuan Hydropower Station in the Midstream; Company Supported, Period, 2012-2016; Head of project, Junxing Yang; Amount: RMB 2.0 million.

三七 RAD 基因组辅助良种选育。企业委托；执行年限：2013-2016；项目负责人：王文；金额：300 万。

RAD Genomic Technology assists Panax pseudoginseng seed selection. RAD Genomic Technology assists Panax pseudoginseng seed selection. Company Supported, Period, 2013-2016; Head of project, Wen Wang; Amount: RMB 3.0 million.

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说明：“#”为并列第一作者，“\*”为通讯作者

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## 获奖 Awards

- 2016 施鹏研究员、孔庆鹏研究员入选国家“万人计划”领军人才  
2016 Prof. Peng Shi and Qingpeng Kong were selected into the second installment of Ten Thousand Talent Program.
- 2016 车静研究员获国家自然科学基金委优秀青年科学基金资助  
2016 Prof. Jing Che was funded by NSFC Excellent Youth Science Foundation.
- 2016 孔庆鹏研究员荣获中科院 2016 年度青促会优秀会员  
2016 Prof. Qingpeng Kong was awarded the outstanding members of Youth Promotion Association Chinese Academy of Sciences in 2016.
- 2016 郑萍研究员荣获 2016 年度“云南省有突出贡献的优秀专业技术人员”三等奖  
2016 Prof. Ping Zheng won the third prize of outstanding-contributions professional and technical personnel of Yunnan Province.
- 2016 张晓明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  
2016 Xiaoming Zhang'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.
- 2016 王明山荣获中科院院长奖学金特别奖  
2016 Mingshan Wang won the Chinese Academy of Sciences Dean scholarship special award.
- 2016 王明山、郭琨荣获朱李月华优秀博士生奖  
2016 Mingshan Wang and Kun Guo won "Zhu Li Yuehua Outstanding PhD Graduate Scholarship of CAS".





## 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334种动物的细胞系2000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 LY, Wang JH, Duan SC, Chen L, Xiang H, Dong Y, Wang W. Systematic evaluation of sericin protein as a substitute for fetal bovine serum in cell culture. *Sci Rep.* 2016, 6:31516.
2. 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, 27:241-252.

### 1. 细胞资源的收集和保藏

2016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114株，其中包括亚洲鳖、高山倭蛙、秃鹫、贡山刺猬、盘羊、金钱豹、高山鼠兔、间颅鼠兔、黑唇鼠兔、北白颊长臂猿等11种野生动物的细胞系29株，建立家猪、山羊和绵羊等家养动物的正常细胞系24株，EBV转化的人淋巴细胞系14株以及人和实验动物的正常细胞系和肿瘤细胞系47株。复苏和扩增各类动物细胞系400株次。



秃鹫



亚洲鳖

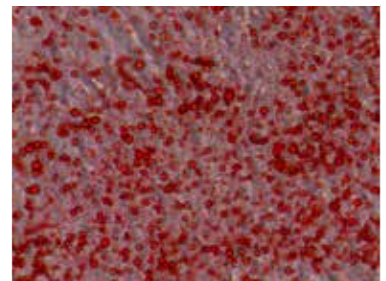
### 2. 对外服务

在2016年度，昆明细胞库为全国各地的391家单位，其中高等院校225家，科研院所91家，企业75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培训5人次、核型分析技术服务6次和STR检测25株次，以及通过电话、邮件及现场指导等方式提供大量的细胞培养技术咨询。

### 3. 小耳猪脂肪前体细胞的分离、培养、纯化和鉴定

脂肪前体细胞是一类具有增殖和向脂肪细胞分化能力的特异化了的细胞。脂肪前体细胞在促脂肪生成因子的作用下细胞内可生成脂滴，转化为成熟的脂肪细胞。因此，脂肪前体细胞的体外培养不仅能完整地认识脂肪组织发生和增生的全过程，并且可以直接观察各种因素对这个过程的调控。小耳猪，俗称版纳小耳猪，是我国优良的地方品种之一，为云南省特有，主产于西双版纳等地区。小耳猪具有皮薄骨细，肉质鲜嫩，口感香糯等特点，并且小耳猪肉不饱和脂肪酸是普通猪肉的3倍。

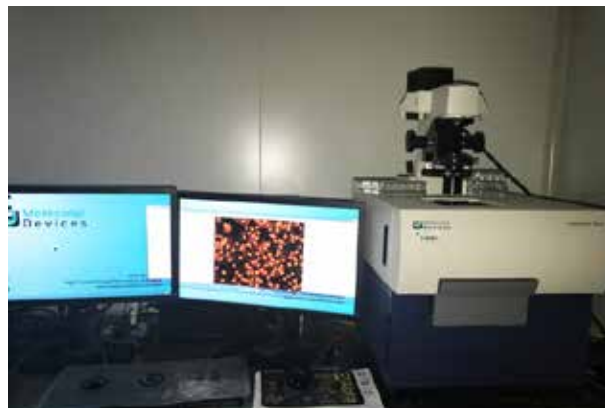
根据中国科学院昆明动物研究所课题组研究的需求，昆明细胞库开展了不同胚胎发育时期的小耳猪脂肪前体细胞系的建立工作。经过多次反复试验，已成功分离和培养了不同胚胎发育时期的小耳猪的脂肪前体细胞，鉴定工作已基本完成，正在进行纯化培养，纯度已达90%以上。目前，昆明细胞库已为该课题组提供了小耳猪的脂肪前体细胞开展后续研究工作。



