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

2014年报
ANNUAL REPORT

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

目录 // CONTENTS

主任致辞

　　2014 年是深入贯彻落实党的十八届三中、四中全会精神，全面深化改革的开局之年，也是中国科学院实施"率先行动"计划的开局之年。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支持下，面向国家和地区的战略需求和学科领域的国际前沿，凝心聚力，全面扎实推进各方面工作，在任务承担、创新研究、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，实验室积极组织策划国家、国际重大科技任务，成效显著。牵头策划的动物复杂性状的进化解析与调控先导专项（B）顺利启动，新争取其它科研项目 48 项，另有 40 项课题圆满结题。年度到位科研经费 5521 万元，人均到位 49.3 万元。目前在研省部级项目 178 项，国际合作项目 8 项，横向协作项目 27 项。在致力于基础研究的同时，实验室也积极推进科技成果的应用转化，例如与企业合作挖掘动植物重要经济性状功能基因，以及根据地区发展需求，与地区交通部门、水电部门等合作研究生态变化，拯救濒危物种等。

　　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，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持续开展深入、系统的研究，2014 年取得了显著进展。发表论文 146 篇，其中 SCI 收录 138 篇（其中 TOP25% 论文 69 篇），EI 收录 1 篇，以第一作者或通讯作者（含并列）发表 SCI 和 EI 收录论文 101 篇，包括发表在 Science、Mol Biol Evol、Nat Commun、Mol Psychiatry、The ISME Journal 等 IF5–year>9 的国际著名期刊论文 10 篇。"基因组多样性与亚洲人群的演化"荣获国家自然科学二等奖。

　　在人才队伍建设方面，实验室"培养 + 引进"的人才队伍建设模式也取得了明显成效。实验室荣获国家基金委创新群体 1 个，入选云南省首批"云岭学者"人才培养工程 1 人，科技部中青年科技创新领军人才 1 人，云南省中青年学术和技术带头人后备人才培养对象 1 人，中国科学院青年创新促进会会员 2 人；荣获王宽诚西部学者突出贡献奖 1 人，王宽诚卢嘉锡青年人才奖 1 人；施鹏研究员在"百人计划"入选者终期评估中获得优秀。此外，新引进青年博士 4 名。研究生培养方面，为国家输送硕士 15 名，博士 13 名，其中李明、姜雨的博士学位论文入选 2014 年度院优秀博士学位论文。此外，实验室还成功举办 2014 年"进化生物学"暑期班，吸引更多有志青年加入实验室。

　　在对外学术交流与合作共享方面，2014 年，实验室继续本着"取长补短、强强联合"的宗旨，继续推动国际条形码中国计划、牵头实施"国际山羊基因组计划"、参与组织"国际绵羊基因组计划"等国际合作项目。继 2013 年解析山羊基因组揭示羊绒生长的基因基础之后，实验室再次携手国内外机构"破译"了绵羊基因组（成果发表于 Science），至此，所有重要家畜动物的基因组密码全部告破。此外，还与美国、加拿大、俄罗斯以及东南亚各国等多家国际一流的学术机构保持着长期稳定的合作关系，进行了多次样品交换和人员互访及合作研究，扩大了实验室国际影响力。2014 年与 34 个国家的 160 余家单位联合发表论文。另外，实验室通过组织和参加高水平的国际学术会议以及与世界各地的知名学者互访开展短期学术交流。人员外出参加国内外学术会议近 60 余人次，其中国外学术会议 10 人次。实验室还积极发挥国内相关研究领域的辐射和带动作用，对外设立开放课题 16 项。

　　骏马腾飞成壮举，灵羊起步赴新程！2015 年，我们将继续遵循"开放、流动、联合、竞争"的运行机制，在学术委员会指导下，发挥自己的学科与资源优势，凝练目标，深化战略规划，强化团队交叉协作，提高自主创新和承担重大项目的能力，力争取得更多系统性、原创性成果，为我国遗传资源的进化与发育研究领域做出重要贡献。

　　实验室的发展离不开各级领导及各位朋友的关心与帮助，在此，我谨代表实验室向大家致以最诚挚的感谢，并希望能得到大家一如既往的关心和支持！

<div align="right">张亚平</div>

Director's Report

The "State Key Laboratory of Genetic Resources and Evolution" has made considerable progress in 2014, with regards to grant awards, scientific research output, talent recruitment and scientific exchange.

Grant awards. – The lab has successfully organized the key project "Analysis of complex traits of animal during evolution" as one of the "Strategic Leading Project (B)" of CAS, which is initiated this year. The lab was also awarded 48 other new grants. In 2014, the grant funds to the lab totaled 55.21 million RMB. Forty grants were successfully completed. Currently the lab holds 178 provincial and ministerial projects, 8 international cooperation projects and 27 horizontal collaboration projects. In addition to basic research, the lab promoted applied researches including the mining of important phenotypic genes of economical plants and animals in cooperation with companies and also ecological studies and conservation of endangered species in cooperation with local government departments .

Publications and Awards. – The lab 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 2014. The lab published in total 138 papers in SCI journals, 1paper in EI journals, including 10 papers in top journals ($IF_{5-year}>9$) such as Science, Nat Commun, Mol Biol Evol, Mol Psychiatry and The ISME Journal. The studies by Prof. Yaping Zhang et al., "Genomic diversity and evolution of Asian populations", was awarded the second prize for National Natural Science Award. The lab has also won one Special award and two First prizes for Natural Science of Yunnan province.

Talent recruitment. - In 2014, the lab has achieved remarkable progress by "training and recruitment ". The lab won one NSFC innovation group. Prof. Bing Su was selected into the first batch of "Yunling Scholar" Training Project in Yunnan Province. Prof. Peng Shi was awarded as "The outstanding contribution prize in Wang kuancheng western scholars, Chinese academy of sciences (CAS)". Drs. Guodong Wang and Lei Shi were selected as members of the "Youth Innovation Association" of CAS. Four young doctors were also recruited. Thirteen Ph.D. and 15 M.Sc. students graduated from the lab in 2014. The doctoral thesis of Ming Li's and Yu Jiang were selected as awarded "the Outstanding Doctoral Dissertation Award" of CAS. Several students were awarded various types of scholarships from CAS. The "Evolutionary Biology" Summer School was successfully held in August, attractting many young people joining the lab.

Scientific exchange. – In 2014, the lab continued to promote high-level international cooperation and scientific exchanges with scholars from US, Canada, Russia and Southeast Asia. In cooperation with an international team, the lab contributed greatly to the decoding of the sheep genome, which was published in Science. Members of the lab attended scientific meetings both at home and abroad for more than 60 times. Twenty-three scholars were invited to visit the lab and to give lectures this year for scientific exchange and co-operation. In 2014, the lab has also funded 16 "open projects" to promote cooperation with scholars in related fields.

In the future, the lab hopes to make more systematic and original achievements in the field of adaptive evolution as well as collection of genetic resources, and exploitation of domesticated animal resources. The goal of the lab is to make major contribution on the researches on genetic resources and evolution in China, and to promote the lab to become an internationally renowned research center in the field.

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

李德铢　　研究员，中国科学院昆明植物研究所
Prof. Dezhu Li, Kunming Institute of Botany, Chinese Academy of Sciences

张亚平　　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

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

基因与基因组的进化
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 112 人，其中博士 72 人，平均年龄 35 岁。拥有中科院院士 1 人，国家杰出青年基金获得者 5 人，中科院"百人计划" 7 人，云南省"高端人才" 3 人。

There are 17 research groups and 3 facility centers in the key lab. Among the 112 staff members, 72of them hold Ph.D. degrees. The average age of the team is 35 years old. The research team includes one academician of CAS, 5 winners of the "National Science Fund for Distinguished Young Scholars", 7 holders of the "Hundred Talents Program" of CAS and 3 holders of "Top talent" project of Yunnan Province.
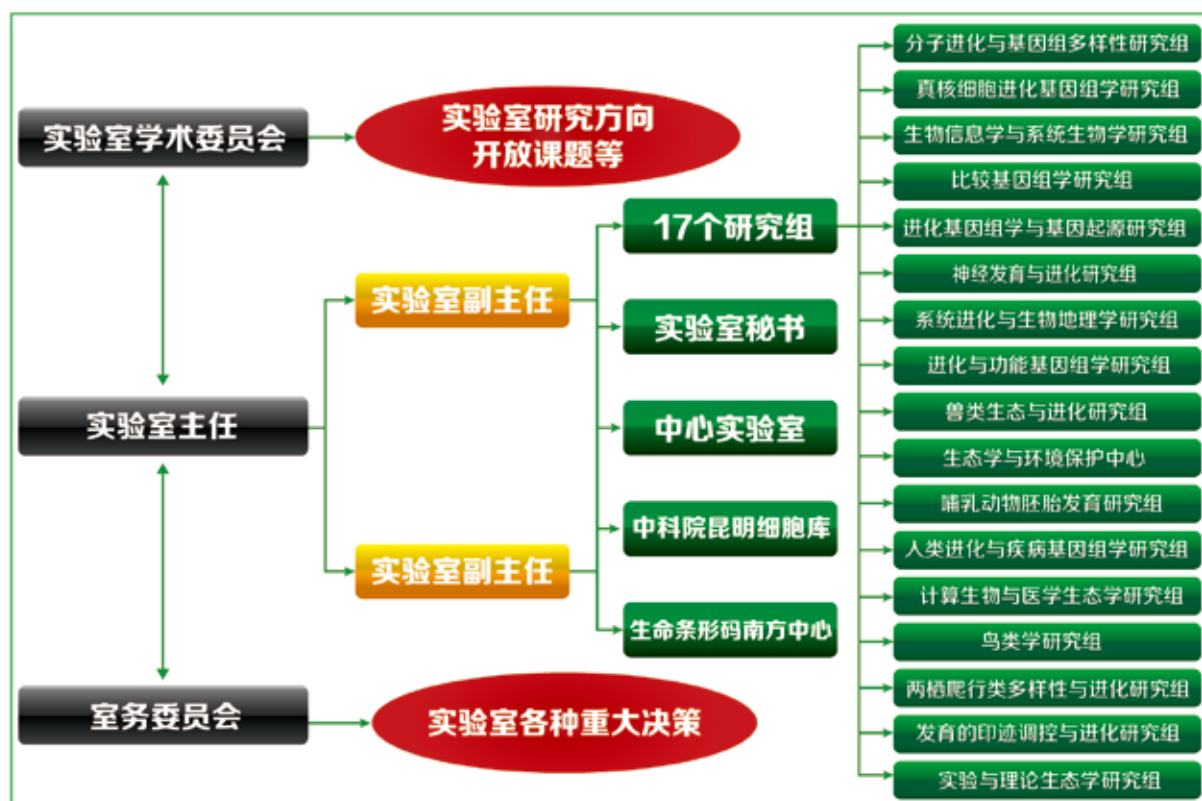
研究方向一：遗传资源多样性的演化与保护 ▶
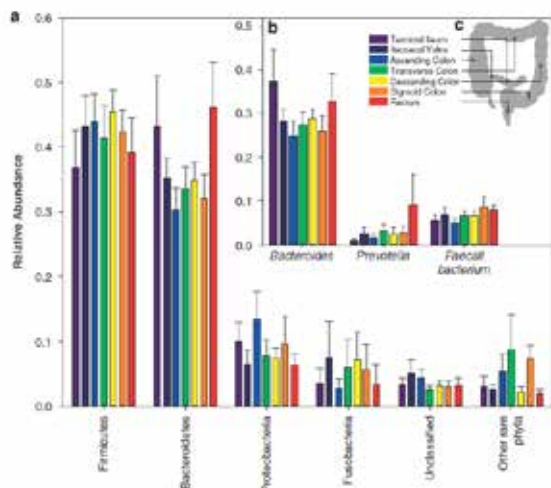
代表性成果一
人体肠道微生物组空间建成模式的研究

ORIGINAL ARTICLE

Spatial heterogeneity and co-occurrence patterns of human mucosal-associated intestinal microbiota

Zhigang Zhang[1,5], Jiawei Geng[2,5], Xiaodan Tang[2], Hong Fan[2], Jinchao Xu[3], Xiujun Wen[4], Zhanshan (Sam) Ma[1] and Peng Shi[1]

[1]State Key Laboratory of Genetic Resources and Evolution, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, China; [2]Department of Gastroenterology, The First People's Hospital of Yunnan Province, Kunming, China; [3]Center for Computational Mathematics and Applications, Department of Mathematics, Pennsylvania State University, University Park, PA, USA and [4]College of Forestry, South China Agricultural University, Guangzhou, China

Human gut microbiota shows high inter-subject variations, but the actual spatial distribution and co-occurrence patterns of gut mucosa microbiota that occur within a healthy human instestinal tract remain poorly understood. In this study, we illustrated a model of this mucosa bacterial communities' biogeography, based on the largest data set so far, obtained via 454-pyrosequencing of bacterial 16S rDNAs associated with 77 matched biopsy tissue samples taken from terminal ileum, ileocecal valve, ascending colon, transverse colon, descending colon, sigmoid colon and rectum of 11 healthy adult subjects. Borrowing from macro-ecology, we used both Taylor's power law analysis and phylogeny-based beta-diversity metrics to uncover a highly heterogeneous distribution pattern of mucosa microbial inhabitants along the length of the intestinal tract. We then developed a spatial dispersion model with an R-squared value greater than 0.950 to map out the gut mucosa-associated flora's non-linear spatial distribution pattern for 51.60% of the 188 most abundant gut bacterial species. Furthermore, spatial co-occurring network analysis of mucosa microbial inhabitants together with occupancy (that is habitat generalists, specialists and opportunist) analyses implies that ecological relationships (both oppositional and symbiotic) between mucosa microbial inhabitants may be important contributors to the observed spatial heterogeneity of mucosa microbiota along the human intestine and may even potentially be associated with mutual cooperation within and functional stability of the gut ecosystem.

　　肠道微生物沿着整个肠道，肠粘膜相关微生物组的建成模式仍然未知。施鹏研究组与马占山研究组合作，从微生物物种和群落的水平，借助经典的宏观生态学理、论和网络生物学分析，首先揭示了正常人体内肠粘膜附着的微生物组存在显著的空间异质性；其次，通过肠道微生物空间共变异网络分析，结合粘膜附着微生物地理分布的特征，进一步解释了空间异质性形成的动力，也鉴定了影响肠道微生物空间扩散的关键细菌。该研究成果第一次为理解正常人体肠道粘膜附着微生物的空间建成机制提供了重要的理论见解，也为进一步研究肠道疾病发生的空间特异性提供了重要的参照。

研究方向一：遗传资源多样性的演化与保护

代表性成果二
榕树－榕小蜂系统研究证实植物也会使用胡萝卜加大棒的策略

Discriminative host sanctions in a fig–wasp mutualism

RUI-WU WANG,[1,4] DEREK W. DUNN,[1,2,5] AND BAO FA SUN[1,3]

[1]*State Key Laboratory of Genetic Resources and Evolution, Kunming Institute of Zoology, Chinese Academy of Science, Kunming, Yunnan 650223 China*
[2]*Statistics and Mathematics College, Yunnan University of Finance and Economics, Kunming, Yunnan 650221 China*
[3]*Disease Genomics and Individualized Medicine Laboratory, Beijing Institute of Genomics, Chinese Academy of Sciences, Beijing 100101 China*

Abstract. In some mutualisms, cooperation in symbionts is promoted by hosts sanctioning "cheats," who obtain benefits but fail to reciprocate. In fig–wasp mutualisms, agaonid wasps pollinate the trees (*Ficus* spp.), but are also exploitative by using some flowers as larval food. *Ficus* can sanction cheats that fail to pollinate by aborting some un-pollinated figs. However, in those un-pollinated figs retained by trees, cheats successfully reproduce. When this occurs, wasp broods are reduced, suggesting sanctions increase offspring mortality within un-pollinated figs. We investigated sanction mechanisms of abortion and larval mortality against wasp cheats in the monoecious *Ficus racemosa* by introducing into figs 1, 3, 5, 7, or 9 female wasps (foundresses) that were either all pollen-laden (P+) or all pollen-free (P−). The abortion rates of P− figs were highest (~60%) when single foundresses were present. Abortion declined with increased foundresses and ceased with seven or more wasps present, irrespective of pollination. In un-aborted figs, wasp fitness (mean offspring per foundress) declined as foundress number increased, especially in P− figs. Reduced broods in P− figs resulted from increased larval mortality of female offspring as foundress number increased, resulting in more male-biased sex ratios. Overall sanctions estimated from both abortion rates and reduced offspring production strengthened as the number of cheats increased. In a second experiment, we decoupled pollination from wasp oviposition by introducing one pollen-free foundress, followed 24 h later by seven pollen-laden ovipositor-excised wasps. Compared with P+ and P− single-foundress figs, delayed pollination resulted in intermediate larval mortality and wasp fitness, which concurred with patterns of female offspring production. We conclude that fig abortion reflects both pollinator numbers and pollen presence. Sanctions within P− figs initiate soon after oviposition and discriminate against female offspring, thus reducing the benefits to cheats from adaptively biasing their offspring sex ratios. We suggest that costs to cheats via these discriminative sanctions are likely to promote stability in this mutualism.

Key words: Agaonidae; cooperation; evolutionary stable strategy; Ficus racemosa; sex ratio; symbiosis.