油红O染色的诱导后的小耳猪脂肪前体细胞

## 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 2000 cell lines from 334 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 2016, we had established and frozen 114 cell lines from various wild and domestic animals. Among these cell lines, 29 cell lines were derived from 11 species of wild animals such as Asiatic softshell turtle, Cinereous vulture, Gongshan hedgehog, Argali, Leopard, Black-lipped pika, Moupin pika, Gansu pika and White-cheek gibbon etc; 24 cell lines were established from domestic animals such as domestic pigs, goats and sheep; 14 cell lines were obtained by EBV-transferred human lymphocytes; and 47 cell lines were normal cell lines and tumor cell lines from human and experimental animals. Four hundreds of frozen-stored cell lines were also resuscitated and subcultured.

### 2. Cell lines service and technical service

In this year, we had provided 398 cell lines, 5 times of karyotype analysis training and 31 times of technical service such as karyotype analysis and STR test for the researchers not only at State key laboratory of genetic resources and evolution, but also at other 391 Chinese universities, scientific research institutions and enterprises. In addition, we also had provided a lot of cell culture technical advisory services by using the telephone and the email.

### 3. The isolation, culture, purification and identification of small-eared pig preadipocytes

Preadipocytes are a kind of specific cells with the ability of proliferation and differentiating to adipocytes. Preadipocytes can generate lipid droplets in the cells under the action of the lipid formation factors and become into mature adipocytes.

Therefore, the preadipocytes in vitro culture can not only understanding the whole process of adipose histogeny and proliferation, and can direct observation of various factors on the process regulation. Small-eared pig, commonly known as Banna small-eared pig, is one of the fine local variety in our country. Mainly produced in Xishuangbanna, the small-eared pig is also the characteristic of Yunnan, with the features of thin skin and bone, succulent fresh flesh, taste etc, and the unsaturated fatty acids in the flesh of small-eared pig is three times as many ordinary pork.

According to the demand of the research group in the Kunming institute of zoology, Chinese Academy of Sciences, the establishment of preadipocyte cell lines was carried out from small-eared pigs during different embryonic development in Kunming cell bank. After several repeating experiments, preadipocytes of small-eared pigs during different embryonic development had been successfully separated and subcultured. The appraisal work had been basically completed, and the purification was under way. The purity was over 90%. At present, the preadipocytes of small-eared pigs have been provided for the group to carry out the follow-up research work.

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The cultured preadipocytes of small-eared pig



## 生命条形码南方中心

生命条形码南方中心，成立于2011年1月，专门从事DNA条形码相关的科学研究、技术革新和应用推广。根据国重室的相关规定和2014年室务会的精神，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；管理云南濒危科委司法鉴定中心，进行分子鉴定；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. Jiao-Jiao Song, **Wen-Zhi Wang**, Newton O. Otecko, Min-Sheng Peng, Ya-Ping Zhang. Reconciling the conflicts between mitochondrial DNA haplogroup trees of *Canis lupus*. ***FSI: Genetics***, 2016, 23: 83–85.
2. Peng-Fei Fan, Kai He, Xing Chen, Alejandra Ortiz, Bin Zhang, Chao Zhao, Yun-Qiao Li, Hai-Bo Zhang, Clare Kimock, Wen-Zhi Wang, Colin Groves, Samue T. Turvey, Kris M. Helgen, Xue-Long Jiang. Description of a new species of Hoolock gibbon (Primates: Hylobatidae) based on integrative taxonomy. ***Am J Primatol***, 2016,

### 1. DNA 条形码揭示蜻蜓多样性

全世界已知的6000余种蜻蜓中大约有1000种生活在中国。它们是中国无脊椎动物中重要的物种资源，也是监测水域生态系统健康以及水环境质量的重要指示生物。研究中心正在广泛开展野外调查工作，全面的采集蜻蜓标本，进行细致的形态分类鉴定，利用分子数据更新和综述若干蜻蜓类群的系统发育关系，并选取了一些特殊样地开展长期监测，用以进行生态系统和蜻蜓栖息地的环境评价。中心已经启动了“中国蜻蜓目DNA条形码计划”，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用标本接近800种，约占中国已知蜻蜓总数的85%。建立中国蜻蜓目的DNA条形码数据库，将有助于快速识别蜻蜓种类，进一步弥补形态分类中的不足和疑难问题，为开展蜻蜓多样性及保护、淡水生态系统的环境评估等方面研究提供重要的研究基础。这项工作对世界蜻蜓学的发展将起到巨大的推动作用。

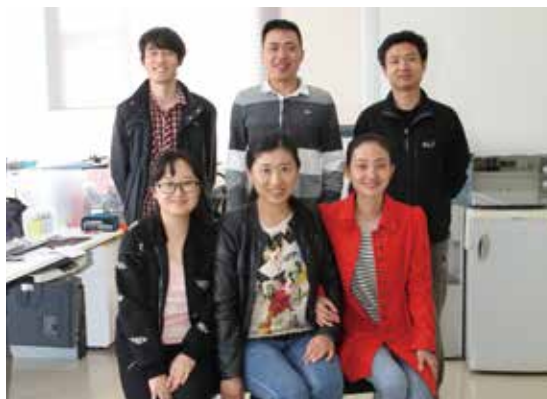
### 2. 在家犬线粒体基因组学研究取得进展

家犬的线粒体DNA (mtDNA) 在分子法医学研究中日益受到重视。mtDNA单倍型类群树可以为mtDNA世系提供高分辨率的系统发生关系。2015年两个部门(张亚平院士研究团队和生命条形码南方中心)分别基于线粒体DNA基因组序列构建了家犬mtDNA的单倍型类群树。由于不同的研究采用了不同的参考序列和数据集，三棵单倍型类群树在世系命名上存在冲突，很可能对后续研究产生干扰。基于此我们进行了以下的工作：将2条参考序列和三棵单倍型类群树进行了详尽的比较分析，并对存在的世系命名冲突进行了协调。同时收集新发表的255条家犬线粒体基因组进行质量过滤并去除24条有问题序列。通过整合新发表的高质量线粒体DNA基因组数据，我们还将DomeTree (<http://www.dometree.org/>) 中家犬和灰狼单倍型类群树进行了更新。相关工作发表于国际法医学知名刊物 *Forensic Science International: Genetics*。宋娇娇(安徽大学联合培养硕士生)和王文智博士为共同第一作者，彭旻晟博士和张亚平院士为共同通讯作者。

## 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 2016, the SCDBC collected more than 10K specimens in wild field, took pictures for over 5000 specimens, got almost 10K standard DNA barcodes, served 19 times for co-research groups. The SCDBC promoted the mitogenomics technologies which was based on the next generation Ion Torrent platform, and had upload 117 amphibian species mitogenomics genome on GeBank.

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### 1. Using DNA Barcoding data to understand the diversity of dragonflies in China

The order Odonata contains over 6000 species worldwide, about 1000 species have been recorded from China. Dragonflies are very important animal resources among the invertebrates, playing an important role for the health assessment of freshwater ecosystem, also they have been used widely as indicators of environmental quality in the aquatic ecosystem. Our center is conducting fieldworks all over China and collecting specimens extensively. Materials would be identified by morphological features firstly, then phylogeny studied will be carried on by genus or family. Meanwhile we have some locations for long-term monitoring, for the health assessment of freshwater ecosystem by dragonflies used as indicators. SCDBC has start the 'Chinese Odonata DNA Barcoding Project', to recognize dragonflies by the DNA Barcoding data. Currently the center has gathered about 800 Chinese species, occupying 85% of the known dragonflies all over China. Establishing the DNA barcoding database of dragonflies will help identifying these insect in a much faster way, solve the taxonomic difficulty, and lay a good foundation for the biodiversity and conservation of dragonflies as well as the assessment of freshwater ecosystem. This project must highly promote the development of global Odonatology.



### 2. Reconciling the conflicts between mitochondrial DNA haplogroup trees of *Canis lupus*

Mitochondrial DNA (mtDNA) haplogroup tree can capture the known mtDNA variation and provide a high-resolution phylogeny for mtDNA lineages. In 2015, three different mtDNA haplogroup trees for *Canis lupus* were released, one of which is from our research. The conflicts of scored variants and haplogroup nomenclatures exist in different trees. To avoid potential chaos and confusions in future related studies, we present the comparisons of the different reference sequences and haplogroup nomenclatures. Re-analyzing 255 dog mitochondrial genomes released recently reveals 24 flawed sequences with potential errors. After incorporating the qualified data, we update the mtDNA haplogroup tree for *Canis lupus* as Build 2 in DomeTree (<http://www.dometree.org/trees/dog.htm>).

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## 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. 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。



##### 4. 实时定量 PCR 仪

Roche LightCycler 480 实时定量 PCR 仪能够实现 96 个样本实时、在线的快速循环 PCR 反应。其通过监测核酸扩增时的荧光，可对产生的结果进行定量检测或基因分型分析。



#### 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，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.

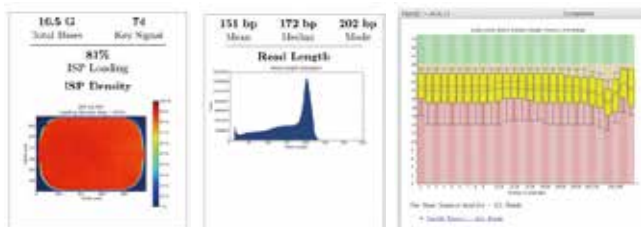
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## The Three Technical Platforms

### I. Genomic Analysis Platform

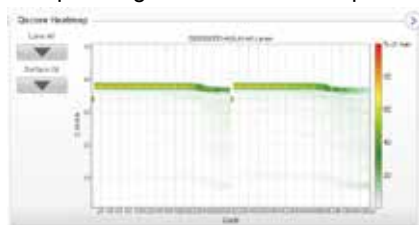
#### 1. Ion Torrent Sequencers

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.