　　王瑞武组在前期系列理论模型与实验研究基础上，推测合作系统可能是一个高度非对称性系统，合作系统的优势方可能通过惩罚机制来抑制投机个体或行为的扩散，而奖励那些主动合作的个体或行为（胡萝卜＋大棒）。该组以著名的榕树－榕小蜂这一种间合作为模式系统，来验证上述理论猜想。与人类社会合作行为极为相似的是：榕树－榕小蜂这一合作系统中，合作的传粉小蜂中有些个体会采取投机性策略，而不给榕树传粉，甚至部分个体完全演化出投机行为的适应性特征————给植物传粉的花粉囊完全退化。试验发现榕树会通过两种方式惩罚这些投机性小蜂。当投机性小蜂数量比较少时，榕树通过果实脱落，将这些投机性小蜂的后代全部杀死。而当投机小蜂个体数量比较多时，榕树则通过抑制这些小蜂后代发育，降低其种群数量，但又维持其一定的数量，这极可能是由于这些投机性小蜂将为植物的花粉散布做出一定的贡献有关。把两种惩罚效应结合起来看，投机者越多，榕树对其惩罚也越大。该研究同时发现：榕树对投机性小蜂的惩罚主要是导致其雌性个体的死亡，而雌性在小蜂种群繁殖中属于真正有效的繁殖个体，因而这种惩罚机制比对雌雄都惩罚的效率要更高。"顺我者昌，逆我者亡"在自然生态系统得以演义。
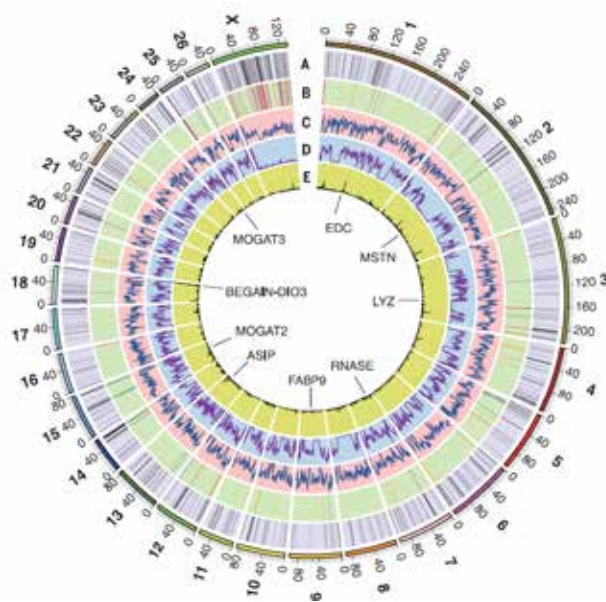
研究方向二：基因与基因组进化 ▶

代表性成果一
绵羊基因组研究取得重大进展

SHEEP GENOME

The sheep genome illuminates biology of the rumen and lipid metabolism

Yu Jiang,[1,2,3]* Min Xie,[4]* Wenbin Chen,[4]* Richard Talbot,[5] Jillian F. Maddox,[6]† Thomas Faraut,[7] Chunhua Wu,[8]† Donna M. Muzny,[9] Yuxiang Li,[4] Wenguang Zhang,[1,10,11] Jo-Ann Stanton,[12] Rudiger Brauning,[13] Wesley C. Barris,[2]§ Thibaut Hourlier,[14,21] Bronwen L. Aken,[14,21] Stephen M. J. Searle,[14] David L. Adelson,[2]|| Chao Bian,[4] Graham R. Cam,[2]¶ Yulin Chen,[3] Shifeng Cheng,[4] Udaya DeSilva,[2]# Karen Dixen,[15] Yang Dong,[1] Guangyi Fan,[4] Ian R. Franklin,[2]** Shaoyin Fu,[10] Pablo Fuentes-Utrilla,[5] Rui Guan,[4] Margaret A. Highland,[16,17] Michael E. Holder,[9] Guodong Huang,[4] Aaron B. Ingham,[2] Shalini N. Jhangiani,[9] Divya Kalra,[9] Christie L. Kovar,[9] Sandra L. Lee,[9] Weiqing Liu,[4] Xin Liu,[4] Changxin Lu,[4] Tian Lv,[4] Tittu Mathew,[9] Sean McWilliam,[2] Moira Menzies,[2] Shengkai Pan,[4] David Robelin,[7] Bertrand Servin,[7] David Townley,[2]†† Wenliang Wang,[4] Bin Wei,[4,18] Stephen N. White,[16,17] Xinhua Yang,[4] Chen Ye,[4] Yaojing Yue,[19] Peng Zeng,[4] Qing Zhou,[4] Jacob B. Hansen,[15] Karsten Kristiansen,[20] Richard A. Gibbs,[9] Paul Flicek,[21] Christopher C. Warkup,[22] Huw E. Jones,[22] V. Hutton Oddy,[23] Frank W. Nicholas,[24] John C. McEwan,[13] James W. Kijas,[2] Jun Wang,[4,20,25,26] Kim C. Worley,[9]‡‡ Alan L. Archibald,[27]‡‡ Noelle Cockett,[8]‡‡ Xun Xu,[4]‡‡ Wen Wang,[1]‡‡ Brian P. Dalrymple[2]‡‡

Sheep (Ovis aries) are a major source of meat, milk, and fiber in the form of wool and represent a distinct class of animals that have a specialized digestive organ, the rumen, that carries out the initial digestion of plant material. We have developed and analyzed a high-quality reference sheep genome and transcriptomes from 40 different tissues. We identified highly expressed genes encoding keratin cross-linking proteins associated with rumen evolution. We also identified genes involved in lipid metabolism that had been amplified and/or had altered tissue expression patterns. This may be in response to changes in the barrier lipids of the skin, an interaction between lipid metabolism and wool synthesis, and an increased role of volatile fatty acids in ruminants compared with nonruminant animals.

　　王文研究组与外单位合作，首次观测到两种在反刍动物（山羊和绵羊）中发生特异蛋白结构改变，且仅在瘤胃中特异高表达的结构蛋白。一种是首次报道和命名的毛透明蛋白类似蛋白，另外一种是小脯氨酸丰富蛋白 II 家族。另外，反刍动物的皮肤也是重要的脂类代谢器官。其中两个重要脂肪代谢的基因，单酰甘油 -O- 酰基转移酶 MOGAT2 和 MOGAT3 基因，在反刍动物早期以及随后在绵羊中进化出了新的重复基因，在绵羊皮肤中这些基因高度表达。在绵羊中 MOGAT2、3 基因仅在皮肤中高表达，提示甘油三脂分解生成羊毛脂所产生的甘油一脂，可在皮肤中直接被回收重新生成甘油三脂。这种新基因重复事件说明新基因的产生对反刍动物和绵羊的特殊生物学性状进化作出了重要贡献。

研究方向二：基因与基因组进化 ▶

代表性成果二
青藏高原家犬高原适应的遗传机制及其与藏族人群的趋同进化

Yan Li,[1,2] Dong-Dong Wu,*[1,2] Adam R. Boyko,[3] Guo-Dong Wang,[1,2] Shi-Fang Wu,[1] David M. Irwin,[1,4,5] and Ya-Ping Zhang*[1,2,6]

[1]State Key Laboratory of Genetic Resources and Evolution, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, China

[2]Kunming College of Life Science, University of Chinese Academy of Sciences, Kunming, China

[3]Department of Biomedical Sciences, College of Veterinary Medicine, Cornell University

[4]Department of Laboratory Medicine and Pathobiology, University of Toronto, Toronto, Ontario, Canada

[5]Banting and Best Diabetes Centre, University of Toronto, Toronto, Ontario, Canada

[6]Laboratory for Conservation and Utilization of Bio-resource, Yunnan University, Kunming, China

*Corresponding author: E-mail: wudongdong@mail.kiz.ac.cn; zhangyp@mail.kiz.ac.cn.

Associate editor: Anna Di Rienzo

Abstract

With the assistance of their human companions, dogs have dispersed into new environments during the expansion of human civilization. Tibetan Mastiff (TM), a native of the Tibetan Plateau, was derived from the domesticated Chinese native dog and, like Tibetans, has adapted to the extreme environment of high altitude. Here, we genotyped genome-wide single-nucleotide polymorphisms (SNPs) from 32 TMs and compared them with SNPs from 20 Chinese native dogs and 14 gray wolves (*Canis lupus*). We identified 16 genes with signals of positive selection in the TM, with 12 of these candidate genes associated with functions that have roles in adaptation to high-altitude adaptation, such as *EPAS1*, *SIRT7*, *PLXNA4*, and *MAFG* that have roles in responses to hypoxia. This study provides important information on the genetic diversity of the TM and potential mechanisms for adaptation to hypoxia.

Key words: high-altitude adaptation, Tibetan Mastiff, domestication.

Mol. Biol. Evol. 31(5):1200−1205

犬是最早随人类活动扩散到全世界的家养动物，和人类适应相同的自然环境。作为青藏高原上的土著犬种，藏獒表现出对高海拔高寒、低氧环境很好的适应性，例如非常厚的皮毛来抵抗低温和强辐射，发达肺脏器官来应对低氧环境等等。然而目前，对藏獒适应极端高原环境的遗传基础尚不清楚。张亚平研究组利用家犬全基因组 SNP 芯片技术获得了藏獒的群体 SNP 数据，并结合中国土狗和灰狼的群体 SNP 数据，详细分析了藏獒的群体特征，并利用群体遗传学方法（如 Fst，XP-EHH 等）挖掘到藏獒基因组中 16 个受选择候选基因，其中 12 个基因可能参与到藏獒的高原适应，包括藏族人群高原适应基因 EPAS1。该研究为藏獒的品种资源保护以及家养动物高原适应的分子机制提供重要信息。
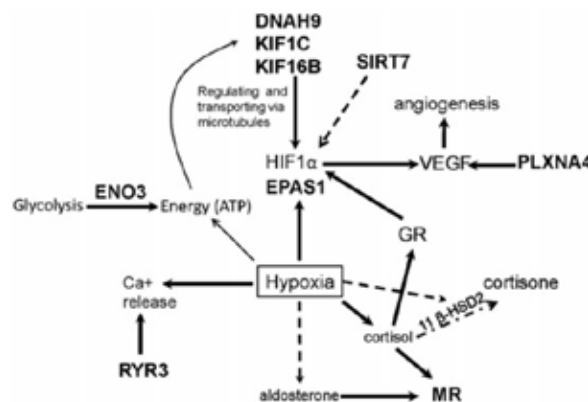
研究方向三： 遗传、发育与进化 ▶

代表性成果一
prestin 基因的平行进化导致回声定位哺乳动物的功能趋同进化

Parallel Sites Implicate Functional Convergence of the Hearing Gene *Prestin* among Echolocating Mammals

Zhen Liu,[1] Fei-Yan Qi,[1,2] Xin Zhou,[1] Hai-Qing Ren,[1] and Peng Shi*[1]

[1]State Key Laboratory of Genetic Resources and Evolution, Laboratory of Evolutionary and Functional Genomics, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, Yunnan, China

[2]University of the Chinese Academy of Sciences, Beijing, China

*Corresponding author: E-mail: ship@mail.kiz.ac.cn.

Associate editor: Naruya Saitou

Abstract

Echolocation is a sensory system whereby certain mammals navigate and forage using sound waves, usually in environments where visibility is limited. Curiously, echolocation has evolved independently in bats and whales, which occupy entirely different environments. Based on this phenotypic convergence, recent studies identified several echolocation-related genes with parallel sites at the protein sequence level among different echolocating mammals, and among these, *prestin* seems the most promising. Although previous studies analyzed the evolutionary mechanism of *prestin*, the functional roles of the parallel sites in the evolution of mammalian echolocation are not clear. By functional assays, we show that a key parameter of *prestin* function, $1/\alpha$, is increased in all echolocating mammals and that the N7T parallel substitution accounted for this functional convergence. Moreover, another parameter, $V_{1/2}$, was shifted toward the depolarization direction in a toothed whale, the bottlenose dolphin (*Tursiops truncatus*) and a constant-frequency (CF) bat, the Stoliczka's trident bat (*Aselliscus stoliczkanus*). The parallel site of I384T between toothed whales and CF bats was responsible for this functional convergence. Furthermore, the two parameters ($1/\alpha$ and $V_{1/2}$) were correlated with mammalian high-frequency hearing, suggesting that the convergent changes of the *prestin* function in echolocating mammals may play important roles in mammalian echolocation. To our knowledge, these findings present the functional patterns of echolocation-related genes in echolocating mammals for the first time and rigorously demonstrate adaptive parallel evolution at the protein sequence level, paving the way to insights into the molecular mechanism underlying mammalian echolocation.

Key words: bat, dolphin, echolocation, convergent evolution, NLC.
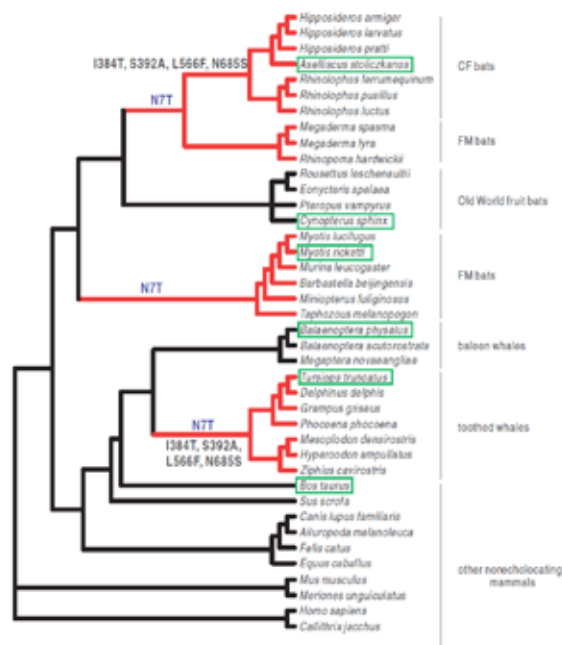
prestin 是哺乳动物听力的关键基因，在此次研究中，施鹏研究组首次从功能出发揭示了 prestin 在独立起源的物种（鲸类和蝙蝠）的回声定位中起着关键作用，有利于其能在昏暗的水下和夜空环境中进行捕食和方向定位。在 prestin 的氨基酸序列的进化分析中显示，T384N 的平行改变，揭示了此位点在哺乳动物高频听力的进化历程中发挥了重要作用。对此，通过进一步的功能结果再一次证明了听力基因 prestin 的氨基酸平行位点的改变导致了功能的趋同。

研究方向三： 遗传、发育与进化 ▶

代表性成果二
揭示灵长类大脑容量调控基因 CENPJ 的低甲基化机制

Human-Specific Hypomethylation of *CENPJ*, a Key Brain Size Regulator

Lei Shi,[†,1,2] Qiang Lin,[†,1,3] and Bing Su[*,1,2]

[1]State Key Laboratory of Genetic Resources and Evolution, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, China

[2]Yunnan Key Laboratory of Primate Biomedical Research, Kunming, China

[3]Kunming College of Life Science, University of Chinese Academy of Sciences, Beijing, China

[†]These authors contributed equally to this work.

*Corresponding author: E-mail: sub@mail.kiz.ac.cn.

Associate editor: Katja Nowick

Abstract

Both the enlarged brain and concurrent highly developed cognitive skills are often seen as distinctive characteristics that set humans apart from other primates. Despite this obvious differentiation, the genetic mechanisms that underlie such human-specific traits are not clearly understood. In particular, whether epigenetic regulations may play a key role in human brain evolution remain elusive. In this study, we used bisulfite sequencing to compare the methylation patterns of four known genes that regulate brain size (*ASPM*, *CDK5RAP2*, *CENPJ*, and *MCPH1*) in the prefrontal cortex among several primate species spanning the major lineages of primates (i.e., humans, great apes, lesser apes, and Old World monkeys). The results showed a human-specific hypomethylation in the 5′ UTR of *CENPJ* in the brain, where methylation levels among humans are only about one-third of those found among nonhuman primates. Similar methylation patterns were also detected in liver, kidney, and heart tissues, although the between-species differences were much less pronounced than those in the brain. Further in vitro methylation assays indicated that the methylation status of the *CENPJ* promoter could influence its expression. We also detected a large difference in *CENPJ* expression in the human and nonhuman primate brains of both adult individuals and throughout the major stages of fetal brain development. The hypomethylation and comparatively high expression of *CENPJ* in the central nervous system of humans suggest that a human-specific—and likely heritable—epigenetic modification likely occurred during human evolution, potentially leading to a much larger neural progenitor pool during human brain development, which may have eventually contributed to the dramatically enlarged brain and highly developed cognitive abilities associated with humans.

Key words: DNA methylation, *CENPJ*, brain evolution, primate, CpG island, epigenetic regulation.

宿兵研究组比较了 4 个灵长类代表物种（人类、黑猩猩、长臂猿和猕猴）大脑前额叶中基因的甲基化模式的差异，发现，CENPJ 基因在人类大脑中是低甲基化的，而在其他所有非人灵长类大脑中的甲基化水平是人类的 2－3 倍；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，并且是可遗传的。由于前人的研究已经表明 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。
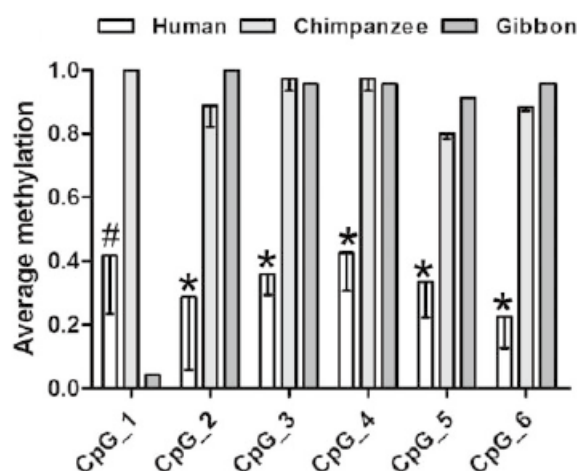
系统进化与生物地理学

杨君兴，博士，研究员，博士生导师。研究方向包括：生物多样的考察监测及评价、系统分类、系统发育与生物地理学；珍稀特有物种的生态学研究和保育；湿地生态系统的恢复研究。本年度共有在研课题 23 项，其中新申请批准的项目 8 项。出版专著 1 章；发表 SCI 论文 2 篇，获授权国家发明专利 1 项。

重要成果（Highlights）
论著（Publications）

1. **Yanfei Huang**, **Junxing Yang***, **Xiaoyong Chen***. 2014. *Stenorynchoacrum xijiangensis*, a new genus and a new species of Labeoninae fish from Guangxi, China (*Teleostei: Cyprinidae*). *Zootaxa* 3793 (3): 379–386.

2. Qiqun Cheng*, Yuxia Zhu, **Xiaoyong Chen***. 2014. High polymorphism and moderate differentiation of chub mackerel, *Scomber japonicus* (Perciformes: Scombridae), along the coast of China revealed by fifteen novel microsatellite markers. *Conservation Genetics* 15 (5):1021-1035.

3. **Xiaofu Pan**, **Xiaoai Wang***, Li Ma, **Zaiyun Li**, **Xiaoyong Chen**, **Junxing Yang**. 2014. Artificial Fertilization and Embryonic Development of Sinocyclocheilus grahami (Regan) from Dianchi Lake, China. *Journal of Biodiversity*, *Bioprospecting and Development* 1(1): 1-6.

4. **Weiying Wang**, Wei Zhou, **Junxing Yang**, **Xiaoyong Chen***. 2014. Morphological and molecular studies on *Garra imberba* and its related speciesi in China. *Zoological Research* 35 (1): 20-32.

5. 王晓爱，潘晓赋，杨君兴，陈小勇. ZL 201310291001.1. 一种滇池金线鲃嗅囊细胞系的构建和超低温冷冻保存方法 （2014.11.19 授权）.

1. 中国野鲮亚科一新属及其模式种的描述

野鲮亚科鱼类是主要分布于亚洲和非洲一类口吸盘高度特化的淡水鱼类，其单系性在形态和分子上都得到了充分的验证。本研究记述了采自中国广西省境内珠江支流野鲮亚科一新属：狭吻鱼属 *Stenorynchoacrum*，和指定的模式种：西江狭吻鱼 *Stenorynchoacrum xijiangensis*。新属与野鲮亚科其他属的相区别的主要特征有：吻皮中间不发达，仅覆盖上颌基部，吻皮侧边发达，往外翻，与下唇相连，唇后沟把下唇分成三部分，下唇侧边后缘游离，下唇中间隆起形成一个圆形肉质垫。

2. 基于微卫星标记的鲐鱼种群遗传多样性分析

鲐鱼，又名日本鲭（*Scomber japonicus*），隶属于鲈形目，鲭科；广泛分布于西北太平洋沿岸水域，是我国最重要的经济鱼类之一。依托本实验室开放课题，研究人员基于 15 个新开发的微卫星标记对中国沿海（黄海—东海—南海）海域 11 个样点的 319 尾鲐鱼进行了遗传多样性分析。结果表明：种群内遗传多样性相对较高，而种群间的遗传分化相对适中。无论是 UPGMA，PCA 还是 Bayesian 分析均表明：中国沿海的鲐鱼种群可以分为三个大的类群，其一包含黄海种群并延伸至南中国海的海南岛东西海岸线，其二包含南中国海中部远离海南岛海岸线的种群，其三包含东海海域中部种群。这一研究对鲐鱼这一重要经济水产资源的可持续利用、有效管理和保护提供了重要基础。

3. 滇池金线鲃人工繁殖状态下胚胎发育研究

滇池金线鲃（*Sinocyclocheilus grahami*）是分布在滇池流域的云南特有珍稀鱼类，历史上曾是昆明周边重要的经济鱼类。但由于上个世纪以来严重的水质污染和过度捕捞等因素，该物种在其原分布区种群剧烈下降，濒临灭绝；并于 1989 年被列为国家 II 级保护动物。2007 年，本课题组首次对该物种人工繁殖成功，到现在为止，其受精卵质量和存活率都得到了极大的提高。本研究对其胚胎发育各阶段进行了详细记录和拍照，根据显微镜下的形态学观察到的特征，将滇池金线鲃受精卵发育划分为 30 个步骤，继而又归类为 6 大阶段。这一研究一方面更全面地了解了滇池金线鲃的个体发育规律，另一方面也为下一步滇池金线鲃育种操作打下良好的基础。

4. 无须墨头鱼及近缘种的形态和分子系统研究

无须墨头鱼（ *Garra imberba*） 是墨头鱼属中为数不多的广布种，包括其亚种 （宜良墨头鱼 *G. imberba yiliangensis* 和海南墨头鱼 *G. imberba hainanensis*）在内， 主要分布在中国的澜沧江、元江、金沙江、南盘江和海南昌江水系。而分布在怒江的怒江墨头鱼（*G. nujiangensis*）和红河水系的高体墨头鱼（ *G. alticorpora*）与无须墨头鱼形态类似，但亲缘关系如何尚不清楚。本研究通过大范围取样的分子谱系地理学分析和详尽的形态对比分析，明确海南墨头鱼、宜良墨头鱼、高体墨头鱼均为无须墨头鱼的同物异名，而怒江墨头鱼为一独立的物种。

Phylogenetics and Biogeography

Dr. Junxing Yang, Professor. The research team is mainly interested in biodiversity monitoring survey and evaluation, fauna taxonomic, phylogenetic and biogeographic; ecology and conservation research to rare and native species; especially focuses on the restoration of wetland ecosystem and application. In 2014, total 23 research programs have been implementing with 8 programs newly approved. Published 1 monograph and 2 SCI papers. One national invention patent licensing.

Email: yangjx@mail.kiz.ac.cn

1. A new genus and a new species of Labeoninae fish

Stenorynchoacrum xijiangens is, a new genus and a new species of Cyprinidae, is described from a tributary of the Zhujiang River (Pearl River) in Guangxi Province, China. It can be distinguished from other genera of Labeoninae by the following characters: middle part of rostral cap undeveloped, narrow, only covering the base of the upper jaw, both sides of rostral cap well developed and extending upward, rostral cap connected the lower lip with free lateral margin, the median part of lower lip protruded to form a round fleshy pad, whose posterior margin continuous with the mental region.

2. Genetic diversity analysis of chub mackerel Scomber japonicus

Genetic diversity and population structure of *Scomber japonicus* along the coast of China were analyzed in 319 individuals from 11 sites using 15 novel microsatellite loci. Relatively high levels of genetic variation within population (Na = 10.20–13.20, Ho = 0.507–0.686, He = 0.678–0.805, and PIC = 0.669–0.776) and moderate level of genetic differentiation among populations (FST = 0.1055) were detected. UPGMA, PCA and Bayesian analyses suggested that *S. japonicus* from YS to SCS can be divided into three major groups. This study will be useful to the sustainable utilization, effective management and conservation of *S. japonicus* resource in the future.

3. Artificial Fertilization and Embryonic Development of Sinocyclocheilus grahami

Sinocyclocheilus grahami, is a cyprinidae fish endemic to Dianchi Lake, Yunnan, China. We have attempted the artificial propagation of *S. grahami* for several years and recorded the success of *S. grahami* artificial fertilization for six years and found that egg quality improved with enhanced broodstock management, with negligible effects on S. grahami artificial fertilization resulting from the injection of LHRH-A2. In this study, we also provide a comprehensive staging series of this species. The eggs have relatively large yolks (1.8–2.2 mm) and are strongly adhesive, with a thick and transparent egg envelope. The embryonic development of *S. grahami* can be divided into thirty stages and further grouped into six periods. Embryos hatched 144.0–168.0 hours after fertilization (HPF).

4. Morphological and molecular studies on Garra imberba

Garra imberba is widely distributed in China. At the moment, both *Garra yiliangensis* and *G. hainanensis* are treated as valid species, but they were initially named as a subspecies of *G. pingi*, a junior synonym of *G. imberba*. *Garra alticorpora* and *G.nujiangensis* also have similar morphological characters to *G. imberba*, but the taxonomic statuses and phylogenetic relationships of these species with *G. imberba* remains uncertain. In this study, 128 samples from the Jinshajiang, Red, Nanpanjiang, Lancangjiang, Nujiang Rivers as well as Hainan Island were measured while 1 mitochondrial gene and 1 nuclear intron of 24 samples were sequenced to explore the phylogenetic relationship of these five species. The results showed that *G. hainanensis*, *G. yiliangensis*, *G. alticorpora* and *G. imberba* are the same species with *G. imberba* being the valid species name, while *G. nujiangensis* is a valid species in and of itself.

员工简介（Lab Staff）
工作人员（Staff）

陈小勇　副研究员
Xiaoyong Chen, Associate Professor
郑兰平　副研究员
Lanping Zheng, Associate Professor
潘晓赋　副研究员
Xiaofu Pan, Associate Professor
刘　倩　秘书
Qian Liu, Secretary
余国华　助理研究员
Guohua Yu, Assistant Professor
杜丽娜　助理研究员
Lina Du, Assistant Professor
蒋万胜　助理研究员
Wansheng Jiang, Assistant Professor
舒树森　助理研究员
Shusen Shu, Assistant Professor
闵　锐　助理研究员
Rui Min, Assistant Professor
王晓爱　助理研究员
Xiaoai Wang, Assistant Professor
刘淑伟　助理研究员
Shuwei Liu, Assistant Professor
王　茉　助理研究员
Mo Wang, Assistant Professor
赵亚鹏　研究实习员
Yapeng Zhao, Research assistant
彭　云　研究实习员
Yun Peng, Research assistant

研究生 Graduate Students

杨坤凤　Kunfeng Yang 2012
程　城　Cheng Cheng 2012
秦　涛　Tao Qin 2012
张源伟　Yuanwei Zhang 2013
陈枳颖　Zhiying Chen 2014
郑　秋　Qiuyang Zheng 2014

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、灵长类及偶蹄类动物为研究对象，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现状及其致危因素分析。

重要成果（Highlights）
论著（Publications）

1. He K, Shinohara A, Jiang XL, Campbell KL*. 2014. Multilocus phylogeny of talpine moles (Talpini, Talpidae, Eulipotyphla) and its implications for systematics. Molecular Phylogenetics and Evolution, 70:513-521.

2. Ni QY, Huang B, Liang ZL, Wang XW, Jiang XL*. 2014. Dietary Variability in the Western Black Crested Gibbon (Nomascus concolor) Inhabiting an Isolated and Disturbed Forest Fragment in Southern Yunnan, China. American Journal of Primatology. 76:217-229.

3. Li XY, Buzzard P, Jiang XL. 2014. Validity of the camera trapping method for abundance estimate and its application to a habitat association analysis for four ungulate species in mountain forests. Population Ecology. 56:251–256.

4. Li XY, Jiang XL. 2014. Implication of musk deer (Moschus spp.) depletion from hunter reports and dung transect data in northwest Yunnan, China. Journal for Nature Conservation. 22:474-478.

5. Hu NQ, Joseph O, Huang B, He K, Jiang XL*. 2014. Isolation and characterization of thirteen microsatellite loci for the western black crested gibbon (Nomascus concolor) by high-throughput sequencing. Conservation Genetics Resources. 6:179-181.

6. He K, Jiang XL*. 2014. Sky islands of southwest China. I: an overview of phylogeographic patterns. Chinese Science Bulletin. 59:585-597.

1. 鼹鼠系统演化研究新进展

中国是世界上鼹科（*Talpidae*）物种资源最丰富的国家，然而我们对该类群的了解仍十分有限。我们与日本宫崎大学、加拿大曼尼托巴大学合作对鼹科鼹族（*Talpini*）的演化进行了研究，测定了线粒体和核基因的 14 个基因片段，并对该族群的系统关系进行了分析。结果有力地支持中国北方的麝鼹属（*Scaptochirus*）与南方的白尾鼹属（*Parascaptor*）是姐妹群关系，首次从系统演化的角度解释了两个属在中耳形态上的相似性。此外我们发现中国和东南亚的东方鼹物种（*Euroscaptor*）与分布于日本的本州鼹（*Euroscaptor mizura*）进化起源不同，后者很可能代表了一个新属。研究结果还表明白尾鼹、东方鼹和缺齿鼹属（*Mogera*）中仍存在未知的新物种，在未来的研究中的，新物种的发现和命名仍将是重要的研究方向。

2. 滇西北地区麝资源的利用与保护

麝是重要的药用动物和香料动物，中国为麝类物种数分布最多的国家，然而由于过度捕猎，我国麝资源量极度下降且难以恢复。访问调查发现，目前麝的主要狩猎工具为颈扣和吊脚扣，分别占到 42.6%（n=26）和 31.1%（n=19）；九十年代初期每人每年收获麝的数量为 7.41±1.8 头，近两年仅有 0.67±0.88 头，并且和 90 年代初期相比，现在狩猎距离显著变远，表明该地区麝资源衰退严重。另外，样线调查发现在非偷猎区的粪堆遇见率是偷猎区的六倍，与访问调查结果一致。在滇西北地区，麝资源的衰退主要是长期过度捕杀导致的，其次是过度放牧和栖息地的规模性破坏。本研究提示对猎人的访谈是有效掌握目标物种现状和濒危原因的方法，并可据此提出有效保护管理措施。

3. 高通量测序法筛选西黑冠长臂猿多态性微卫星位点

作为极度濒危物种西黑冠长臂猿（*Nomascus concolor*），限制其分子遗传保护学研究发展的不仅有样品来源不易，还有其不完备的分子标记系统。我们采集了来自无量山 6 个不同种群 12 个个体的粪便样品并利用 454 高通量测序 1/8 板的方法成功筛选出 13 个西黑冠长臂猿特异性的多态性微卫星位点。平均每个位点观测等位基因数位 3–8 个。观测杂合度 （H_o）为 0.333–0.917，期望杂合度（H_e）为 0.424–0.822。13 个位点个体鉴定的不可排除率为 $1.58×10^{-11}$。该结果将成为西黑冠长臂猿社群结构和种群遗传学进一步研究的有效工具。

Mammal Ecology and Evolution

Dr. 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.

Email: jiangxl@mail.kiz.ac.cn

1. Multilocus phylogeny reveal cryptic diversity in shrew like moles (Uropsilus, Talpidae, Mammalia)

The tribe Talpini is a group of strictly sub-terranean moles distributed across the EurasianContinent whose phylogenetic relationships and taxonomy remain unresolved. Here we report a multi-locus nuclear-mitochondrial DNA dataset (9468 bp) from 11 talpine species en-compassing all five recognized genera, to-gether with analyses of their divergence times and evolutionary affinities inferred from maximum likelihood and Bayesian approaches. Our results resolved all relationships except the root of the four recognized Asian genera, which was placed sister to the genus Talpa. We provide the first molecular support for a sister-taxon relationship between Parascaptor and Scaptochirus and confirm that the genus Euroscaptor is paraphyletic. Our species delimitation analyses support the existence of at least two genetically distinct, and hence potentially cryptic species. These findings argue that generic status should be given to E. mizura and illustrate that the taxonomic diversity of the tribe Talpini in mountainous regions of southwestern China and Southeast Asia is underestimated.
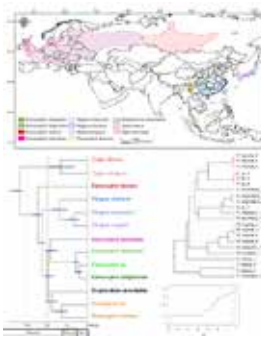
2. Dietary Variability in the Western Black Crested Gibbon (Nomascus concolor) Inhabiting an Isolated and Disturbed Forest Fragment in Southern Yunnan

Forest fragmentation and isolation can reduce the size of available habitat and lead to lower food availability. The persistence of nonhuman primates in fragments depends largely on their ability to adjust their diet in response environmental change. The western black crested gibbon (Nomascus concolor) is distributed mainly in southwestern China, but little is known about its diet except from studies in the well-protected forests at Mt. Wuliang and Mt. Ailao, central Yunnan. We studied food abundance and diet over 2 years in a small group surviving in an isolated and disturbed forest at Bajiaohe, southern Yunnan, and drew a comparison with the population at Dazhaizi in Mt. Wuliang. We found that gibbons at Bajiaohe consumed mostly fruit, but did not eat figs, unlike most other gibbon populations. Liana fruits and mature leaves were used as alternative during periods of tree fruit scarcity. Our indicate that gibbons in Bajiaohe respond to habitat fragmentation and isolation by consuming a variety of plant species, depending on those that are locally available, and increasing time spent feeding on fruits of trees and lianas rather than increasing time spent consuming leaves.

员工简介（Lab Staff）
工作人员（Staff）

饶定齐　副研究员
Rao Dingqi, Associate Professor
何　锴　助理研究员
He Kai, Assistant Professor
黄　蓓　助理研究员
Huang Bei, Assistant Professor
李学友　助理研究员
Li Xueyou, Assistant Professor
张栋儒　助理研究员
Zhang Dongru, Assistant Professor
辉　洪　高级工程师
Hui Hong Senior Engineer
林　苏　助理实验师
Lin Su, Assistant Engineer
刘　硕　研究实习员
Liu Shuo   Research Assistant
何　锬　研究实习员
He Tan   Research Assistant
布　超　研究实习员
Bu Chao Research Assistant

研究生 (Graduate Students)

胡道清　Hu Naiqing, 2009
万　韬　Wan Tao, 2010
张　斌　Zhang Bin, 2012
陈中正　Chen Zhongzheng, 2012
李　权　Li Quan, 2012
赵启龙　Zhao Qilong, 2012
黄　程　Huang Cheng, 2013
宁文鹤　Ning Wenhe, 2013
杜宜清　Du Yiqing, 2103
程　峰　Chengfeng, 2013
宋心强　Song Xinqiang, 2012

鸟类学

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

重要成果（Highlights）
论著（Publications）

1. **Dong F**, Zou FS, Lei FM, Liang W, Li SH*, **Yang XJ***. Testing hypotheses of mitochondrial gene-tree paraphyly: unraveling mitochondrial capture of the Streak-breasted Scimitar Babbler (Pomatorhinus ruficollis) by the Taiwan Scimitar Babbler (Pomatorhinus musicus), *Molecular Ecology*, 2014, 23: 5855-5867.

2. **Dong F**, Li SH, Zou FS, Lei FM, Liang W, Yang JX, **Yang XJ***. Molecular systematics and plumage coloration evolution of an enigmatic babbler (Pomatorhinus ruficollis) in East Asia. *Molecular Phylogenetics and Evolution*, 2014, 70: 76-83.

3. **Xia J**, **Wu F**, **Hu WZ**, Fang JL, **Yang XJ**. The coexistence of seven sympatric fulvettas in Ailao Mountains, Ejia Town, Yunnan Province. *Zoological Research*, 2015, 36: 18-28.

4. Hung CM, Hung HY, Yeh CF, Fu YQ, Chen D, Lei FM, Yao CT, Yao CJ, **Yang XJ**, Lai YT and Li SH. Species delimitation in the Chinese bamboo partridge Bambusicola thoracica (Phasianidae; Aves), *Zoologica Scripta*, 2014, 43: 562-575.

5. Luo ST, Wu YC, Chang Q, Liu Y, **Yang XJ**, Zhang ZW, Zhang M, Zhang Q and Zou FS. Deep phylogeographic divergence of a migratory passerine in Sino- Himalayan and Siberian forests: the Red- flanked Bluetail (Tarsiger cyanurus) complex. *Ecolggy and Evolution*, 2014, 4:977-986.

6. Wang WJ, Dai CY, Alstrom P, Zhang CL. Qu YH, Li SH, **Yang XJ**, Zhao N, Song G, Lei FM 2014 Past hybridization between two East Asian long-tailed tits (Aegithalos bonvaloti and A. fuliginosus). *Frontiers in Zoology*, 2014, 11:40

1. 棕颈钩嘴鹛与台湾钩嘴鹛的分化历史研究

线粒体基因树上的物种水平并系性是分类学和系统学中的一个常见问题。这一问题可有多种解释，但目前的方法不易将其进行区分。本研究基于四个线粒体基因和九个核基因使用多种统计方法解析棕颈钩嘴鹛线粒体基因树上并系性的成因。线粒体系统发育分析揭示棕颈钩嘴鹛相对于台湾钩嘴鹛为并系群，而核基因却支持二者的姐妹群关系。溯组模拟分析暗示这一并系性很可能由台湾钩嘴鹛对棕颈钩嘴鹛的线粒体袭夺导致。进一步的近似贝叶斯分析暗示两物种自更新世后期分化以来，存在由棕颈钩嘴鹛向台湾钩嘴鹛的显著水平的单向基因流。研究中我们列举了线粒体渐渗和核基因渐渗结果相异的可能原因。本研究强调多基因数据在物种界定中的优势，以及检验线粒体基因树上物种水平并系性成因假说的重要性。
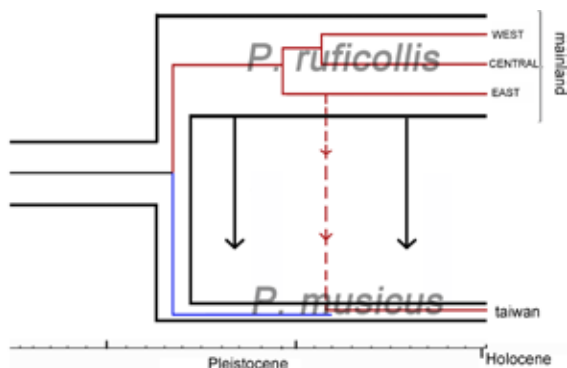
2. 哀牢山 7 种雀鹛共存机制的研究

生态习性相似物种的共存机制的研究是群落生态学研究的核心问题。2012−2014 年，通过网捕结合样点观察的方法，从空间生态位利用和形态分化的角度，对云南哀牢山鄂嘉地区同域分布的 7 种雀鹛属鸟类的共存机制进行了初探。研究结果表明：7 种雀鹛在海拔分布、栖位高度、对生境中植被盖度的选取上均具有显著差异；判别分析结果中约 90.3% 的样本被正确归类，除白眉雀鹛（*Alcippe vinipectus, 65.40%*）与褐头雀鹛（*Alcippe cinereiceps, 74.60%*）外，其余鸟种判别正确率较高（*91.20%-100%*），7 种雀鹛被分为 4 个集团。各集团相对独立的形态特征与其资源利用方式相关，保证了在分布重叠区内集团间鸟种资源利用的分离。通过空间生态位维度多尺度的分化以及分布重叠区内不同集团资源利用的差异，7 种雀鹛最大限度的减少了生态位的重叠，缓解了种间竞争压力，促进了共存。

Ornithology

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

Email:yangxj@mail.kiz.ac.cn

1. Molecular systematics of the streak-breasted scimitar babbler

Species-level paraphyly inferred from mitochondrial gene trees is a prevalent phenomenon in taxonomy and systematics, but there are several potential causes that are not easily explained by currently used methods. This study aimed to test the underlying causes behind the observed paraphyly of Streak-breasted Scimitar Babbler (Pomatorhinus ruficollis) via statistical analyses of four mitochondrial (mtDNA) and nine nuclear (nuDNA) genes. Mitochondrial gene trees show paraphyly of P. ruficollis with respect to the Taiwan Scimitar Babbler (Pomatorhinus musicus), but nuclear genealogies support a sister-group relationship. Predictive coalescent simulations imply several hypothetical explanations, the most likely being mitochondrial capture of P. ruficollis by P. musicus for the observed cyto-nuclear incongruence. Further approximate Bayesian computation suggests a unidirectional introgression model with substantial level of gene flow from P. ruficollis to P. musicus during their initial divergence during the Late Pleistocene. This specific observation frames several potential causes for incongruent outcomes of mitochondrial and nuclear introgression in general, and on the whole, our results underscore the strength of multiple independent loci for species delimitation and importance of testing hypotheses that explain disparate causes of mitochondrial gene-tree paraphyly.