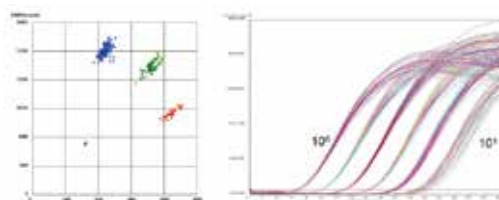
#### 2. MiSeq Sequencer

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.



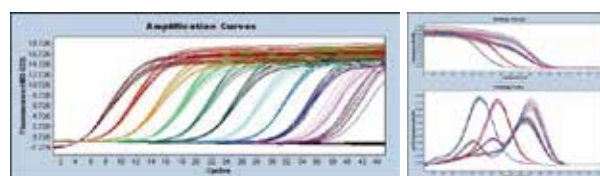
#### 3. QuantStudio 12K Flex 实时定量 PCR 仪

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.



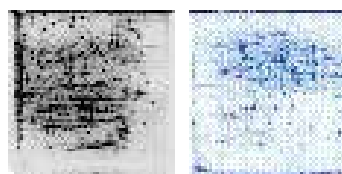
#### 4. Roche LightCycler 480

The LightCycler 480 System enables you to perform real-time, online PCR combined with rapid cycling of up to 96 samples. After monitoring fluorescence during nucleic acid amplification, results can be analyzed, for example, by quantification or genotyping. The outstanding thermal homogeneity and cycling speed of the LightCycler 480 System provide exact results in a short time.



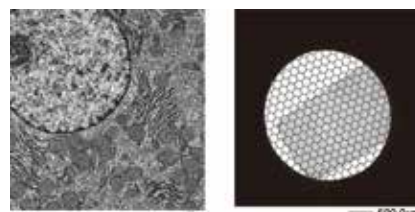
### II. Proteomic Analysis Platform

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.  $\times 10$ ) to the MAG mode (max. mag.  $\times 1.2$  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	健康长寿人群老年性疾病低发的遗传学基础研究 (特邀)	孔庆鹏	中国心脏大会	北京	8月11-14日
2	RNF220-mediated K63-linked ubiquitination and sequestration shapes the Gli gradient required for ventral spinal patterning (特邀)	毛炳宇	2016 全国发育生物学大会	杭州	10月20日
3	基因组时代下的生物资源挖掘 (特邀)	施鹏	苏州大学药学院第六届研究生学术论坛	苏州	12月18日
4	抗冻百合和荧光百合组培 (特邀)	王文	2016 年宁夏农业综合开发院地科技合作项目落实会	宁夏	4月6-8日
5	生物技术的新发展与羊绒产业的新机会 (特邀)	王文	第二十三届全国绒毛会议暨首届全国绒毛产业发展峰会	北京	3月28-29日
6	CRISPR in butterflies (特邀)	李学燕	美国昆虫学会太平洋分会 2016 年年会	美国夏威夷	4月2-4月9日
7	ESC-specific Filia/Floped/Blm complex regulates replication stress response and safeguards genomic stability (特邀)	赵博	国际干细胞协会 2016 年年会	美国旧金山	6月22-25日
8	Down-Regulation of EPAS1 Transcription and Genetic Adaptation of Tibetans to High-Altitude Hypoxia	宿兵	分子生物学与进化 2016 年会 (SMBE2016)	澳大利亚	7月3-7日
9	Whole-genome sequence of the Tibetan frog <i>Nanorana parkeri</i> and the comparative evolution of tetrapod genomes	孙艳波	分子生物学与进化 2016 年会 (SMBE2016)	澳大利亚	7月3-7日
10	Cloning and characterization of luciferases from a <i>Diplocladon</i> starworm and a <i>Lamprigera</i> firefly	李学燕	第 19 届国际生物荧光和化学荧光大会	日本筑波	5月28日 -6月4日
11	Gene loss and its role in adaptive evolution of subterranean mammals	郑智中	香港中文大学生物医学研究院 2016 年研究生年会	香港	11月9-12日
12	Phylogeographic studies of amphibians and reptiles on the Qinghai-Tibetan plateau	车静	国际生物地理学会年会 2016- 生态与生物地理	北京	5月4-7日
13	River islands, refugia and genetic structuring in the endemic brown frog <i>Rana kukunoris</i> (Anura, Ranidae) of the Qinghai-Tibetan Plateau	周炜炜	国际生物地理学会年会 2016- 生态与生物地理	北京	5月4-7日
14	Red River barrier and Pleistocene climatic fluctuations shaped the genetic structure of <i>Microhyla fissipes</i> complex (Anura: Microhylidae) in southern China and Indochina	袁智勇	国际生物地理学会年会 2016- 生态与生物地理	北京	5月4-7日