2. The coexistence of seven sympatric fulvettas in Ailao Mountains

The coexistence of ecologically similar species sharing sympatric areas is a central issue of community ecology. Niche differentiation is required at least in one dimension to avoid competitive exclusion. From 2012-2014, by adopting the methods of mist-nets and point counts to evaluate spatial niche partitioning and morphological differentiations, we explored the coexistence mechanisms of seven sympatric fulvettas in Ailao Mountains, Ejia town, Yunnan Province, China. The microhabitats of these seven fulvettas were significantly different in elevation, roost site height and vegetation coverage, indicating a spatial niche segregation in different levels. Approximately, 90.30% of the samples were correctly classified by linear discriminant analysis (LDA) with correct rates at 91.20%-100%, except the White-browed fulvetta (Alcippe vinipectus) (65.4%) and the Streak-throated fulvetta (A. cinereiceps) (74.6%). The seven fulvettas were classified into four guilds based on their specific morphological characters, suggesting that the species in each guild use their unique feeding ways to realize resource partitioning in the overlapped areas. These finding indicate that through multi-dimensional spatial niche segregation and divergence in resource utilizing, the inter-specific competition among these seven fulvettas is minimized, whereas, coexistence is promoted.

员工简介（Lab Staff）
工作人员（Staff）

吴 飞 博士 助理研究员
Fei Wu, Assistant Professor
伍和启 博士 助理研究员
HeQi Wu, Assistant Professor
董 锋 博士 助理研究员
Feng Dong, Assistant Professor
岩 道 硕士 研究实习员
Dao Yan, Research Assistant
高建云 硕士 研究实习员
Jianyun Gao, Research Assistant
李欣磊 硕士 研究实习员
Xinlei Li, Research Assistant

研究生（Graduate Students）
董好岩 博士生 HaoYan Dong 2012
王荣兴 博士生 RongXing Wang 2011
卢光义 博士生 GuangYi Lu 2014
胡莞钊 硕士生 Wanzhao Hu 2013

生态学与环境保护中心 (ECEC)

Douglas W. Yu, 博士, 研究员, 博导。主要关注三个方面的研究内容: Metabarcoding 技术在快速生物多样性评估中的应用; 保护生物学和对热带森林保护的方针、政策; 互利共栖的演化。有 90 篇研究成果分别发表于 Nature, Science, PNAS, PLoS Biology, Ecology Letters, Ecological Monographs, Ecology, American Naturalist, Evolution, J. Animal Ecology and Proceedings of the Royal Society of London B.

重要成果（Highlights）
论著（Publications）

1. Harris, R.B., Zhou, J.K., Ji, Y.Q., Kai, Z., Yang, C.Y., Yu, D.W. (2014) Evidence that the Tibetan fox is an obligate predator of the plateau pika: conservation implications. Journal of Mammalogy,95,1207-1221.

2. Edwards, D.P., Magrach, A., Woodcock, P., Lim, N.T.L., Edwards, F.A., Larsen, T.H., Hsu, W.W., Benedick, S., Khen, C.V., Chung, A.Y.C., Hamer, K.C., Wilcove, D.S., Yu, D.W. (2014) Selective-logging and oil palm: multitaxon impacts, biodiversity indicators, and trade-offs for conservation planning. Ecological Applications 24(8), 2029–2049.

3. Yang, C.X., Wang, X.Y., Miller, J.A., de Blécourt, M., Ji, Y.Q., Yang C.Y., Harrison, R.D., Yu, D.W. (2014) Using metabarcoding to ask if easily collected soil and leaf-litter fauna can be used as a general biodiversity indicator. Ecological Indicators 46, 379-389.

4. He, D., Wu, R., Feng, Y., Li, Y., Ding, C. & Wang, W., Yu, D. W. (2014) China's transboundary waters: Water and ecological security through applied ecology. Journal of Applied Ecology. doi: 10.1111/1365-2664.12298.

5. Bohmann, K., Evans, A., Gilbert, M.T.P., Carvalho, G.R., Creer, S., Knapp, M., Yu, D.W., de Bruyn, M. (2014) Environmental DNA for wildlife biology and biodiversity monitoring. TREE 29, 358–367.

6. Bayliss, J., Schaafsma, M., Balmford, A., Burgess, N.D., Green, J.M.H., Madoffe, S.S., Okayasu, S., Peh, K.S-H., Platts, P.J., Yu, D.W. (2014) The current and future value of nature-based tourism in the Eastern Arc Mountains of Tanzania. Ecosystem Services 8:75-83.

1. 利用 metabarcoding 探究是否易采样的土壤和腐殖质样本能用作常规生物多样性指标

Chenxue Yang, Xiaoyang Wang, Jeremy A. Miller, Marleen de Blécourt, Yinqiu Ji,Chunyan Yang, Rhett D. Harrison, Douglas W. Yu

将含分类信息的基因标记进行目标测序即为 metabarcoding 技术，该技术可以对真核生物多样性进行快速、低价、综合的评估，并可以重复实验，也适于第三方审核。Metabarcoding 能帮助科学家们扫清物种鉴定障碍，降低描述及鉴定物种的困难，提高我们检测及应对自然环境变化的能力。如今，采样成为了生物多样性评估的难点，为了减少采样时间，我们用中国南部及越南的节肢动物样本来探究是否土壤、腐殖质样本和地上样本一样都能提供相似的生态学信息。土壤或腐殖质样本在几分钟内就可以采集到，但是地上样本如马氏网样本或冠层喷雾采样则很费时间，而且同时我们的地上样本可能会遭到各种破坏及污染。我们本次实验结果表明土壤和腐殖质样本的分类组成与地上样本的组成虽然非常不一样，但是它们都能在物种丰度及 β 多样性上得到相似的生态学信息。实际上，腐殖质样本在检测栖息地差异上比马氏网及冠层喷雾样本更有效。因此，我们认为土壤及腐殖质样本的 metabarcoding 技术可以广泛用于陆地生态系统快速环境监测。

2. 高原鼠兔的专性捕食者——藏狐及其保护

RICHARD B. HARRIS, ZHOU JIAKE, JI YINQIU, ZHANG KAI, YANG CHUNYAN, DOUGLAS W. YU

藏狐（Vulpes ferrilata）普遍被认为是捕食善于挖洞的高原鼠兔（Ochotona curzoniae）的专家，但是这一说法是否正确还没有定论。我们估计了 62 个栖息样地藏狐的分布，反应出中国青海地区藏狐分布环境的连续性。 我们用点占据模型（site–occupancy modeling）来量化高原鼠兔的数量，并用点变量来预测藏狐的分布。我们也通过收集并测序藏狐的粪便来确定藏狐的分布。鼠兔的数量及其洞穴的数量是用于支持藏狐分布预测模型唯一的协变量。若某样点鼠兔数量越多，则藏狐存在的可能性越高; 鼠兔不在该样点出现的话，藏狐存在的可能性则接近于 0。近99% 的藏狐粪便含有鼠兔 DNA 序列，97% 的则主要含鼠兔序列，73% 的只含有鼠兔序列。因此，我们认为这一区域的藏狐不仅善于捕食高原鼠兔，而且还专食鼠兔。青藏高原地区的高原鼠兔数量仍然非常多，并不断增长，因此其是一种有害物种，政府也致力于消除其危害。藏狐目前没有灭绝的危险，但是如果鼠兔还继续扩大、繁殖的话，则藏狐有可能灭绝。

藏狐及高原鼠兔在中国西南地区的分布图

Ecology, Conservation, & Environment Center (ECEC)

Dr. Douglas W. Yu. Yu's research covers the conservation biology of tropical forests and the evolution and ecology of mutualisms. In the first area, we have developed new methods for estimating and projecting the impact of hunting on large vertebrates in Amazonian forests. 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.

E-mail: dougwyu@gmail.com

1. Using metabarcoding to ask if easily collected soil and leaf-littersamples can be used as a general biodiversity indicator

Chenxue Yang, Xiaoyang Wang, Jeremy A. Miller, Marleen de Blécourt, Yinqiu Ji,Chunyan Yang, Rhett D. Harrison, Douglas W. Yu

The targeted sequencing of taxonomically informative genetic markers, sometimes known as metabar-coding, allows eukaryote biodiversity to be measured rapidly, cheaply, comprehensively, repeatedly,and verifiably. Metabarcoding helps to remove the taxonomic impediment, which refers to the greatlogistical difficulties of describing and identifying species, and thus promises to improve our ability todetect and respond to changes in the natural environment. Now, sampling has become a rate-limitingstep in biodiversity measurement, and in an effort to reduce turnaround time, we use arthropod sam-ples from southern China and Vietnam to ask whether soil, leaf litter, and aboveground samples providesimilar ecological information. A soil or leaf-litter sample can be collected in minutes, whereas an above-ground sample, such as from Malaise traps or canopy fogging, can require days to set up and run, duringwhich time they are subject to theft, damage, and deliberate contamination. Here we show that whilethe taxonomic compositions of soil and leaf-litter samples are very different from aboveground sam-ples, both types of samples provide similar ecological information, in terms of ranking sites by speciesrichness and differentiating sites by beta diversity. In fact, leaf-litter samples appear to be as or more pow-erful than Malaise-trap and canopy-fogging samples at detecting habitat differences. We propose thatmetabarcoded leaf-litter and soil samples be widely tested as a candidate method for rapid environmentalmonitoring in terrestrial ecosystems.

2. Evidence that the Tibetan fox is an obligate predator of the plateau pika: conservation implications

RICHARD B. HARRIS, ZHOU JIAKE, JI YINQIU, ZHANG KAI, YANG CHUNYAN, DOUGLAS W. YU

The Tibetan fox (Vulpes ferrilata) is generally acknowledged to be a specialist forager on its preferred prey, the burrowing lagomorph plateau pika (Ochotona curzoniae), but whether true dependency characterizes the relationship remains unclear. We estimated the presence of Tibetan foxes in 62 habitat patches that reflected a continuum of environmental conditions within their known geographic distribution within Qinghai Province, China. We used site-occupancy modeling and quantified the abundance of plateau pikas as well as other site variables that could plausibly predict fox presence. We quantified fox presence by collecting and sequencing DNA from scats. The number of pikas and the number of their burrows were the only covariates supported in predictive models of Tibetan fox presence. The probability of site occupancy by foxes increased with pika abundance, and was close to 0 when pikas were absent even within habitat patches otherwise generally suitable. DNA-based diet analysis also allowed us to identify prey species consumed by Tibetan foxes. Approximately 99% of fox scats contained pika DNA sequences, 97% contained predominantly pika sequences, and 73% contained only pika sequences. We conclude that Tibetan foxes in this region are not merely foraging specialists of plateau pikas, but that they are obligate predators on pikas. Plateau pikas, while presently still abundant on the Qinghai-Tibetan Plateau, are considered a pest by government policy and are subject to extensive, governmentfunded poisoning programs. The Tibetan fox is currently at no substantial risk as a species, but this could change if pika poisoning increases in scope, intensity, or effectiveness.

员工简介（Lab Staff）
工作人员（Staff）

朱建国　副研究员
Dr. Zhu Jianguo
Associate Researcher
zhu@mail.kiz.ac.cn
季吟秋　助理研究员
Dr. Ji Yinqiu
Assistant Researcher
jiyinqiu@hotmail.com
杨春燕　助理研究员
Dr. Yang Chunyan
Assistant Researcher
yangyahan@mail.kiz.ac.cn
杨晨雪　助理研究员
Dr. Yang Chenxue
Assistant Researcher
xu_anwomingren_happy@126.com
王　林　研究实习员
Mr. Wang Lin,
Research Assistant
汪嘉欣　研究实习员
Ms.Wang Jiaxing,
Research Assistant
吴春莹　助理实验师
Ms. Wu Chunying,

研究生（Graduate Students）

张　凯　Zhang Kai
王晓阳　Wang Xiaoyang
于龙龙　Yu Longlong
Catharine Powell

实验与理论生态学

王瑞武，研究员，实验与理论生态学组 PI，中科院优秀青年生命科学家专项资助获得者。现任中国科学院昆明动物研究所实验与理论生态学学科组负责人，中国科学院昆明动物所青年科学小组组长。

重要成果（Highlights）
论著（Publications）

1. **He JZ**, **Wang RW***, Jensen, C.X. J., Li YT. 2014.Asymmetric interaction paired with a super-rational strategy might resolve the tragedy of the commons without requiring either recognition or negotiation. *Scientific Reports*. 5, 7715 (IF2013=5.08).

2. **Wang RW*** **Dunn DW**, Sun BF. 2014. Discriminative host sanction in fig-fig wasp mutualism. *Ecology*. 95(5):1384–1393 (IF2012=6.37).

3. **Wang B**, Geng XZ, Ma LB, Cook JM, **Wang RW***. 2014. A trophic cascade induced by predatory ants in a fig-fig wasp mutualism. *Journal of Animal Ecology*. 83, 1149–1157. (IF2012=5.17).

4. **He JZ**, **Wang RW*** Li YT*. 2014. Evolutionary Stability in the Asymmetric Volunteer's Dilemma. *PLOS one*. 9(8): e103931. (IF2012=4.24).

5. **Wang YQ**. Li YT. **Wang RW***. 2014. The optimal sex ratio in cooperatively breeding populations. *Chinese Science Bulletin*. 59(35):5047-5079(IF2011=1.40).

6. **Wang RW*** **Yang Y**. Wiggins NL. 2014. Asymmetric and/or diffusive co-evolution generate meta-populations in fig-fig wasp mutualisms. *Science China: life science*. 57(6): 596-602. (IF2012=2.02).)

1. 发现解决"公共地悲剧"或无需谈判或识别机制

研究基于"志愿者困境"博弈模型，结合合作系统中存在着"非对称相互关系（强、弱参与者或主导方和从属方等）"、参与者之间因信息的不完全的而实施"超理性策略（个体只根据自己的收益值决定如何选择自己的策略）"的实际，建立了一个具超理性的非对称"志愿者困境"博弈模型。模型发现：强、弱参与者的提供公共品（合作）行为强烈依赖于社群的大小且存在一临界值，即当社群大小大于该临界值时弱参与者的不合作频率将随其增大而增大，然而强参与者的不合作频率却随社群大小增大而增减小。也即是说，如果合作系统的非对称度不是太大而社群又较大时，强参与者比弱参与者具有更大的意愿提供公共品（合作）。而系统的非对称度对强、弱参与者的影响却与社群大小的影响相反，即非对称度的增大会使得强参与者的不合作频率上升而使得弱参与者的不合作频率下降。此外，在所有参与者都采取超理策略时，系统的公共品被提供的概率却随社群或系统非对称度的增大而增大。结果显示社会合作系统"公共地悲剧"的解决可以不依赖于复杂的谈判行为或认知、识别能力，在一个非对称性的系统，个体完全可以根据自身的利益而选择自己的最优策略，合作机制同样也可以建立。该结果 Scientific Reports 已发表。

2. 植物也会使用胡萝卜加大棒的策略

对于任何一个合作系统而言，总是存在投机的、不合作的行为或个体。这些投机行为或投机个体的在合作系统中的扩散将会导致合作系统的解体。然而，是什么机制能够阻止这种投机行为，从而避免合作系统的解体至今仍是一个争议很大的科学问题。由于合作双方存在信息、演化路径的不对称性，投机的个体或行为能够得以共存。为了进一步检验这种理论猜想的可信性，该课题组以著名的榕树－榕小蜂这一种间合作为模式系统，来验证上述理论猜想。与人类社会合作行为极为相似的是：榕树－榕小蜂这一合作系统中，合作的传粉小蜂中有些个体会采取投机性策略，而不给榕树传粉，甚至部分个体完全演化出投机行为的适应性特征 ————给植物传粉的花粉囊完全退化。试验发现榕树会通过两种方式惩罚这些投机性小蜂。当投机性小蜂数量比较少时，榕树通过果实脱落，将这些投机性小蜂的后代全部杀死。反之，榕树则通过抑制这些小蜂后代发育，降低其种群数量，但又维持其一定的数量，这极可能是由于这些投机性小蜂将为植物的花粉散布做出一定的贡献有关。把两种惩罚效应结合起来看，投机者越多，榕树对其惩罚也越大。该结果已于 Ecology 发表。

Experimental and Theoretical Ecology

Dr. Ruiwu Wang, Professor, Principal Investigator of Experimental and Theoretical Ecology, Kunming Institute of Zoology, Chinese Academy of Sciences.Research interests: (1) evolution and maintenance of cooperative systems, especially in insect-plant mutualisms; (2) mathematical and statistical modeling on the evolution of cooperation and species co-existence; (3) evolution of biodiversity under the influence of climate change; (4) sex ratio evolution under the selective pressure of environment. Study system involves: fig-fig wasps, plant- endofungi, and insect-fungi symbiosis.

Email: wangrw@mail.kiz.ac.cn

1. Asymmetric interaction paired with a super-rational strategy might resolve the tragedy of the commons without requiring recognition or negotiation

Avoiding the tragedy of the commons requires that one or more individuals in a group or partnership "volunteer", benefiting the group at a cost to themselves. Recognition and negotiation with social partners can maintain cooperation, but are often not possible. If recognition and negotiation are not always the mechanism by which cooperative partnerships avoid collective tragedies, what might explain the diverse social cooperation observed in nature? Assuming that individuals interact asymmetrically and that both "weak" and "strong" players employ a super-rational strategy, we find that tragedy of the commons can be avoided without requiring either recognition or negotiation. Whereas in the volunteer's dilemma game a rational "strong" player is less likely to volunteer to provide a common good in larger groups, we show that under a wide range of conditions a super-rational "strong" player is more likely to provide a common good. These results imply that the integration of super-rationality and asymmetric interaction might have the potential to resolve the tragedy of the commons. By illuminating the conditions under which players are likely to volunteer, we shed light on the patterns of volunteerism observed in variety of well-studied cooperative social systems, and explore how societies might avert social tragedies

2. Discriminative host sanction in a fig-fig wasp mutualism.

In some mutualisms, cooperation in symbionts is promoted by hosts sanctioning "cheats," who obtain benefits but fail to reciprocate. In fig–wasp mutualisms, agaonid wasps pollinate the trees (Ficus spp.), but are also exploitative by using some flowers as larval food. Ficus can sanction cheats that fail to pollinate by aborting some un-pollinated figs. However, in those un-pollinated figs retained by trees, cheats successfully reproduce. When this occurs, wasp broods are reduced, suggesting sanctions increase offspring mortality within un-pollinated figs. We investigated sanction mechanisms of abortion and larval mortality against wasp cheats in the monoecious Ficus racemosa by introducing into figs 1, 3, 5, 7, or 9 female wasps (foundresses) that were either all pollen-laden (P+) or all pollen-free (P−). The abortion rates of P− figs were highest (~60%) when single foundresses were present. Abortion declined with increased foundresses and ceased with seven or more wasps present, irrespective of pollination. In un-aborted figs, wasp fitness (mean offspring per foundress) declined as foundress number increased, especially in P− figs. Reduced broods in P− figs resulted from increased larval mortality of female offspring as foundress number increased, resulting in more male-biased sex ratios. Overall sanctions estimated from both abortion rates and reduced offspring production strengthened as the number of cheats increased.