15	SPECIES IDENTIFICATION AND BIODIVERSITY STUDIES ON HERPETOFAUNA BASED ON MOLECULAR TOOL IN NIGERIA, WEST AFRICA	Lotanna	国际生物地理学会年会 2016- 生态与生物地理	北京	5月4-7日
16	AmphibiaChina: an online database of Chinese Amphibians	车 静	The 8th World Congress of Herpetology	杭 州	8月15-21日
17	Whole-genome sequence of the Tibetan frog <i>Nanorana parkeri</i> and the comparative evolution of tetrapod genomes	孙艳波	The 8th World Congress of Herpetology	杭 州	8月15-21日
18	Contrasting population structure and demographic history generated by different geographic features in eastern Qinghai-Tibet Plateau	周炜韩	The 8th World Congress of Herpetology	杭 州	8月15-21日
19	Red River barrier and Pleistocene climatic fluctuations shaped the genetic structure of <i>Microhyla fissipes</i> complex (Anura: Microhylidae) in southern China and Indochina	袁智勇	The 8th World Congress of Herpetology	杭 州	8月15-21日
20	Transcriptomes reveal the genetic mechanisms underlying ionic regulatory adaptations to salt in the crab-eating frog	邵 永	The 8th World Congress of Herpetology	杭 州	8月15-21日
21	Genetic survey reveals human influence on Chinese Giant Salamander	Robert Murphy	The 8th World Congress of Herpetology	杭 州	8月15-21日
22	Taxonomic revision of the Chinese <i>Limnonectes</i> (Anura, Dicroglossidae) with the description of a new species from China and Myanmar	Champ	The 8th World Congress of Herpetology	杭 州	8月15-21日
23	The diversity of herpetofauna in Tibet Autonomous Region, China	蒋珂	The 8th World Congress of Herpetology	杭 州	8月15-21日
24	Loss is less? Lesson from two subterranean rodents, Naked mole rat and Blind mole rat	郑智中	苏州大学药学院第六届研究生学术论坛	苏 州	12月18日
25	澜沧江鱼类资源现状	刘淑伟	中国动物学会第23届学术年会暨鱼类学分会学术讨论会	武 汉	10月29-31日
26	滇池金线鲃的保护、恢复与产业化开发	潘晓赋	中国动物学会第23届学术年会暨鱼类学分会学术讨论会	武 汉	10月29-31日
27	滇池金线鲃精子冷冻保存及其精子质量评价	王晓爱	中国动物学会第23届学术年会暨鱼类学分会学术讨论会	武 汉	10月29-31日
28	基于先进成像的洞穴鱼类头部形态与演变	和 友	同步辐射与先进生物医学成像技术发展研讨会	北 京	8月22-23日
29	dometree.org 家养动物线粒体 DNA 单倍型类群分型系统	彭昱晟	第三届(2016)科学数据大会	上 海	8月25-26日
30	喝酒脸红的故事	彭昱晟	中国科学院青年创新促进会 2016 年学术年会暨会员代表大会	成 都	11月16-18日
31	A cryptic mitochondrial DNA link between North European and West African dogs	Adeniyi C.Adeola	2016 国际生物地理大会	北 京	5月1-4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)
GREKF16-01	高建军	副研究员	云南大学	大苹果蝇种组的繁殖生态及非遗传多型	10
GREKF16-02	王江新	教授	深圳大学	贾第虫的单细胞核转录组研究	10
GREKF16-03	陈永久	副教授	浙江海洋学院	黄鱼与梅童鱼生长相关 SNP 标记及比较基因组学	10
GREKF16-04	欧珠罗布	教授	西藏大学	藏族人群高原适应关键基因 EPAS1 和 EGLN1 的互作机制及其功能解析	10
GREKF16-05	李杰晶	副教授	昆明理工大学附属云南省第一人民医院	Elp3 调控神经嵴迁移的机制研究	10
GREKF16-06	和友	副研	中国科学院上海应用物理研究所	洞穴金线鲃头部三维形态及适应演化研究	10
GREKF16-07	唐利洲	教授	曲靖师范学院	银星竹鼠的遗传多样性与分子系统地理学研究	10
GREKF16-08	俄广鑫	中级	西南大学	山羊 SSR 和 MHC 的进化关系及群体结构分析	10
GREKF16-09	Taal Levi	副教授	美国俄勒冈州立大学	利用环境 DNA 技术动态监测美国阿拉斯加的三文鱼资源	10
GREKF16-10	蔡望伟	教授	海南医学院	线粒体 DNA 拷贝数及其异质性对长寿的影响和调控机制研究	10
GREKF16-11	邹权	研究员	天津大学	基于 Hadoop 的大规模 DNA 进化树构建算法	10
GREKF16-12	Cameron David Siler	助教	University of Oklahoma & Sam Noble Oklahoma Museum of Natural History	Comparative phylogeography of agamid lizards of the genus Japalura across montane-river corridors in the Hengduan Mountain Region	10
GREKF16-13	敖磊	副高	昆明中英安琪儿妇产医院	lncRNA 做为胚胎植入前分子标记物的探讨分析	10
GREKF16-14	张佳进	讲师	云南农业大学	灵长类动物模型表型与遗传数据库和可视化系统构建	10
GREKF16-15	丁利	副研究员	中国科学院成都生物研究所	温泉蛇 <i>Thermophis baileyi</i> 青藏高原适应性的遗传机制研究	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	Yoshihiro Ohmiya	National Institute of AIST, Biomedical Research Institute, Japan	1月15日	Basic and application of multicolor bioluminescence system using ATTO equipment
2	Victor Luria	Harvard Medical School, USA	3月31日	De novo genes in evolution: the invention of protein structure and the flux of genes through genomes
3	Changlu Wang	Rutgers University, USA	4月20日	Recent advances in urban insect pest research
4	陈敬洲	中国医学科学院阜外医院心血管病国家重点实验室	5月26日	高血压发生机制及其靶器官损害
5	秦燕	中国科学院生物物理研究所	6月3日	蛋白质翻译调控因子 EF4 通过调控线粒体和细胞代谢促进肿瘤发生
6	David Irwin	University of Toronto, Canada	6月6-6月8日	Course about molecular evolution and Scientific writing
7	Bernald L. Odera Agwan-da	National Museum, Kenya	6月18日	Uncovering cryptic diversity in mammals: lesson learnt & knowledge gaps in Kenya
8	Laurent A.F. Frantz	Oxford university, UK	6月23日	Of dogs, pigs and chickens: studying animal domestication in the genomic era
9	Michael Turelli	University of California, USA	7月8-15日	On the origin of species: Definitions, patterns and processes, with the roles of geography and reinforcement revealed by phylogenies, meta-analyses and genetics
10	张建之	University of Michigan, USA	7月15日	Testing the neutral hypothesis of phenotypic evolution
11	廖本扬	台湾健康研究所	7月15日	Histone modifications maintain mRNA dosage of duplicated genes in model Eukaryotes deficient in cytosine DNA methylation
12	Taoyang Wu	University of East Anglia, UK	7月26日	Phylogenetic networks
13	Michael Lynn Arnold	University of Georgia, USA	8月2日	The Web-of-Life — An Evolutionary Stimulus in Changing Environments?
14	叶承曦	University of Maryland, USA	8月8日	第三代测序数据组装算法及软件研究进展
15	Joseph Daniel Orkin	University of Calgary, Canada	8月9日	Landscape genetics of western black crested gibbons ( <i>Nomascus concolor</i> ) in the Wuliang Mountains with a scat detection dog
16	David M. Hillis	University of Texas, USA	8月12日	The Evolution of Animal Nervous Systems
17	David Cannatella	University of Texas, USA	8月12日	Why don't poison frogs poison themselves
18	Pierre Taberlet	University of Grenoble, France	8月22-23日	Evolutionary biology, systematic taxonomy, genetics
19	Eric Coissac	University of Grenoble, France	8月23日	The PhyloAlps Project: Sequencing the whole alpine flora PhyloAlps
20	周欣	中国农业大学	8月23日	PCR-free mitochondrial metagenomics, are we ready?
21	Anthony Chariton	CSIRO Oceans and Atmosphere, Australia	8月24日	1. Applying DNA metabarcoding to environmental policies; 2. Network analysis of ecological communities