员工简介（Lab Staff）
工作人员（Staff）

Derek William Dunn 副研究员
Associate Researcher
杨　燕　研究实习员
Yang Yan, Research Assistant
吴　佳　研究实习员
Wu Jia, Research Assistant

博士后（Postdoctoral Fellows）
贺军州 He Junzhou
黄　强 Huang Qiang
陈　春 Chen Chun
Riccardo Pansini

研究生（Graduate Students）
文晓岚 Wen Xiaolan 2012
李肇天 Li Zhaotian 2012
罗天逊 Luo Tianxun 2013
黄　俊 Huang Jun 2014

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，2014 年重点开展了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，揭示了多种家养动物在驯化过程中复杂生物功能（如视觉、和行为驯化、脂肪沉积和抗逆性等）发生变化的进化机制和藏獒、藏猪和藏鸡高原适应机制的异同，发现家青藏高原家犬在高原适应过程中与藏族人群的趋同进化。在 *Mol Biol Evol, Genome Biol Evol, Mol Evol* 等国际刊物发表 *SCI* 文章 *28* 篇。实验室在家养动物方面的研究成果受到了国际广泛关注，国际著名杂志 *Ann Rev Anim Biosci* 特邀张亚平院士撰写了关于家养动物驯化基因组学研究的综述论文："Domestication Genomics: Evidence from Animals"。2014 年度获国家自然科学奖二等奖一项。

重要成果（Highlights）

2014 年度 国家自然科学奖二等奖
"基因组多样性与亚洲人群的演化"

论著（Publications)

1. Li Y, **Wang GD**, Wang MS, Irwin DM, **Wu DD***, **Zhang YP***. Domestication of the Dog from the Wolf Was Promoted by Enhanced Excitatory Synaptic Plasticity: A Hypothesis. *Genome Biology and Evolution*, 2014, 6:3115-3121.
2. 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, 31:1200-1205.
3. Liu J, Wang XP, Cho S, Lim BK, **Irwin DM**, Ryder OA, **Zhang YP**, Yu L. Evolutionary and Functional Novelty of Pancreatic Ribonuclease: a Study of Musteloidea (order Carnivora). *Scientific Reports*, 2014, 4.
4. Luo J, **Gao Y**, Ma W, Bi XY, **Wang SY**, Wang J, Wang YQ, Chai J, Du R, **Wu SF**, Meyer A, Zan RG, Xiao H, **Murphy RW**, Zhang YP*. Tempo and mode of recurrent polyploidization in the Carassius auratus species complex (Cypriniformes, Cyprinidae). *Heredity*, 2014, 112:415-427.
5. **Shi NN**, Fan L, Yao YG, **Peng MS***, **Zhang YP***. Mitochondrial genomes of domestic animals need scrutiny. *Molecular Ecology*, 2014, 23:5393-5397.
6. **Wang GD**, Fan RX, Zhai WW, Liu F, Wang L, Zhong L, Wu H, Yang HC, **Wu SF**, **Zhu CL**, **Li Y**, **Gao Y**, Ge RL, Wu CI, **Zhang YP***. Genetic Convergence in the Adaptation of Dogs and Humans to the High-Altitude Environment of the Tibetan Plateau. *Genome Biology and Evolution*, 2014, 6:2122-2128.
7. **Wang GD**, **Xie HB**, **Peng MS**, Irwin D, and **Zhang YP***. Domestication Genomics: Evidence from Animals. *Annual Review of Animal Biosciences*, 2014, 2:65-84.
8. Zhou ZY, Li AM, Adeola AC, Liu YH, **Irwin DM**, **Xie HB***, **Zhang YP***. Genome-Wide Identification of Long Intergenic Noncoding RNA Genes and Their Potential Association with Domestication in Pigs. *Genome Biology and Evolution*, 2014, 6:1387-1392.

1. 家犬高原适应进化的遗传基础

作为长期生活在海拔超过 3500 米的青藏高原的土著犬种，藏獒表现出优秀的高原适应性。为研究其适应极端环境的遗传基础，本实验室通过家犬基因组 SNP 芯片扫描了藏獒、中国土狗以及灰狼群体，发现藏獒群体中有 12 个参与响应低氧、高寒代谢通路的基因表现出显著的选择信号。杂志当期和 Science daily 均做了专题报道。进一步对藏獒、藏土狗、中国平原土狗以及品种犬四个群体基因组重测序，结合高原犬与平原犬的血红蛋白指标，揭示藏犬与藏族人群相似的适应模式，提示相同的生存环境在不同物种趋同进化过程中有重要作用。随后在不同海拔高度的 17 个家犬群体中，对趋同进化的两个基因 EPAS1 和 HBB 进行检测，证实其突变型频率与海拔高度呈现显著的正相关。以上研究揭示了家犬的高原适应遗传机制，并为藏獒的品种资源保护提供了重要信息。

【Li Y et al. 2014 *Mol Biol Evol*, IF=14.308】
【Wang DG et al. 2013 *Genome Biol Evol*, IF=4.532】
【Fan RX et al. 2013 J *Genet Genomics*, IF=2.924】

图 1. 家犬高原适应的相关新闻报道

2. 家养动物数据库及数据质量

家养动物的驯化研究对于理解人类自身的文明发展有着至关重要的作用，本室在家养动物核基因组 SNP 数据库构建及线粒体数据质量控制方面取得了新的进展。第一项研究收录了家犬参考 SNP 数据集及 69 个家犬、8 个灰狼的核基因组重测序数据，构建了第一个家犬、灰狼核基因组 SNP 数据库（DoGSD:*DoGSD.big*.ac.cn）。该数据库的构建弥补了原有参考数据集包含 SNP 数量少、采样及测序覆盖度偏差大等问题，合理的组织、存储了日益增长的家犬、灰狼重测序数据，为家犬驯化研究提供了高质量的研究平台。

第二项研究对来自 8 种家养动物（家犬、家牛、牦牛、家猪、马、山羊、绵羊和家鸡）共计 1342 条 mtDNA 基因组序列进行了系统的评估，运用基于 mtDNA 单倍型类群树的系统发育分析策略，一共发现 194 条存在质量问题的序列。结果对今后家养动物 mtDNA 研究提出了警示与告诫，说明采纳严谨的质量控制措施是十分必要的。

【Bai B et al. 2014 *Nucleic Acids Res*, 5 Year-IF=7.417】
【Shi NN et al. 2014 *Mol Ecol*, 5 Year-IF=6.347】

Molecular Evolution and Genome Diversity

Dr. 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 machenism of the high-altitude adaptation in domesticated animals. We revealed the genetic machenism and convergence in the adaptation of dogs and humans to the high-altitude of the Tibetan Plateau. We constructed whole genome SNP database of dog, pig etc and raise the caution of data quality of domesticated animals. Within 2014, the above research progress were published 28 SCI papers, including **Mol Biol Evol** (1), **Nat Commun** (1), **Sci Rep** (1), **Mol Evol** (2), **Nucleic Acids Res**(1).

Email: zhangyp@mail.kiz.ac.cn

1. The genetic basis underlying the high-altitude adaptation of dogs

Being human cloest companions, dogs have dispersed into new environments as human civilization expanded since ancient times. Among these dogs was the Tibetan Mastiff (TM), which has adapted to the extremely high altitude of the Tibetan Plateau (typically over 3,500m).

To investigate the genetic basis underlying the adaptation, we scanned three populations from the TM, Chinese native dog and the gray wolf and identified 12 genes with significant selective signatures that associated with functions roles in high-altitude adaptation. Next, we re-sequenced four populations including the TM, Tibetan native dog, plain native dog and several breeds. We also revealed the genetic convergence in the adaptation of dogs and humans to the high-altitude of the Tibetan Plateau. A subsequent verification of two genes, EPAS1 and HBB, from 17 populations further revealed that the proportion of derived alleles positively correlated with the altitude, with a significant statistics.

These results will not only shed novel lightsinto the molecular mechanisms of high-altitude adaptation of domestic animals, but also help the resource conservation of the TM.
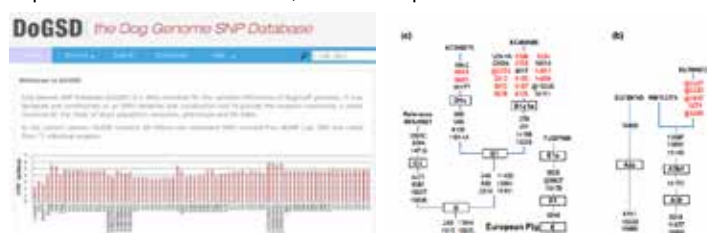

Figure 3. The data processing pipeline of DoDSD

2. Domesticated Animals' Database and Data Quality

Studies of wild animal domestication tremendously promote the understanding of human civilization development. We have obtained some achievements in the database construction and necessity of quality control of domesticated animal data. We constructed the first dog/wolf whole genome SNP database (DoGSD:DoGSD.big.ac.cn), which contains ~19M high-quality and high-density SNPs. DoGSD collected the current dog reference SNP dataset, whole genome resequencing data of 69 dogs, 8 wolves as data sources and performed SNP calling, etc. DoGSD not only compensated for the data scarcity, high sampling and sequencing coverage biases of the current reference SNP dataset, but also serves as a high-standard dog domestication research platform. Moreover, we evaluated 1342 mtDNA sequences of 8 domesticated animals (dog, cattle, yak, pig, horse, goat, sheep and chicken). By phylogenetic analysis of haplotype group trees, we find 194 of them are flaw sequences.

This result warns us that the strict data quality control strategy is necessary in the future studies of domesticated animal's mtDNA.

研究人员（Researchers）

Dr. Robert W. Murphy, Visiting Professor
Dr. David Irwin, Visiting Professor
高 云 副研究员
Dr. Yun Gao, Associate Professor
吴东东 副研究员
Dr. DongDong Wu, Associate Professor
彭旻晟 副研究员
Dr. MinSheng Peng, Associate Professor
王国栋 副研究员
Dr. GuoDong Wang, Associate Professor
谢海兵 助理研究员
Dr. HaiBing Xie, Assistant Professor
陈 睿 助理研究员
Dr. Rui Chen, Assistant Professor
何 静 助理研究员
Ms. Jing He, Assistant Professor
马云飞 研究实习员
Mr. YunFei Ma, Resarch Assistant
韩徐曼 研究实习员
Ms. XuMan Han Ma, Resarch Assistant

工程技术人员（Technicians）

吴世芳 Ms. ShiFang Wu
朱春玲 Ms. ChunLing Zhu
杨敏敏 Ms. MinMin Yang
邓家坤 Mr. JiaKun Deng

博士后（Postdoctoral Fellows）

李家堂 Dr. JiaTang Li，2009
周传江 Dr. ChuanJiang Zhou, 2011
李 艳 Dr. Yan Li, 2012
季林丹 Dr. LinDan Ji, 2012
倪 刚 Dr. Gang Ni, 2013

研究生（Graduate Students）

刘鹤群 Liu, HQ 刘 杰 Liu, J
杨贺川 Yang, HC 曹 雪 Cao, X
袁智勇 Yuan, ZY 杨 阳 Yang, Y
周中银 Zhou, ZY 邵 永 Shao, Y
王明山 Wang, MS 徐 丹 Xu, D
徐海波 Xu, HB 曾 琳 Zeng, L
叶凌群 Ye, LQ 姚 瑶 Yao, Y
尹婷婷 Yin, TT 汪 轩 Wang, X
黄翠萍 Huang, CP 史妮妮 Shi, NN
霍永霞 Huo, YX 王运梅 Wang, YM
吕梦蝶 Lu, MD 沈全宽 Shen, QK
芦方茹 Lu, FR 宋娇娇 Song, JJ
Nguyen Ngoc Sang   Adeola Adeniyi Charles
Otecko Newton Otieno

两栖爬行类多样性与进化

车静，博士，研究员。昆明动物研究所"青年科学家小组"人才项目获得者。动物学会两爬分会理事，中科院青年创新促进会理事。2011 年获"中国科学院卢嘉锡青年人才"奖。本课题组长期活跃在中国和东南亚这一重要区域，以两栖爬行动物为研究对象，系统开展隐存物种发掘，物种形成与分化，大尺度生物多样性格局的形成及演化规律，以及生物适应性方面的研究。目前已在 PNAS、ME、MPE 等国内外本领域重要杂志刊物发表论文 40 余篇。

重要成果（Highlights）
论著（Publications）

1. **Zhou WW**, **Zhang BL**, **Chen HM**, **Jin JQ**, **Yang JX**, Wang YY, Jiang K, Murphy RW, Zhang YP*, **Che J***. DNA barcodes and species distribution models evaluate threats of global climate changes to genetic diversity: a case study from Nanorana parkeri (Anura: Dicroglossidae). *Plos One*, 2014, 9(8) : e103899

2. Hou M, Wu YK, Yang KL, Zheng S, **Yuan ZY**, Li PP*. A missing geographic link in the distribution of the genus Echinotriton (Caudata: Salamandridae) with description of a new species from southern China. *Zootaxa*, 2014, 3895(1):89–102

3. **Yuan ZY**, Zhao HP, Jiang K, Hou M, He LZ, Murphy RW, **Che J***. Phylogenetic Relationships of the Genus Paramesotriton (Caudata: Salamandridae) with the Description of a New Species from Qixiling Nature Reserve, Jiangxi, Southeastern China and a Key to the species. *Asian Herpetological Research*, 2014, 5(2): 67–79

4. Ngyyen SN, **Jin JQ**, **Zhou WW**, Vo BD, Nguyen LT, **Che J***, Murphy RW*, Zhang YP*. DNA barcoding of Vietnamese bent-toed geckos (Squamata: Gekkonidae: Cyrtodactylus) and the description of a new species. *Zootaxa*, 2014, 3784(1): 48–66

5. Chen X, Jiang K, Guo P, Huang S, Rao DQ, Ding L, Takeuchi H, **Che J**, Zhang YP, Myers EA, Buebeink FT*. Assessing species boundaries and the phylogenetic position of the rare Szechwan ratsnake, Euprepiophis perlaceus (Serpentes: Colubridae), using coalescent-based methods. Molecular *Phylogenetics and Evolution*, 2014, 70: 130–136

6. Theodore P, **Yan F**, Wang YY, Todd P. A survey for the Chinese giant salamander (Andrias davidianus; Blanchard, 1871) in the Qinghai Province. *Amphibian and reptile conservation*, 2014, 8(1) : 1–6

1. DNA 条形码技术应用于物种多样性保护

人类活动造成的全球气候变化严重威胁着生物多样性。DNA 条形码技术可以快速确定物种遗传多样性分布格局。同时结合使用物种分布模型可以用来评估气候变化对物种，及其遗传多样性的潜在影响。高山蛙（*Nanorana parkeri*）是青藏高原南部分布较为广泛的本地特有物种。以高山蛙为例，我们结合 DNA 条形码技术和物种分布模型预测了全球气候变化对两栖类的影响。DNA 条形码标记鉴定出高山蛙的两个支系（Fig.1）。支系 W 起源于单一避难点而支系 E 起源于三个避难点。所有的避难点都位于河谷中，并对现在的种内遗传多样性有巨大的影响。物种分布模型显示在全球气候变化背景下，高山蛙避难点中的两个将不再适合高山蛙的生存，因此气候变化对高山蛙，尤其是其遗传多样性影响巨大。
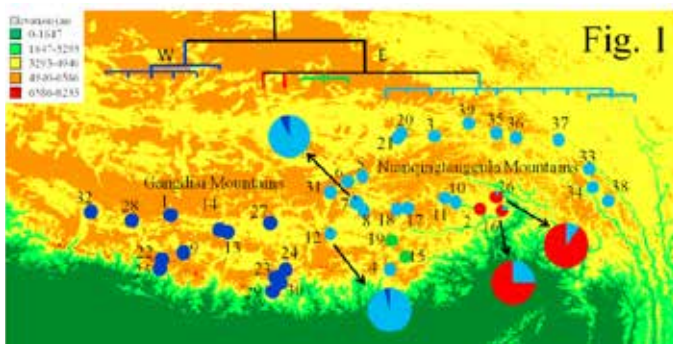
2. DNA 条形码技术揭示隐存多样性

以越南地区分布的裸趾虎属为例，研究显示 DNA 条形码技术作为物种鉴定的有效工具，有利于对隐存多样性的认识，并对生物多样性保护具有积极的作用。

我们使用 DNA 条形码（COI）对越南地区已有的 21 个物种进行了遗传分化的研究。系统发育树恢复了所有已知物种，并揭示出未被描述的新支系（如图）。已有物种之间的遗传距离为 4.3% 到 28.7%，平均为 $21.0 \pm 4.2\%$。我们的研究揭示现有的数据包括 5 个潜在新种，2 个来自越南，2 个来自老挝，还有 1 个来自中国。本文中，基于形态和分子数据，我们描述了其中分布于越南的 1 个新种 *Cyrtodactylus puhuensis*。
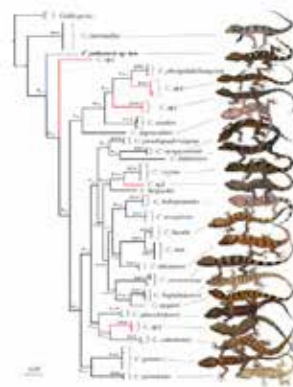
Herpetological Diversity and Evolution

Dr. Jing Che, Principal Investigator. Using amphibian and reptile as model, we often explore the biodiversity issue and evolutionary questions within a phylogenetic framework mostly concentrating on species inhabiting three regions: China's Qinghai-Tibetan Plateau and Hengduan Mountain Range, Southeast Asia, and the mainland of East China and nearby islands.

Email: chej@mail.kiz.ac.cn

1. DNA Barcodes and Species Distribution Models Evaluate Threats of Global Climate Changes to Genetic Diversity

Anthropogenic global climate changes are one of the greatest threats to biodiversity. Distribution modeling can predict the effects of climate changes and potentially their effects on genetic diversity. DNA barcoding quickly identifies patterns of genetic diversity. As a case study, we use DNA barcodes and distribution models to predict threats under climate changes in the frog Nanorana parkeri, which is endemic to the Qinghai-Tibetan Plateau. Barcoding identifies major lineages W and E. Lineage W has a single origin in a refugium and Lineage E derives from three refugia. All refugia locate in river valleys and each greatly contributes to the current level of intraspecific genetic diversity. Species distribution models suggest that global climate changes will greatly influence N. parkeri, especially in the level of genetic diversity, because two former refugia will fail to provide suitable habitat (Fig. 2). Our pipeline provides a novel application of DNA barcoding and has important implications for the conservation of biodiversity in southern areas of the Qinghai-Tibetan Plateau.
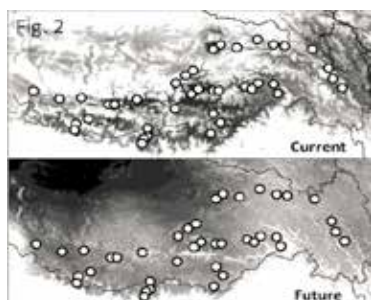
A new species Cyrtodactylus puhuensis

2. DNA barcoding of Vietnamese bent-toed geckos (Squamata: Gekkonidae: Cyrtodactylus) and the description of a new species

Species of bent-toed gecko (*Cyrtodactylus*) in Vietnam have been described at a rate of nearly four species per year since 2007 mostly based on morphological data. A tool that guides species delimitation will accelerate the rate of documentation, and at a time when the recognition of species greatly benefits conservation. We use DNA barcoding using COI to re-examine the levels of genetic divergence and taxonomic status of 21 described species of Vietnamese bent-toed geckos. Tree-based analyses resolve all sampled species and identify potential undescribed taxa. Kimura 2-parameter genetic distances between the described species average 21.0±4.2% and range from 4.3% to 28.7%. Further, our analyses

discover two potentially new species from Vietnam, two from Laos and one from China. Herein we describe the new species *Cyrtodactylus puhuensis* sp. nov. from Vietnam on the basis of both genetics and morphology.

员工简介（Lab Staff）
工作人员（Staff）

周炜帏　博士　副研究员
Weiwei Zhou, Associate Professor

孙艳波　博士　副研究员
Yanbo Sun, Associate Professor

颜　芳　博士　助理研究员
Fang Yan, Assistant Professor

陈宏满　硕士　助理工程师
Hongman Chen, Assistant Engineer

金洁琼　学士　实验师
Jieqiong Jin, Technician

研究生（Graduate Students）
袁智勇　Zhiyong Yuan 2010

高　伟　Wei Gao 2013

付婷婷　Tingting Fu 2014

联合培养
杨军校　Junxiao Yang 2010

邵　勇　Yong Shao 2011

张宝林　Baolin Zhang 2012

陈进民　Jinmin Chen 2012

邹大虎　Dahu Zou 2013

进化基因组学与基因起源

王文，博士、研究员，中德马普进化基因组学青年科学家小组组长。本年度作为首席科学家之一获得中科院先导 B 类项目和重大突破择优支持项目资助。继 2013 年解析山羊基因组揭示羊绒生长的基因基础之后，2014 年携手国内外机构"破译"了绵羊基因组。

实验室主页：http：//159.226.149.45/wangw/wangwen2010.htm

重要成果（Highlights）
论著（Publications）

1. **Jiang Y** , et al., **Wang W***. The sheep genome illuminates biology of the rumen and lipid metabolism. *Science*, 2014, 344 (6188):1168-1173; 10.1126/science.1252806.

2. Lyu J , et al., **WangW***. A genomic perspective on the important genetic mechanisms of upland adaptation of rice. *BMC Plant Biology*, 2014, JUN 11, 14 10.1186/1471-2229-14-160.

3. Su RR , et al., **Wang W***. Identification of a novel fumarase C from Streptomyces lividans TK54 as a good candidate for malate production. *Molecular Biology Reports*, 2014,41 (1):497-504; 10.1007/s11033-013-2885-8.

4. Tosser-Klopp G , et al., **Wang W**, **Zhang WG***. Design and Characterization of a 52K SNP Chip for Goats. *Plos One*, 2014, 9 (1):10.1371/journal.pone.0086227.

5. Du X , et al., **Wang W***, Zhao* S. An update of the goat genome assembly using dense radiation hybrid maps allows detailed analysis of evolutionary rearrangements in Bovidae. *BMC Genomics*, 2014, 15 10.1186/1471-2164-15-625.

6. Wu J , **Xiang H*** , et al. Adaptive Evolution of the STRA6 Genes in Mammalian. *Plos One*, 2014, 9 (9):10.1371/journal.pone.0108388.

7. **Lei Chen**, et al., **Wen Wang*** and Guojie Zhang*. Advances in genome editing technology and its promising application in evolutionary and ecological studies. *GigaScience*, 2014, 3:24.

1. 获得中国科学院战略性先导科技专项 B 类"动物复杂性状的进化解析与调控"（XDB13000000）资助，王文研究员作为首席科学家之一，承担了项目一课题五：脊椎动物大脑进化关键物种复杂基因组的解析（XDB13010500）

动物复杂性状是动物长期适应进化的结果，是动物多样性存在的主要基础，其调控的失衡是人类重大慢性病发生的内在原因，对其研究对家养动物经济性状的改良和动物特殊功能的仿生有重要意义。本专项通过大尺度、跨物种的进化比较，系统整合不同动物物种遗传因子－发育网络进化－表型适应性三个层面的全面数据，有望突破静态描述和表象关联的局限，解析动物复杂性状的成因。我们把这种研究动物复杂性状的新思路称之为 eGPS（evolutionary Genotype－Phenotype Systems biology）。本专项以系统集成的、多学科交叉的 eGPS 范式的建立，开辟动物复杂性状研究的新思路，引领复杂生命现象的研究，使我国在新一轮生物科学和技术革命中能占据一个重要的制高点。

2. 绵羊基因组研究取得重大进展

山羊和绵羊是反刍动物的典型代表动物，而瘤胃是反刍动物独有的消化器官。科学家们首次观测到两种在反刍动物中发生特异蛋白结构改变，且仅在瘤胃中特异高表达的结构蛋白。一种是首次报道和命名的毛透明蛋白类似蛋白，另外一种是小脯氨酸丰富蛋白 II 家族。它们发挥瘤胃表面基板的作用，通过转谷氨酰胺酶介导交联瘤胃表达的角蛋白，从而构成瘤胃壁粘膜层的坚韧的角质化表面。与消化吸收密切联系的是代谢。研究发现除了肝脏，反刍动物的皮肤也是重要的脂类代谢器官。 成果发表在美国 Science 杂志上（http://www.sciencemag.org/content/344/6188/1168.full）。

3. STRA6 基因在脊椎动物进化过程中的适应性改变

光照周期对生物的最直接影响就是生物节律，而生物节律可调控一系列生理和代谢途径。生物钟由复杂的转录和翻译反馈通路组成，通过激活特异的转录因子，调节 10% 左右的细胞转录本的表达量来实现。接收光照最主要的器官就是眼睛，视黄酸刺激因子 6(Stimulated by retinoic acid 6,STRA6) 是视黄酸结合受体蛋白，负责将视黄酸转运到眼睛，最终形成视觉。通过研究 STRA6 在脊椎动物中的进化情况我们发现，在物种分化后 STRA6 基因的进化率随即发生了变化。STRA6 蛋白的细胞外卷曲部分氨基酸发生了加速进化。支位点模型结果显示除了啮齿类动物外，其他的哺乳动物中都存在加速进化，这表明栖息环境与物种间的相互作用驱动了 STRA6 基因的适应性改变。在物种分化后，由于 STRA6 功能发生变化导致一些氨基酸残基发生变化。这些结果暗示脊椎动物的不同分支与栖息环境相适应，STRA6 基因在物种分化过程中发生了适应性进化。该研究结果发表在 PLoS ONE（9(9)：e108388．doi:10.1371）上。

Origin and Evolution of New Genes

Dr. Wen Wang, Professor, Head of CAS–Max Planck Junior Research Group, KIZ, CAS. This year we mainly focused on the sheep genome which illuminated biology of the rumen and lipid metabolism. Dr. Wen Wang was one of chief scientists, and got the funding from Proposal for Strategic Priority Research Programs (B) of Chinese Academy of Sciences (CAS) .

E-mail: wwang@mail.kiz.ac.cn

1. Proposal for Strategic Priority Research Programs (B) of Chinese Academy of Sciences (CAS) "Evolutionary analysis and functional regulation of animal complex traits"

Complex traits critically contribute to the beautiful and endless forms of animals. Understanding the genetic basis of complex traits of animals has been an extraordinary challenge in modern biology, but such understanding would shed light on the mechanisms underpinning normal body functions and phenotypic variation as well as non-communicable.Given that all animal traits were formed and selected by nature during long-term evolution, we propose an evolutionary genotype-phenotype systems biology (eGPS) approach to decipher animal complex traits. This approach takes advantage of powerful -omics technologies, such as genomics, proteomics and transcriptomics, and integrates multiple research disciplines including genetics, developmental biology, evolutionary biology, computational biology as well as state-of-the-art transgenic animal models. By collecting cross-species genomic, transcriptomic, and proteomic data, we will identify genetic and developmental regulation networks related to the three traits. The results will also allow us to address whether morphological (brain size) and physiological (metabolism and altitude adaptation) traits are controlled by different genetic mechanisms, which has been a major controversy in evolutionary developmental biology. We will conduct genetic manipulation using mouse, monkey, and tree shrew, which is a small mammal closely related to primate, to test the functional significance of the identified key genes and networks.

2. The sheep genome illuminates biology of the rumen and lipid metabolism

Sheep (Ovis aries) are a major source of meat, milk, and fiber in the form of wool and represent a distinct class of animals that have a specialized digestive organ, the rumen, that carries out the initial digestion of plant material.We have developed and analyzed a high-quality reference sheep genome and transcriptomes from 40 different tissues. We identified highly expressed genes encoding keratin cross-linking proteins associated with rumen evolution. We also identified genes involved in lipid metabolism that had been amplified and/or had altered tissue expression patterns. This may be in response to changes in the barrier lipids of the skin, an interaction between lipid metabolism and wool synthesis, and an increased role of volatile fatty acids in ruminants compared with nonruminant animals.

3. Adaptive Evolution of the STRA6 Genes in Mammalian

Stimulated by retinoic acid 6 (STRA6) is the receptor for retinol binding protein and is relevant for the transport of retinol to specific sites such as the eye. we have investigated different aspects of vertebrate STRA6 evolution and used molecular evolutionary analyses to detect evidence of vertebrate adaptation to the lightless habitat. Free-ratio model revealed significant rate shifts immediately after the species divergence. The amino acid sites detected to be under positive selection are within the extracellular loops of STRA6 protein. Branch-site model A test revealed that STRA6 has undergone positive selection in the different phyla of mammalian except for the branch of rodent. The results suggest that interactions between different light environments and host may be driving adaptive change in STRA6 by competition between species. In support of this, we found that altered functional constraints may take place at some amino acid residues after speciation. We suggest that STRA6 has undergone adaptive evolution in different branch of vertebrate relation to habitat environment.

工作人员 (Staff)

相 辉 博士 副研究员
Dr. Hui Xiang, Associate Professor
xiangh@mail.kiz.ac.cn
李学燕 博士 助理研究员
Dr. Xueyan Li, Assistant Professor
lixy@mail.kiz.ac.cn
时晓菲 博士 助理研究员
Dr. Xiaofei Shi, Assistant Professor
shixiaofei1@163.com
赵若苹 本科 实验师
Ms. Ruoping Zhao, Assistant Professor
zhaorp@mail.kiz.ac.cn
刘贵春 硕士 研究实习员
Ms. Guichun Liu, Assistant Professor
liuguichun@mail.kiz.ac.cn

博士后 (Postdoctoral Fellows)

张文广 Wenguang Zhang, 2010
刘 斌 Bin Liu, 2012
苏 蕊 Rui Su, 2013

研究生 (Graduate Students)

徐 讯 Xun Xu, 2007
张业胜 Yesheng Zhang, 2010
刘 晖 Hui Liu, 2010
张 田 Tian Zhang, 2011
陈 垒 Lei Chen, 2011
沈文菁 Wenjing Sheng, 2011
刘力源 Liyuan LIU, 2012
苟志恒 Zhiheng Gou, 2011
王 筱 Xiao Wang, 2011
任彦栋 Yandong Ren, 2013
赵颖俊 Yingjun Zhao, 2013
张 如 Ru Zhang, 2013
曾 严 Yan Zeng, 2014
生承晔 Chengye Sheng, 2014
陈海涛 Haitao Chen, 2014

比较基因组学

宿兵，博士、研究员、博士生导师，中国科学院知识创新工程学科带头人，中科院"百人计划"引进人才、国家基金委杰出青年基金获得者、"新世纪百千万人才工程"国家级人选，从事灵长类大脑演化的遗传学机制以及现代人类起源、迁徙与适应性进化的遗传学研究。已在《*Science*》、《*Nature*》、《*Nat Rev Genet*》、《*PNAS*》、《*Am J Hum Genet*》、《*Genome Res*》、《*Mol Biol Evol*》、《*Hum Mol Genet*》等国际核心刊物上发表研究论文 120 余篇。

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

重要成果（Highlights）
论著（Selected Publications）

1. **Li M, Luo XJ**, ….., **Su B.*** 2014. Allelic differences between Europeans and Chinese for CREB1 SNPs and their implications in gene expression regulation, hippocampal structure and function, and bipolar disorder susceptibility. *Mol Psychiatry*. 19:452-461.

2. **Shi L, Lin Q**, **Su B***. 2014. Human-specific hypomethylation of CENPJ, a key brain size regulator. *Mol Biol Evol* 31:594-604.

3. **Zhang Q***, **Su B***. 2014. Evolutionary origin and human-specific expansion of a cancer/testis antigen gene family. *Mol Biol Evol*. 31:2365-2375.

4. **Li M**, Ohi K, Chen C, He Q, **Liu JW**, Chen C, **Luo XJ**, Dong Q, Hashimoto R, **Su B***. 2014. Failure of replicating the association between hippocampal volume and 3 single-nucleotide polymorphisms identified from the European genome-wide association study in Asian populations. Neurobiol Aging 35:2883 e2881-2882.

5. **Yang L**, **Zhang R**, Li M, Wu X, Wang J, Huang L, Shi X, Li Q, **Su B***. 2014. A functional MiR-124 binding-site polymorphism in IQGAP1 affects human cognitive performance. **PLoS One** 9:e107065.

6. **Zhang X**#, Kampuansai J#, **Qi X**#, Yan S, **Yang Z**, Serey B, Sovannary T, Bunnath L, Aun HS, Samnom H, Kutanan W, **Luo X**, **Liao S**, Kangwanpong D, Jin L, **Shi H***, **Su B***. 2014. An updated phylogeny of the human Y-chromosome lineage O2a-M95 with novel SNPs. **PLoS One** 9:e101020.

7. **Qi X**, Cui C, Ouzhuluobu, Wu T, **Su B***. 2014. Prehistoric Colonization and Demographic History of Modern Humans on the Tibetan Plateau. In. *eLS*: John Wiley & Sons, Ltd. p. 1-10.

1. 揭示灵长类大脑容量调控基因 CENPJ 的低甲基化机制

巨大的大脑容量和复杂的认知能力是人类区别于我们的近亲－非人灵长类的重要特征之一。然而，在人类起源中发生这一显著变化的遗传学机制尚不清楚，特别是表观遗传调控在人类大脑进化中的作用我们知之甚少。 最近，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。他们通过亚硫酸氢盐测序比较了 4 个灵长类代表物种（人类、黑猩猩、长臂猿和猕猴）大脑前额叶中这 4 个基因的甲基化模式的差异。研究结果发现，CENPJ 基因在人类大脑中是低甲基化的，而在其他所有非人灵长类大脑中的甲基化水平是人类的 2–3 倍；理论上，低甲基化往往对应高的基因转录活性。如预期的一样，他们在人的大脑中检测到比非人灵长类高得多的 CENPJ 的表达。因此，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，并且是可遗传的。由于前人的研究已经表明 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。研究结果发表在国际知名分子进化学术刊物 *Molecular Biology and Evolution 31:594-604(2014)*。

2. 灵长类物种中 CT 抗原家族 CTAGE 的快速进化模式与功能效应

在人类基因组中存在一类由生殖系基因编码的肿瘤／睾丸抗原（简称 CT 抗原）。在人类的很多肿瘤中 CT 抗原会异常表达。宿兵实验室和美国哈佛大学张渠博士（宿兵实验室前实习学生）合作，系统研究了 CT 抗原的一个家族 CTAGE(cutaneous T cell lymphoma–associated antigen) 在灵长类中的分子进化模式及其功能效应。通过对包括人类在内的灵长类代表物种的比较，他们发现 CTAGE 在灵长类的进化中发生了快速的扩张，在新旧大陆灵长类分开之前的祖先中发生了一次反转座（retroposition）事件，而后在旧大陆灵长类特别是在人类的基因组中产生了多个单外显子基因拷贝。同祖先多外显子基因相比，CTAGE 家族中的单外显子拷贝基因受到明显的达尔文正选择的作用，有可能对人类早期进化中适应性表型的产生有贡献。该项研究成果发表于国际知名分子进化刊物 *Molecular Biology and Evolution 31: 2365-2375(2014)*

3. 揭示梭形神经元等人和灵长类大脑认知相关的特定细胞的基因表达模式与生物学功能

梭形神经元是一类胞体很长可以远距离传递信息的神经元 ，它不同于其它神经元的是在人脑中这类神经元的数量和细胞体积都显著大于其他非人灵长类。 目前发现这类神经元只存在于具有高级认知能力的大型群居哺乳动物大脑的三个区域，前扣带回、前岛叶皮层、背外侧前额叶。梭形神经元在智力的发育、对环境改变的适应能力和认知失调中扮演着重要作用。目前由于技术的限制该类细胞的转录组一直没有得到解析。为了能够解析不同神经元的转录组，找出更多认知相关基因，了解不同类型神经元在认知过程中所起的作用，我们将激光捕获显微切割和单细胞测序技术有效结合，得到了高质量的 cDNA 并且经过二代测序得到了 3 个人脑 B24 区梭形神经元、大锥体神经元、小锥体神经元和 B32 区的大锥体神经元的四类神经元的转录组数据。通过初步的数据分析,我们发现不同类型的神经元其表达谱存在一定的差异。这些差异基因的真实性和潜在功能还有待于进一步验证。研究结果正在进行深入的生物学功能验证。

4. 人类高级认知相关基因 IQGAP1 的遗传进化机制研究

IQGAP1 是广泛表达的细胞骨架蛋白，它参与很多细胞行为，例如细胞粘附、细胞迁移及调节细胞骨架。该基因的表达与否直接影响到神经元上神经突触棘的数量，IQGAP1 敲除小鼠表现出学习记忆的缺失。我们推测位于该基因 3'UTR 区的一个单核苷酸突变可能会影响到与之相互作用的小 RNA 对它的调控能力，进而影响该基因的表达，甚至可能有与之相关的认知表型。为了证明这个推测，我们首先做了体内和体外表达差异实验，证明了该多态位点可以影响到 IQGAP1 的表达，然后我们利用行为学实验证明了该位点与亚洲男性的触觉记忆相关，最后我们对该位点做了群体进化分析发现该位点所在区域可能存在近期正选择。我们的研究结果表明 IQGAP1 基因的表达量可以影响到小鼠的学习记忆能力，此外另一个研究小组发现在该基因的 3'UTR 区存在一个单核苷酸突变可能受到正选择，该突变位点的存在可能影响到 miR–124 对 IQGAP1 的表达调控。我们推测该位点不仅可以改变 IQGAP1 的表达，也可能会在人群中造成学习记忆的表型差异。研究成果发表在 *PLOS One,9:e107065(2014)*。

Comparative Genomics

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

E-mail: sub@mail.kiz.ac.cn

1. Human-Specific Hypomethylation of CENPJ, a Key Brain Size Regulator

Both the enlarged brain and concurrent highly developed cognitive skills are often seen as distinctive characteristics that set humans apart from other primates. Despite this obvious differentiation, the genetic mechanisms that underlie such human-specific traits are not clearly understood. In particular, whether epigenetic regulations may play a key role in human brain evolution remain elusive. In this study, we used bisulfite sequencing to compare the methylation patterns of four known genes that regulate brain size (ASPM, CDK5RAP2, CENPJ, and MCPH1) in the prefrontal cortex among several primate species spanning the major lineages of primates (i.e., humans, great apes, lesser apes, and Old World monkeys). The results showed a human-specific hypomethylation in the 5'-UTR of CENPJ in the brain, where methylation levels among humans are only about one-third of those found among nonhuman primates. Similar methylation patterns were also detected in liver, kidney, and heart tissues, although the between-species differences were much less pronounced than those in the brain. Further in vitro methylation assays indicated that the methylation status of the CENPJ promoter could influence its expression. We also detected a large difference in CENPJ expression in the human and nonhuman primate brains of both adult individuals and throughout the major stages of fetal brain development. The hypomethyla- tion and comparatively high expression of CENPJ in the central nervous system of humans suggest that a human- specific—and likely heritable—epigenetic modification likely occurred during human evolution, potentially leading to a much larger neural progenitor pool during human brain development, which may have eventually contributed to the dramatically enlarged brain and highly developed cognitive abilities associated with humans. *Shi L, Lin Q, Su B. Molecular Biology and Evolution 31:594-604 (2014)*.

2. Evolutionary Origin and Human-Specific Expansion of a Cancer/Testis Antigen Gene Family

Cancer/testis (CT) antigens are encoded by germline genes and are aberrantly expressed in a number of human cancers. Interestingly, CT antigens are frequently involved in gene families that are highly expressed in germ cells. Here, we presented an evolutionary analysis of the CTAGE (cutaneous T-cell-lymphoma-associated antigen) gene family to delineate its molecular history and functional significance during primate evolution. Comparisons among human, chimpanzee, gorilla, orangutan, macaque, marmoset, and other mammals show a rapid and primate specific expansion of CTAGE family, which starts with an ancestral retroposition in the haplorhini ancestor. Subsequent DNA-based duplications lead to the prosperity of single-exon CTAGE copies in catarrhines, especially in humans. Positive selection was identified on the single-exon copies in comparison with functional constraint on the multiexon copies. Further sequence analysis suggests that the newly derived CTAGE genes may obtain regulatory elements from long terminal repeats. Our result indicates the dynamic evolution of primate genomes, and the recent expansion of this CT antigen family in humans may confer advantageous phenotypic traits during early human evolution. *Zhang Q, Su B. Molecular Biology Evolution 31:2365-2375 (2014)*.