22	Aaron Ellison	Harvard University, USA	10月8日	Identifying, anticipating, and intervening in ecological regime shifts
23	温秀军	华南农业大学	10月8日	昆虫信息化学物质及其应用
24	Ziheng Yang	University College London, UK	10月12日	Statistical inference using genomic sequence data from multiple closely related species
25	朱天琪	中国科学院数学与系统科学研究院应用数学所	10月12日	An isolation with migration model for three species for testing speciation with gene flow
26	ROYA. MARI-UZZA	University of Maryland, USA	11月15日	Structural Insights into the Evolution of Adaptive Immunity
27	邹 权	天津大学	12月28日	高性能并行计算在生物信息学中的应用

## 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	芦方茹, 黎武略, 李明莉, 马 成, 许明敏, 周其俊	杨 阳, 胡靖扬, 叶凌群, 尹婷婷, 曾 琳, 黄翠萍, 李建波, 吕梦蝶, 王运梅, 沈全宽, 耿伟航, David Heriel Mauki, 马云飞, Otecko Newton Otieno, Saber Khederzadeh, Hadi Charati	倪 刚
2	彭旻晟	宋娇娇, Felista Kasyoka Kilunda, Said Ismail Nganga		
3	王国栋	林 娜		
4	杨君兴	郑秋吻, 牛诚祎	杨坤凤, 张源伟, Marco Endruweit, 杜丽娜	
5	车 静	米 雪, 付婷婷, 徐 伟	张宝林, 陈进民, 高伟, NNEJI/LOTANNA MICAHA	Chatmongkon Suwannapoom
6	焦保卫	郭 璐, 杨 星, 马玉洁	柯 浩, 赵丽娜, 徐海波, 赵丽敏	张洪磊
7	孔庆鹏	葛明侠, 杨杏丽, 董 蕾, 王昊天	王晓雄, 余 琴, 刘耀文, 田骄阳, 吴 焕, 江建军, 夏王晓, ZIA UR RAHMAN	
8	毛炳宇	任碧玉, 杜加诚, 朱 良	王晓磊, 杨相彩, 刘晓亮	
9	宿 兵	周亚楠, 黄 俊, 张栋秦, 李 敏, 袁佳妙, 胡 庭, 孟晓宇, 胡 艳	林 强, 刘杰伟, 杨晏冬, 罗 鑫, 和耀喜, 姜 瑾	
10	王 文	陈海涛, 曾 严, 生承晔, 刘 威, 王 宝, 何金武, 朱亚楠 (联培)	奎 玲, 向志丹, 沈文菁, 刘力源, 李永鑫, 任彦栋, 王 筱	刘斌, 吴江鸿, 苏 蕊

11	文建凡	邱兰, 吕章夏	薛敏, 叶青青, 李毓劲, 刘芳	
12	郑萍	孙春丽, 李聪, 李秀峰	何大健, 王鑫轶, 李朝晖, 郭琨, 陈忠良, 张伟道, 李竞争	
13	马占山	李杰	夏尧	
14	施鹏	张佳, 陈杰, 郭媛婷, 吴群富, 蔡婉芷, 雷孟龙, 杨丽丽	罗杰, 郑智中, 李媛媛, 朱磊, 张涛, 刘奇	
15	黄京飞	李慧娟, 安三琪, 李文兴, 陈碧雯	郑俊娟, 刘家倩, 王倩	
16	蒋学龙	杜宜青, 程峰, 牛晓炜, 甘霖, 于秋鹏, KENNETH OTIENO ONDITI	宋文字, NARAYAN PRASAD KOJU, Laxman Khanal, 李权, 宁文鹤, 黄程	陈顺德
17	饶定齐	宋心强		
18	Douglas W Yu	蔡望、罗明洁	王晓阳	
19	杨晓君	田天祺, 胡菀钊, 范闯, MURIITHI JACINTA MURINGI, 黎思涵, 何书航	王荣兴, 卢光义, 单鹏飞, 王继山	
20	吴东东			郭兴

## 毕业生一览表 (Students Graduated)

序号	姓名	学位	导师姓名	毕业时间
1	袁志勇	博士	车静	2016-06
2	陈中正	博士	蒋学龙	2016-12
3	张斌	博士	蒋学龙	2016-12
4	李肇天	博士	蒋学龙	2016-12
5	许东明	博士	施鹏	2016-12
6	陈垒	博士	王文	2016-07
7	董好岩	博士	杨晓君	2016-07
8	李朝晖	博士	郑萍	2016-06
9	郭义成	博士	黄京飞	2016-06
10	吴宏	博士	张亚平	2016-11
11	王明山	博士	张亚平	2016-11
12	邵永	博士	张亚平	2016-06
13	柴静	博士	张亚平	2016-06
14	杨贺川	博士	张亚平	2016-03
15	徐丹	博士	张亚平	2016-06
16	袁智勇	博士	张亚平	2016-01
17	张煦	博士	宿兵	2016-12
18	张凯	博士	Douglas W Yu	2016-12
19	郭雨龙	硕士	施鹏	2016-12



20	胡莞钊	硕士	杨晓君	2016-07
21	何一博	硕士	宿兵	2016-05
22	虎恩志	硕士	宿兵	2016-05
23	程乐华	硕士	孔庆鹏	2016-11
24	樊萌萌	硕士	马占山	2016-12
25	王娅丽	硕士	马占山	2016-12
26	张如	硕士	王文	2016-07
27	赵颖俊	硕士	王文	2016-07
28	姚瑶	硕士	张亚平	2016-05

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

一等奖 (4 篇, 影响因子  $\geq 9$ ):

**The First prize(4, IF $\geq 9$ )**

王明山 Mingshan Wang(Nature Genetics,IF32.197)

王明山 Mingshan Wang(Cell Research,IF11.178)

沈全宽 Quankuan Shen(The American Journal of Human Genetics, IF10.79)

李媛媛 Yuanyuan Li(Molecular Biology and Evolution, IF13.649)

二等奖 (2 篇,  $6 \leq$  影响因子  $< 9$ ):

**The Second prize(2,  $6 \leq$  IF  $< 9$ )**

许东明 Dongming Xu(Current Biology, IF10.134, 并列一作)

王明山 Mingshan Wang(Journal of Molecular Cell Biology,IF6.983)

三等奖 (4 篇,  $4 \leq$  影响因子  $< 6$ ):

**The third prize(4,  $4 \leq$  IF  $< 6$ )**

杨相彩 Xiangcai Yang(Scientific Reports,IF5.597)

吕梦蝶 Mengdie Lv(Scientific Reports,IF5.525)

张煦 Xu Zhang(Scientific Reports,IF5.525)

李肇天 Zhaotian Li(Scientific Reports,IF5.525)

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 journals are the journal's five-year average impact factor at the time of application.

## 大事记 Major Events

(1) 2016年3月2日, 实验室第二届学术委员会第五次会议在昆明召开。

The fifth meeting of the second academic committee of the key lab was held in Kunming on March 2nd, 2016.