3. A Functional MiR-124 Binding-Site Polymorphism in IQGAP1 Affects Human Cognitive Performance

As a product of the unique evolution of the human brain, human cognitive performance is largely a collection of heritable traits. Rather surprisingly, to date there have been no reported cases to highlight genes that underwent adaptive evolution in humans and which carry polymorphisms that have a marked effect on cognitive performance. IQ motif containing GTPase activating protein 1 (IQGAP1), a scaffold protein, affects learning and memory in a dose-dependent manner. Its expression is regulated by miR-124 through the binding sites in the 39UTR, where a SNP (rs1042538) exists in the core-binding motif. Here we showed that this SNP can influence the miR-target interaction both in vitro and in vivo. Individuals carrying the derived T alleles have higher IQGAP1 expression in the brain as compared to the ancestral A allele carriers. We observed a significant and male-specific association between rs1042538 and tactile performances in two independent cohorts. Males with the derived allele displayed higher tactual performances as compared to those with the ancestral allele. Furthermore, we found a highly diverged allele-frequency distribution of rs1042538 among world human populations, likely caused by natural selection and/or recent population expansion. These results suggest that current human populations still carry sequence variations that affect cognitive performances and that these genetic variants may likely have been subject to comparatively recent natural selection. *Yang L, Zhang R, Li M, Wu X, Wang J, …, Bing Su. PLoS ONE 9(9): e107065 (2014).*

员工简介（Lab Staff）
工作人员（Staff）

祁学斌 博士 副研究员
Dr. Xuebin Qi, Associate Professor
qixuebin@mail.kiz.ac.cn
张 慧 硕士 助理研究员
Ms. Hui Zhang, Research Associate
zhanghui@mail.kiz.ac.cn
郭 彦 本科 助理研究员
Ms. Yan Guo, Research Associate
Guoyan@mail.kiz.ac.cn
彭 忆 博士，助理研究员
Dr. Yi Peng, PhD. Research Assistant
石 磊 博士，助理研究员
Dr. Lei Shi, PhD. Research Assistant
张晓明 博士，助理研究员
Dr. Xiaoming Zhang, PhD. Research Assistant
杨立新 博士，助理研究员
Dr. Lixin Yang, PhD. Research Assistant

研究生（Graduate Students）

2005-present
罗雄剑　Xiongjian Luo, 2005
王金凯　Jingkai Wang, 2005
杨若林　Ruolin Yang, 2005
黄 琳　Ling Huang, 2005
韩 冷　Leng Han, 2005
牛傲蕾　Aolei Niu, 2006
孙正华　Zhenghua Sun, 2006
彭 忆　Yi Peng, 2007
石 磊　Lei Shi, 2007
张雁峰　Yanfeng Zhang, 2007
李 明　Ming Li, 2008
杨立新　Lixin Yang, 2008
彭应梅　Yingmei Peng, 2008
杨召辉　Zhaohui Yang, 2009
曹向宇　Xiangyu Cao, 2009
向 坤　Kun Xiang, 2010
王 毅　Yi Wang, 2010
张 煦　Xu Zhang, 2010
林 强　Qiang Lin, 2011
刘杰伟　Jiewei Liu, 2012
杨晏冬　Yandong Yang, 2012
廖世玉　Shiyu Liao, 2012
罗 鑫　Xin Luo, 2013
何一博　Yibo He, 2013
和耀喜　Yaoxi He, 2014
李 敏　Min Li, 2014
张栋秦　Dongqin Zhang, 2014
袁佳妙　Jiamiao Yuan, 2015
周亚楠　Yanan Zhou, 2015

生物信息学与系统生物学

黄京飞，研究员，博士生导师，中国科学院昆明动物研究所副所长，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 50 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. Gao, Yue-Dong, **Yuqi Zhao**, and **Huang JF***. Metabolic Modeling of Common Escherichia coli Strains in Human Gut Microbiome. *BioMed research international*. 2014.

2. Zhao, Y., Ji, S., Wang, J., **Huang JF***., & Zheng, P. mRNA-Seq and microRNA-Seq whole-transcriptome analyses of rhesus monkey embryonic stem cell neural differentiation revealed the potential regulators of rosette neural stem cells. *DNA Research*. 2014, dsu019.

3. Wang, R. R., Yang, Q. H., Luo, R. H., Peng, Y. M., **Dai, S. X**., Zhang, X. J., **Huang JF** & Zheng, Y. T. Azvudine, A Novel Nucleoside Reverse Transcriptase Inhibitor Showed Good Drug Combination Features and Better Inhibition on Drug-Resistant Strains than Lamivudine In Vitro. *PloS one*. 2014, 9(8): e105617.

4. Cheng D Q, Li Y, Huang J F*. Molecular Evolution of the Primate Alpha/Theta Defensin Multigene Family. PloS one. 2014, 9(5): e974252.

5. **Chen S**, **Gao S**, **Cheng D**, **Huang JF***. The characterization and comparison of amyloidogenic segments and non-amyloidogenic segments shed light on amyloid formation. *Biochemical and biophysical research communications*. 2014, 447(2): 255-262.

6. Li GH, Huang JF*. Inferring therapeutic targets from heterogeneous data: HKDC1 is a novel potential therapeutic target for cancer. *Bioinformatics*. 2014 Mar 15;30(6):748-52.

1. 抗肿瘤分子靶标的发掘研究

肿瘤是目前世界人口死亡的第一原因。除了传统的放化疗等方法外，靶向治疗是肿瘤研究的热点和发展趋势。因此找到合适的肿瘤靶标是靶向治疗的基础和关键。由于癌症相关数据的剧增，使得我们能够充分利用计算生物学方法来推断治疗靶点。我们实验室研究开发了一个新的系统生物学模型来发掘肿瘤靶标。基于该模型，该研究组预测了 50 个针对肺癌的靶标。结果表明在预测的前 20 个靶标中，有 19 个是已知的肿瘤靶标，提示该数学模型具有较高的准确率。而这些靶标中，只有一个己糖激酶家族成员（HKDC1）目前尚未应用到临床。通过整合与 HKDC1 相关的各类生物学、药学等数据提示，HKDC1 可能是一个新型的针对肺癌的肿瘤靶标。上述结果已在顶级计算生物学杂志《Bioinformatics》上发表。

2. 灵长类 α/θ 防御素基因家族的分子进化研究

灵长类 α/θ 防御素多基因家族编码一类内源性阳离子型和两亲型的多功能肽，这些肽具有广谱的抗细菌、真菌和病毒活性。虽然已有报道 α/θ 防御素（DEFA/DEFT）基因经历了快速进化和伴随着频繁基因复制的生－灭演化过程。但是灵长类 DEFA/DEFT 基因家族的系统发育关系、相近物种之间具有相似抗菌谱的遗传基础、环状 θ 防御素在旧大陆猴的出现以及在人类中的功能丢失等问题还没有澄清。因此，我们对灵长类和树 的 DEFA/ DEFT 基因家族进行了详细的系统发育分析，序列和结构分析，选择压力和比较基因组学分析。研究结果表明在 treeshrew，Prosimian 和 simian 中，所有的 DEFA/DEFT 基因可分为两个主要分支，分别是肠组织特异和髓组织特异的防御素。这些基因进一步可以分为序列结构功能以及选择压力迥异的六个功能基因簇，这反映了相近物种抗菌谱的相似性。物种特异的基因复制和假基因预示着物种抗菌谱的不断变化以此来应对多变的外界环境。最后，我们提出 less－is－hitchhiking 的假说来解释 DEFTP 假基因的扩张以及功能性基因 DEFT 的丢失。上述结果已在《PLoS ONE》上发表。

3. 淀粉样片段和非淀粉样片段的特征比较揭示淀粉样斑的形成

蛋白质或多肽的淀粉样聚集涉及到一些神经退行性疾病发生发展，并且是疾病治疗过程的一个重要难题。这类蛋白常在其短区域淀粉样蛋白片段中发生聚合，理解短区域淀粉样蛋白片段聚合和淀粉样病变的机制对于治疗神经退行性疾病十分重要。我们研究了淀粉样蛋白片段特定的理化性能，并将其与非淀粉样蛋白片段进行比较。首先，与非淀粉样片段相比，淀粉样片段具较低平均静电荷值、静电电位、溶剂表面可及区域、温度因子等特点。其次，他们有丰富的疏水残基并倾向于形成氢键。因此，淀粉样蛋白片段与非淀粉样蛋白片段的理化性质有明显的差异。第三，我们的分子动力学模拟研究支持了淀粉样蛋白片段的柔韧性平均值低于非淀粉样蛋白片段的假说。上述结果已在《Biochemical and Biophysical Research Communications》上发表。

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 50 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.

Email: huangjf@mail.kiz.ac.cn

1. Inferring therapeutic targets from heterogeneous data: HKDC1 is a novel potential therapeutic target for cancer

The discovery of therapeutic targets is important for cancer treatment. Although dozens of targets have been used in cancer therapies, cancer remains a serious disease with a high mortality rate. Owing to the expansion of cancer-related data, we now have the opportunity to infer therapeutic targets using computational biology methods. Here, we describe a method, termed anticancer activity enrichment analysis, used to determine genes that could be used as therapeutic targets. The results show that these genes have high likelihoods of being developed into clinical targets (>60%). Combined with gene expression data, we predicted 50 candidate targets for lung cancer, of which 19 of the top 20 genes are targeted by approved drugs or drugs used in clinical trials. A hexokinase family member, hexokinase domain-containing protein 1 (HKDC1), is the only one of the top 20 genes that has not been targeted by either an approved drug or one being used in clinical trials. Further investigations indicate that HKDC1 is a novel potential therapeutic target for lung cancer. We developed a protocol to identify potential therapeutic targets from heterogeneous data. We suggest that HKDC1 is a novel potential therapeutic target for lung cancer.

2. Molecular Evolution of the Primate α-/θ-Defensin Multigene Family

The primate α-/θ-defensin multigene family encodes versatile endogenous cationic and amphipathic peptides that have broad-spectrum antibacterial, antifungal and antiviral activity. in this study, the DEFA/DEFT gene repertoires from primate and treeshrew were collected, followed by detailed phylogenetic, sequence and structure, selection pressure and comparative genomics analyses. The simian enteric and myeloid α-defensins are classified into six functional gene clusters with diverged sequences, variable structures, altered functional constraints and different selection pressures, which likely reflect the antimicrobial spectra among closely related species. Species-specific duplication or pseudogenization within each simian cluster implies that the antimicrobial spectrum is ever-shifting, most likely challenged by the ever-changing pathogen environment. The DEFT evolved from the myeloid DEFA8. Lastly, a less-is-hitchhiking hypothesis was proposed as a possible explanation for the expansion of pseudogene DEFTP and the loss of functional DEFT, where the gain or loss of the hitchhiker is determined by its adjacent driver gene during the birth-and-death evolutionary process.

3. The characterization and comparison of amyloidogenic segments and non-amyloidogenic segments shed light on amyloid formation

Amyloid fibrillar aggregates of proteins or peptides are involved in the etiology of several neurodegenerative diseases and represent a major problem in healthcare. Short regions in the protein trigger this aggregation. It is important to understand the basis of such short regions aggregation and amyloidosis for therapeutic intervention. In this study, we describe specific physico-chemical properties of amyloidogenic segments and compare them with non-amyloidogenic segments. First, amyloidogenic segments are characterized by lower values for average net charge, electrostatic potential, solvent accessible surface area and B-factor when compared to the non-amyloidogenic segments of the same proteins. Second, they are enriched in hydrophobic residues and have a tendency to form hydrogen bonds. Thus, amyloidogenic segments have distinct physico-chemical properties that are different from those of non-amyloidogenic segments. Third, and quite unexpectedly, our dynamic simulation studies support the hypothesis that amyloidogenic segments have lower average flexibility than non-amyloidogenic segments. Furthermore, the presence of amyloidogenic segments in disordered proteins does not contradict the observation that amyloidogenic segments are less flexible.

员工简介（Lab Staff）
工作人员（Staff）

李功华 博士 助理研究员
Dr Gong-Hua Li, Assistant Professor
ligonghua@mail.kiz.ac.cn
代绍兴 博士 助理研究员
Dr Shao-Xing Dai, Assistant Professor
daishaoxing@mail.kiz.ac.cn
廖爱文 秘书
Ms.Ai-Wen Liao, Secretary
awliao@mail.kiz.ac.cn
刘衡 技术员
Ms. Heng Liu, Technician
liuh@mail.kiz.ac.cn

研究生（Graduate Students）
郑俊娟 Jun-juan zheng
韩菲菲 Fei-Fei Han
郭义成 Yi-Cheng Guo
刘家倩 Jia-qian Liu
张 琳 Lin zhang
廉 婷 Ting Lian
王 倩 Qian Wang
李文兴 Wen-xing Li
安三琪 San-qi An

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。

重要成果(Highlights)

1. Zhang D, Qi JF, Yu J, Huang JL, Sun T, Li SP, **Wen JF**, Hettenhausen C, Wu JS, Wang L, Zhuang HF, Wu JQ* and Sun GL*. 2014. Root parasitic plant Orobanche aegyptiaca and shoot parasitic plant Cuscuta australis obtained Brassicaceae-specific strictosidine synthase-like genes by horizontal gene transfer. *BMC Plant Biology* 14:19

2. Feng XM, Yang CL, Zheng WY, **Wen JF***. Structural and evolutionary characteristics of pyruvate phosphate dikinase in Giardia lamblia and other amitochondrate protozoa. Chinese *Medical Journal 2014; 127 (23)*

3. 陈兵，文建凡* 2014. 血吸虫的寄生适应性研究及其应用价值 中国血吸虫病防治杂志 26(1)：84-89

1. 解开了衣藻利用乙酸作为唯一碳源进行非光合生长之谜

莱茵衣藻作为研究光合作用的首选模型，具有以乙酸为唯一碳源进行非光合生长的特性，这种非光合生长是如何实现的？一般推测乙酸进入细胞后活化为 acetyl-CoA，部分供给 TCA 循环产生能量，部分经过乙醛酸循环同化为 C4 酸作为生物合成反应前体，然后通过糖异生途径合成碳水化合物；但是，衣藻在黑暗中乙酸同化的研究仍然缺乏，乙酸同化的一些细节并不清楚，例如，acetyl-CoA 不能自由的通过线粒体膜，那么它是如何进入线粒体参与 TCA 循环的呢？更重要的是，衣藻中缺少一般生物中参与糖异生途径的胞质型 FBPase，不能确保糖异生途径的完整性。现有的研究并没有解决衣藻非光合生长是如何实现的这一问题。为了破解衣藻非光合生长之谜，我们对衣藻在黑暗中的乙酸同化机制进行了全面系统的研究，发现一个新型的 FBPase 打通了衣藻在黑暗中的糖异生途径，而 acetyl-CoA 从胞质到线粒体的转运是通过肉碱穿梭的方式完成的。基于此，我们重构了衣藻在黑暗中乙酸同化的主要碳代谢途径，破解了衣藻非光合生长之谜：乙酸进入细胞后，在胞质中形成 acetyl-CoA，活化的 acetyl-CoA 部分通过肉碱穿梭的方式进入线粒体参与 TCA 循环产生能量，部分则通过乙醛酸循环将其中的 C 固定为琥珀酸，琥珀酸可进入线粒体，经部分 TCA 循环生成苹果酸，苹果酸进入胞质，形成草酰乙酸，然后通过糖异生途径生成己糖（磷酸），此产物可以合成淀粉，也可以成为其他生物合成反应碳骨架。

2. 果糖 1-6 二磷酸醛缩酶基因从真核生物到原核生物转移的发现与意义。

果糖 1-6 二磷酸醛缩酶（FBA）是参与卡尔文循环、糖酵解／糖异生途径以及戊糖磷酸途径等核心碳代谢的中的重要酶。我们的调查发现：真核生物几乎全都具有 I 型 FBA，而极大部分原核生物具有 II 型 FBA；但也有不少原核生物除具有 II 型 FBA 外，还具有是 I 型 FBA。FBA 在整个生物界中的这一分布现象是如何形成的呢？我们的分子系统发生分析显示：原核生物 I 型 FBA 基因是由真核生物水平基因转移获得，且具有多个独立的起源。一枝起源于硅藻胞质型定位的 FBA；一枝从红藻和褐藻的共同祖先中获得了质体型定位的 FBA；一枝来源于红藻质体型定位的 FBA；而另有一枝则可能来源于硅藻和金藻共同祖先中质体型定位的 FBA，可以看出，原核生物中 I 型 FBA 的获得至少发生了 4 次独立的水平基因转移。FBA 在原核生物中形成了 I 型 II 型并存，甚至仅有 I 型存在的特殊分布模式。进一步调查发现，原核生物的卡尔文循环、糖酵解／糖异生途径中参与反应的仍然以其本身的 II 型 FBA 为主，而获得的 I 型 FBA 可能从事了一种"第二职业"，即执行了"Moonlighting protein"功能。

Evolutionary Genomics of Eukaryotic Cells

Dr. 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.

Email: wenjf@mail.kiz.ac.cn

1. The riddle of non-photosynthetic growth of Chlamydomonas reinhardtii on acetate

Chlamydomonas reinhardtii is able to utilize the organic carbon in the form of acetate and remain viable in the dark, photosynthetic genes can be disrupted in C. reinhardtii to the isolation of numerous non-photosynthetic mutants, making it become the premier organism for studying the molecular genetics of photosynthesis. In order to explain of the mechanism of non-photosynthetically growth of C. reinhardtii, we here report an in-depth investigation on the related metabolic pathways of acetate assimilation in the dark. In the research, we discovered a novel FBPase and have reconstructed the central carbon metabolism of chlamydomonas reinhardtii on acetate under dark conditions and then reveal the mystery of non-photosynthetically growth of C. reinhardtii on acetate as sole carbon and energy source: Once enter the cells in the cytosol, acetate is firstly activated to acetyl-CoA. The acetyl-CoA is partially transport into mitochondria by cartinine shuttle for energy production via the TCA cycle, and partially used for biosynthesis via the glyoxylate cycle and gluconeogenesis.

2. Fructose-bisphosphate aldolase I in prokaryotes and the eukaryote-to-prokaryote transfer of this gene is not a rare event

As a core carbon metabolic enzyme, fructose-bisphosphate aldolase (FBA) has two non-homologous but functionally equivalent types, and typically eukaryotes possess FBA I and prokaryotes FBA II. Here, a comprehensive investigation of phylogenetic distribution of FBA in diverse Prokaryotes was made, then the origin of the Prokaryotes FBA I and the transfer mechanisms were explored by phylogenetic. These FBA I were acquired independently of each other from at least four eukaryotic original sources, through much more than four gene transfer events. Thus, eukaryote-to-prokaryote horizontal gene transfer (HGT) seems to be not a rare phenomenon in the transfer of FBA I, and through it three types of combinations of FBA I and II enzymes formed in Prokaryotes. The FBA I probably have performed the "Moonlighting protein" function.