(2) 2016年5月14日, 实验室参与举办昆明动物所第十二届“公众科学日”活动。实验室以科普报告及生动有趣的科普游戏向市民们主要普及了关于保护动物及其生存环境的理念。

The key lab participated in the twelfth “Public Science Day” of Kunming Institute of Zoology on May 14th, 2016. The lab organized some interesting talks and games intending to protecting animals and their environment.



(3) 2016年6月18-20日, 实验室主办的“家犬基因组学术峰会”在北京召开。同时, 由实验室张亚平院士、美国加州大学 Robert K. Wayne 教授、美国国立卫生研究院 Elaine A. Ostrander 研究员以及实验室王国栋副研究员共同发起的家犬基因组研究联盟在京正式成立。

“The academic summit of dog genomes” was held by the key lab in Beijing, on June 18-20, 2016. At the same time, Dog10K genomes consortium was established associate co-sponsored by Academician Yaping Zhang, Prof. Robert K. Wayne from the United States of America University of California, Prof. Elaine A. Ostrander from United States National Institutes of Health, and Dr. Wang Guodong of the key lab.



(4) 2016年7月15-16日,“第一届进化遗传青年科学家论坛”在昆明举办。

"The 1st Young Scientists Forum on Evolutionary Genetic" was held in Kunming on July 15-16, 2016



(5) 2016年7月17-7月22日,实验室与所研究生部在昆明联合举办“2016年进化生物学暑期班”。

On July 17-22, 2016, the Evolutionary Biology Summer Course was held in Kunming organized by the key lab and the Office of Postgraduate Affairs of KIZ.



(6) 2016年8月15-21日,实验室参与承办的“第八届世界两栖爬行动物学大会”在杭州召开。

"The 8th World Congress of Herpetology (WCH8)" was co-organized by the key lab in Hongzhou on August 15-21, 2016.



(7) 2016年8月22-26日, 第六届国际DNA高通量条形码(DNA Metabarcoding)培训班在昆明举办。  
The sixth international DNA Metabarcoding training courses was held by the lab in Kunming on August 22-26, 2016.

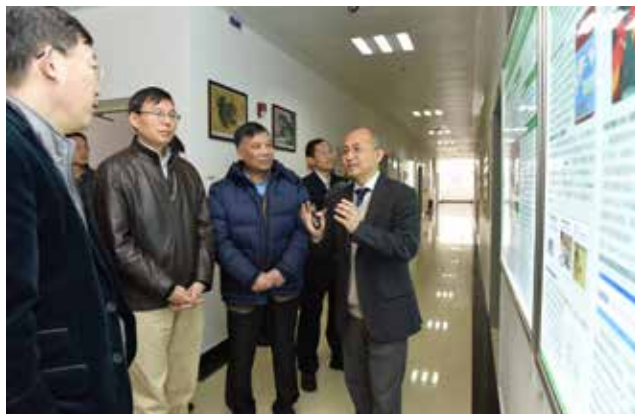


(8) 2016年12月17日, “遗传资源与进化青年学者论坛”2016年总决赛举办, 经过2016年9场论坛报告筛选, 共决出6名研究生代表和5名青年骨干代表参加此次决赛。

On December 17th, 2016, "Final Forum of 2016 for Young Scholars on Genetic Resources and Evolution" was held after 9 forums in 2016, six graduates and five young scholars gave talks in the Final Forum.



(9) 2016年12月30日, 科技部组织的生命科学领域国家重点实验室评估专家组对实验室进行了现场评估。  
On Dec 30th, 2016, the assessment experts group of the Ministry of Science and Technology assessed the key lab.







## 固定人员名单 (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	吴东东	杨君兴	杨晓君	佺文惠
郑 萍	施 鹏	宿 兵	黄京飞	焦保卫	蒋学龙

### 其他工作人员

Adeola Adeniyi Charles	万 韬	马鹏程	王 茉	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	王晓爱	石 磊	代绍兴	朱建国	朱春玲
伍和启	刘 振	刘 倩	刘 熙	刘 衡	刘贵春
刘淑伟	刘鹤群	祁学斌	许绍斌	孙艳波	苏伟婷
李玉春	李功华	李欣磊	李学友	李学燕	李宗煦
李桂梅	李朝翠	李连伟	杨 钦	杨 晖	杨双娟
杨立新	杨利琴	杨春燕	杨敏敏	肖富辉	时晓菲
吴 飞	吴世芳	吴春莹	何 错	何水旺	何永捍
余 蕊	余国华	邹 丽	闵 锐	张 慧	张业胜
张志刚	张栋儒	张晓明	张浩淼	陈 兵	陈小琼
陈中正	陈宏满	陈忠良	邵 永	邵静茹	岩 道
季吟秋	金洁琼	周中银	周炜帏	郑兰平	赵 博
赵玉琪	赵亚鹏	赵若苹	郝军军	饶定齐	高 云
高建云	郭 彦	唐 嘉	浦绍艳	常云艳	彭 云
彭 忆	彭旻晟	董 锋	蒋万胜	韩徐曼	程乐华
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## 2016年报

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