员工简介（Lab Staff）
工作人员（Staff）

陈 兵 助理研究员
Bing Chen
Research Assistant
chenbing@mail.kiz.ac.cn

邵静茹 助理实验师
Jingru Shao
Experimentalist
shaojr@mail.kiz.ac.cn

研究生（Graduate Students）

叶青青 Qingqing Ye 2010
李毓劲 Yujing Li 2011
谢钢琴 Gangqin Xie 2011
王文敏 Wenmin Wang 2011
姚友旭 Youxu Yao 2012
黄海波 Haibo Huang 2013
薛 敏 Min Xue 2013
吕章夏 Zhangxia Lv 2014

进化与功能基因组学

施 鹏，博士，研究员。中科院昆明进化与遗传国家重点实验室 PI，进化和功能基因组学科组负责人。2008 年入选中科院"百人计划"，长期从事进化基因组学和功能基因组学研究。本研究室的研究兴趣集中在以下三个方面：

1）动物如何通过感觉系统的整合来适应它们所处的环境

2）如何通过自然选择的理论来探讨基因型与表型的关系

3）哺乳动物高原适应性进化的机制机理

重要成果（Highlights）
论著（Publications）

1. Liu Z, Qi FY, Zhou X, Ren HQ, **Shi P**#. Parallel sites implicate functional convergence of the hearing gene prestin among echolocating mammals. Mol. Biol. Evol. (2014). **(5-Year IF=11.221)**

2. Liu Z, Wang W, Zhang TZ, Li GH, He K, Huang JF, Jiang XL, Murphy RW and **Shi P**#. Repeated functional convergent effects of NaV1.7 on acid insensitivity in hibernating mammals. Proc. R. Soc. B-Biol. Sci. (2014) 281(1776): 20132950. **(5-Year IF=5.832)**

3. Zhang Z, Geng J, Tang X, Fan H, Xu J, Wen X, Ma ZS# and **Shi P**# Spatial heterogeneity and co-occurrence patterns of human mucosal-associated intestinal microbiota. ISME J. (2014) 8(4): 881-893. **(5-Year IF=8.927)**

1. 听力基因 prestin 的平行进化位点导致回声定位哺乳动物的功能趋同进化

回声定位是某些特定哺乳动物利用声波进行方向定位和捕食的感觉系统，尤其是在视觉受限的环境中。令人惊奇的是，对于蝙蝠和鲸类动物，二者的生存环境完全不一样，竟独立进化出了回声定位这一特异性状。基于二者在回声定位这一表型上表现出的趋同进化，现在很多研究通过氨基酸序列的平行进化位点于不同回声定位哺乳动物中鉴定出了很多与回声定位相关的基因，而听力基因 prestin 更为突出。虽然在先前的研究中分析了 prestin 在哺乳动物听力中的进化机制，但是相关的平行进化位点在哺乳动物回声定位的进化历程中所起的功能作用却不清楚。通过功能分析，我们发现 prestin 的一个重要的参数 $1/\alpha$ 值在回声定位哺乳动物中显著增高，而使得这个功能参数的趋同的分子机制正是 7 号（N7T）氨基酸趋同位点。另外，对于参数 V1/2 则在齿鲸的宽吻海豚（Tursiops truncatus）和恒频蝙蝠的三叶蹄蝠（Aselliscus stoliczkanus）中偏向于去极化的方向，I384T 氨基酸平行进化位点的存在是使得齿鲸和恒频蝙蝠在 V1/2 这一功能参数的趋同的重要分子基础。Prestin 的两个参数 $1/\alpha$ 和 V1/2 与哺乳动物的高频听力密切相关，这进一步揭示 prestin 功能在回声定位哺乳动物中的的趋同改变可能对哺乳动物的回声听力起着关键性作用。在此次研究中，首次通过回声定位哺乳动物相关基因的功能模式揭示了蛋白序列水平的适应性平行进化，为弄清楚回声定位哺乳动物潜在的分子机制提供了新的思路。（*Molecular biology and evolution, 2014*）
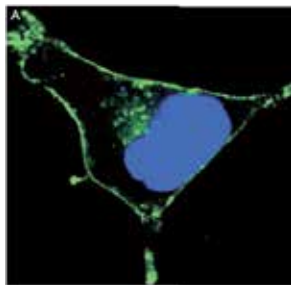
Confocal images showing the plasma membrane location of the prestin-GFP constructs.

2. 冬眠动物中酸不敏感基因的多次功能趋同效应

冬眠动物需要对酸刺激不敏感从而适应高二氧化碳的生活环境。然而，动物对酸耐受的分子机制依然不为人们所知。裸鼹鼠和一些冬眠动物有着相似的生存环境和生理特征。研究指出，在裸鼹鼠中，酸刺激不敏感性与钠离子通道蛋白 Nav1.7 的一个功能域直接相关。这一结论给我们研究其他动物动物酸耐受机制提供了很好的机会。我们对包括 22 种冬眠动物的 71 种哺乳动物 Nav1.7 功能趋同的情况进行了检测。结果显示在氨基酸水平上，冬眠哺乳动物至少独立出现了 6 次趋同演化。进一步的进化分析发现：这种功能上的趋同是既有功能域上氨基酸的平行进化导致，也有氨基酸的趋异进化导致。我们这一研究不仅发现了与酸耐受直接相关的功能分子，也开创了一个研究哺乳动物酸耐受分子机制的新方法。（*Proceedings. Biological sciences / The Royal Society, 2014*）

Evolutionary and Functional Genomics

Dr. Peng Shi, Principal Investigator. There are three major topics in our lab. (1) Exploring the genetic mechanisms of animals adaptation to the extreme environments using large-scale data. (2) Functionally resolving the molecular mechanisms of adaptive evolution for animals using functional platforms. (3) Evolution of plateau adaptation. My lab investigates these questions using a combination of empirical and computational approaches to analyze the large-scale data.

Email: ship@mail.kiz.ac.cn

1. Parallel Sites Implicate Functional Convergence of the Hearing Gene Prestin among Echolocating Mammals

Echolocation is a sensory system whereby certain mammals navigate and forage using sound waves, usually in environments where visibility is limited. Curiously, echolocation has evolved independently in bats and whales, which occupy entirely different environments. Based on this phenotypic convergence, recent studies identified several echolocation related genes with parallel sites at the protein sequence level among different echolocating mammals, and among these, prestin seems the most promising. Although previous studies analyzed the evolutionary mechanism of prestin, the functional roles of the parallel sites in the evolution of mammalian echolocation are not clear. By functional assays, we show that a key parameter of prestin function, $1/\alpha$, is increased in all echolocating mammals and that the N7T parallel substitution accounted for this functional convergence. Moreover, another parameter, V1/2, was shifted toward the depolarization direction in a toothed whale, the bottlenose dolphin (Tursiops truncatus) and a constant-frequency (CF) bat, the Stoliczka's trident bat (Aselliscus stoliczkanus). The parallel site of I384T between toothed whales and CF bats was responsible for this functional convergence. Furthermore, the two parameters ($1/\alpha$ and V1/2) were correlated with mammalian high-frequency hearing, suggesting that the convergent changes of the prestin function in echolocating mammals may play important roles in mammalian echolocation. To our knowledge, these findings present the functional patterns of echolocation-related genes in echolocating mammals for the first time and rigorously demonstrate adaptive parallel evolution at the protein sequence level, paving the way to insights into the molecular mechanism underlying mammalian echolocation. (*Molecular biology and evolution, 2014*)

2. Repeated functional convergent effects of NaV1.7 on acid insensitivity in hibernating mammals

Hibernating mammals need to be insensitive to acid in order to cope with conditions of high CO_2; however, the molecular basis of acid tolerance remains largely unknown. The African naked and hibernating mammals share similar environments and physiological features. In the naked mole-rat, acid insensitivity has been shown to be conferred by the functional motif of the sodiumion channelNaV1.7. There is now an opportunity to evaluate acid insensitivity in other taxa. In this study, we tested for functional convergence of NaV1.7 in 71 species of mammals, including 22 species that hibernate. Our analyses revealed a functional convergence of amino acid sequences, which occurred at least six times independently in mammals that hibernate. Evolutionary analyses determined that the convergence results from both parallel and divergent evolution of residues in the functional motif. Our findings not only identify the functional molecules responsible for acid insensitivity in hibernating mammals, but also open new avenues to elucidate the molecular underpinnings of acid insensitivity in mammals. (*Proceedings. Biological sciences / The Royal Society, 2014*)

工作人员（Staff）

刘　振 博士 副研究员
Dr. Zhen Liu, Associate Professor
张志刚 博士 副研究员
Dr. Zhigang Zhang, Associate Professor
杨　晖 博士 助理研究员
Dr. Hui Yang, Assistant Professor
郝军军 博士 助理研究员
Dr. Junjun Hao, Assistant Professor
胡玲玲 博士 助理研究员
Dr. Lingling Hu, Assistant Professor
余　蕊 实验员
Technician
任海清 实验员
Technicians
周　鑫 实验员
Technicians
祁飞燕 研究实习员
Resarch Assistant
李媛媛 研究实习员
Resarch Assistant

研究生（Graduate Students）

王　维 Wei Wang, 2009
许东明 Dongming Xu, 2010
罗　杰 Jie Luo, 2011
郑智中 Zhizhong Zheng, 2012
李　芸 Yun Li, 2013
郭雨龙 Yulong Guo, 2013
张　涛 Tao Zhang, 2014
张　佳 Jia Zhang, 2014

人类进化与疾病基因组学

孔庆鹏，中国科学院昆明动物研究所，研究员、博士生导师。目前已在 *Am J Hum Genet*、 *Mol Biol Evol*、*PNAS* 及 *Hum Mol Genet* 等国际重要 SCI 期刊上接受发表论文 60 余篇，论文被各类 SCI 刊物累计引用 2400 余次，H 指数 24。主持有国家基金委面上及优秀青年基金项目，并于 2013 年入选科技部科技创新中青年领军人才计划。研究组目前的主要研究方向：东亚人群源流历史与人类重大疾病及重要性状的遗传学基础。

重要成果（Highlights）

（一）论著（Publications）

1. **He YH**, Zhang YX, **Yang LQ**, Liao XP, Cai WW*, **Kong QP***. Assessment of the health status of centenarians in the South of China: A cross-sectional study. *J Am Geriatr Soc*, 2014a, 62:1402-1404.

2. **He YH**, Chen XQ, Yan DJ, **Xiao FH**, **Liu YW**, Lin R, Liao XP, Cai WW*, **Kong QP***. Thyroid function decreases with age and may contribute to longevity in Chinese centenarians' families. *J Am Geriatr Soc*, 2014b (In press)

3. **He YH#**, **Lu X#**, **Wu H**, Cai WW*, **Yang LQ**, Sun HP, **Kong QP***. MtDNA content contributes to healthy aging in Chinese: a study from nonagenarians and centenarians. *Neurobiol Aging*, 2014, 35:1779.e1-1779.e14.

4. **He YH#**, **Lu X#**, **Yang LQ**, Xu LY, **Kong QP***. Association of the insulin-like growth factor binding protein 3 polymorphism with longevity in Chinese nonagenarians and centenarians. *Aging-US*, 2014, 6:N11.

5. **He YH#**, **Lu X#**, Bi MX, **Yang LQ**, Xu LY, **Kong QP***. The reduction of vascular disease risk mutations contributes to longevity in Chinese. *Meta Gene*, 2014, 2:761-768.

6. **Xiao FH#**, **He YH#**, **Li QG**, **Wu H**, Luo LH, **Kong QP***. A genome-wide scan reveals important roles of DNA methylation in human longevity by regulating age-related disease genes. *PLoS One*, 2014 (In press).

7. **Tian JY**, Wang HW, **Li YC**, Zhang W, Yao YG, van Straten J., Richards M., and **Kong QP***. A genetic contribution from the Far East into Ashkenazi Jews via the ancient Silk Road. *Sci Rep*, 2015a, 5:8377.

8. **Li YC**, Wang HW, **Tian JY**, Liu LN, **Yang LQ**, Zhu CL, Wu SF, Kong QP*, and Zhang YP*. Ancient inland human dispersals from Myanmar into interior East Asia since the Late Pleistocene. *Sci Rep*, 2015b, 5:9473.

（二）奖励（Awards）

国家自然科学二等奖（"基因组多样性与亚洲人群的演化"；张亚平，**孔庆鹏**，吴东东，彭旻晟，孙昌；2014）

1. 基于百岁老人研究挖掘长寿的遗传保护因子

研究发现，长寿老人，特别是百岁老人，往往能逃脱常见衰老相关疾病的困扰，提示长寿老人可能拥有某些规避衰老相关疾病的保护因子。围绕该假设，我们从流行病学、长寿家系、线粒体基因、核基因及表观遗传等视角开展了系统研究并取得阶段性成果：1）流行病学调查揭示：535 位长寿老人的肝脏、肾脏功能及营养代谢指标都处于正常生理学范围；无人患恶性肿瘤且 2 型糖尿病、高血脂和高血压的患病率要显著低于普通老年人群（*JAGS* 2014a）；2）长寿家系研究显示：甲状腺功能随年龄增加而下降，且长寿老人的甲状腺功能可以遗传给后代（*JAGS* 2014b）；3）线粒体基因研究发现：线粒体 DNA（mtDNA）含量和年龄呈负相关关系，但长寿老人的 mtDNA 含量反而要显著高于老年组，提示维持相对稳定的 mtDNA 含量为长寿所必须（*Neurobiol Aging* 2014）；4）核基因研究表明：长寿老人不但拥有一些长寿相关变异位点（*Aging-US* 2014），也缺少某些疾病风险突变位点（*Meta Gene* 2014）；5）表观遗传研究：百岁老人和对照人群的差异甲基化位点主要富集在一些老年性疾病如心血管疾病、2 型糖尿病等相关易感基因上（*PLoS One* 2014）。

2. 犹太人群存在古丝绸之路的远东母系遗传贡献

现今犹太人在保留中东祖先遗传印记的同时，也受到了欧洲等周围群体的遗传影响。丝绸之路留下了大量犹太人与中国人密切交流的考古历史证据，但犹太人是否受到过远东地区的遗传贡献还未可知。为解决这个问题，我们对欧亚范围内 55,595 条线粒体 DNA 数据进行分析，发现源自中国南部的单倍型类群 M33c 的子类群 M33c2 广泛分布于来自多个国家的德系犹太人群，进一步分析提示 M33c2 很可能于 640−1400 年前引入犹太人群，与古丝绸之路的时间范围和历史考古记录相吻合。研究工作表明，古代犹太人与中国人通过古丝绸之路的历史交流不仅限于经济文化方面，而且也体现在遗传方面（*Sci Rep* 2015a）。

3. 早期人类沿内陆迁徙路线从缅甸进入东亚内陆

由于东南亚和东亚之间有大量的河流相连接，早期人类在到达东南亚后，除了沿海岸线迁徙以外，也可能沿不同河流直接进入东亚内陆。在本研究中，我们采集了来自缅甸的 14 个群体的 845 个个体的 mtDNA 高变区数据，并结合分析了已报道的缅甸及其周边群体的数据。我们发现缅甸人群中存在大量的古老的 mtDNA 基部世系，其中一部分局限分布于缅甸和中国西南，表明这两个地区存在一定的遗传联系。进一步的系统发育分析表明，这些遗传联系一部分是近期基因流的结果，而另一部分则很可能是缘于从缅甸到中国西南的古老迁徙事件（25−10 kya）。我们的结果表明，除了沿海路线以外，早期人类还经内陆迁徙路线从东南亚直接进入东亚内陆（*Sci Rep* 2015b）。

Molecular Anthropology

Dr. Qing-Peng Kong, Professor, Kunming Institute of Zoology, Chinese Academy of Sciences. My laboratory is mainly interested in the following fields: (1) mtDNA phylogenomics in eastern Asia and reconstructing the prehistory of Asian populations by using multiple genetic markers; (2) understanding the genetic basis of longevity and major diseases such as cancer.

E-mail: kongqp@mail.kiz.ac.cn

1. Digging protective factors contributing to longevity by studying Chinese centenarians

Aging is an irreversible biological process. However, people realize an extreme aging phenotype, that is, longevity. Epidemiological surveys show that: the healthy long-lived elderly, especially the centenarians, can usually escape from common age-related diseases (such as cardiovascular disease, cancer, Alzheimer's disease), suggesting that they may carry some protective factors which may fight effectively against age-related diseases. Based on this hypothesis, we carried out the following studies focusing on epidemiology, longevity family, mitochondrial DNA, nuclear gene and epigenetic:(1) Epidemiological study: all indicators of liver function, renal function and nutritional metabolism were within normal physiological range, no one suffered from malignant tumor in 535 centenarians. The prevalence of type 2 diabetes, hyperlipidemia and hypertension was significantly lower than general elderly population (*JAGS* 2014a); (2) Longevity family: the thyroid function decreased with increasing age, until the centenarians. Hypothyroidism may cause decreased metabolism, which is similar to energy restriction which can prolong the lifespan. Interestingly, the thyroid function of centenarians can be passed on to their offspring (*JAGS* 2014b); (3) Mitochondrial DNA: a negative correlation between the mtDNA content and age were revealed, namely the older, the lower the content of mitochondria, however there is an exception for centenarians with higher mtDNA content than general old people (*Neurobiol Aging* 2014); (4) Single nucleotide polymorphism: longevity subjects not only carried some longevity mutations (e.g. insulin signaling) (*Aging-US* 2014), but also lack some disease risk loci (e.g. vascular disease) (*Meta Gene* 2014); (5) Epigenetics: centenarians carried some specific methylation sites which are mainly enriched in age-related disease (such as cardiovascular disease, type 2 diabetes mellitus) genes (*PLoS One* 2014).

2. A genetic contribution from the Far East into Ashkenazi Jews via the ancient Silk Road

Contemporary Jews retain a genetic imprint from their Near Eastern ancestry, but obtained substantial genetic components from their neighboring populations. Whether they received any genetic contribution from the Far East remains unknown, but frequent communication with the Chinese has been observed since the Silk Road period. To address this issue, mtDNA variation from 55,595 Eurasians are analyzed. Eastern Eurasian haplogroup M33c2 in eastern Ashkenazi Jews supports an East Asian genetic contribution. Further evidence indicates that this connection can be attributed to a gene flow event that occurred 640-1400 years ago, which fits well with the Silk Road scenario, historical records and archaeological discoveries. This observed genetic contribution demonstrates that the historical exchange between Ashkenazim and the Far East was not confined to the cultural sphere but also extended to an exchange of genes (*Sci Rep* 2015a).

3. Ancient inland human dispersals from Myanmar into interior East Asia

Given the existence of plenty of river valleys connecting Southeast and East Asia, it is possible that some inland route(s) might have been adopted by the initial settlers to migrate into the interior of East Asia. Here we analyzed mtDNA HVS variants of 845 newly collected individuals from 14 Myanmar populations and 5,907 published individuals from Myanmar and its surroundings. Enrichment of basal lineages with ancient ages in Myanmar suggests that Myanmar was likely one of the differentiation centers of early modern humans. Intriguingly, some haplogroups were merely shared by populations from Myanmar and southwestern China, hinting certain genetic connection between both regions. Further analyses revealed that such connection was attributed to either recent gene flow or ancient dispersals from Myanmar to southwestern China during ~25-10 kya, suggesting that, besides the coastal route, the early modern humans also adopted an inland dispersal route to populate the interior of East Asia (*Sci Rep* 2015b).

员工简介（Lab Staff）
工作人员（Staff）

何永捍　助理研究员
He Yonghan, Assistant Professor
刘　佳　助理研究员
Liu Jia, Assistant Professor
程耀霆　助理研究员
Cheng Yaoting , Assistant Professor
李其刚　研究实习员
Li Qigang, Research Assistant
蒲绍艳　研究实习员
Pu Shaoyan, Research Assistant
杨利琴　实验师
Yang Liqin, Technician
陈小琼　助理实验师
Chen Xiaoqiong, Assistan Technician

研究生（Graduate Students）

李玉春　Li Yuchun 2009
肖富辉　Xiao Fuhui 2010
王晓雄　Wang Xiaoxiong 2011
刘耀文　Liu Yaowen 2012
田娇阳　Tian Jiaoyang 2012
吴　焕　Wu Huan 2012
余　琴　Yu Qin 2013
夏王晓　Xia Wangxiao 2014
程乐华　Cheng Lehua　2014

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（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。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。是总部设在英国伦敦的"Faculty 1000 of Biology & Medicine"成员［也是目前该机构在 Microbial Evolution & Genomics 领域的唯一华人］，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. Ma ZS (2014a). Towards computational models of animal cognition, an introduction for computer scientists. Cognitive Systems Research, vol. 33:42-69

2. Ma ZS (2014b). Towards computational models of animal communication, an introduction for computer scientists. Cognitive Systems Research, vol. 33:70-99

3. Ye CX, Hill C, Koren S. Ruan J, **Ma ZS***, Yorke JA, Zimin A (2014). DBG2OLC: efficient assembly of large genomes using the compressed overlap graph. http://adsabs.harvard.edu/cgi-bin/bib_query?arXiv:1410.2801 Software: http://sites.google.com/site/dbg2olc/

4. Zhang ZG, Geng JW, Tang XD, Xu JC, Wen XJ, **Ma ZS***, **P. Shi*** (2014) Spatial heterogeneity and co-occurrence patterns of human mucosal associated intestinal microbiota. The ISME Journal, vol. 8, 881–893

5. Li H, Ye DD, Wang X, Settles ML, Wang J, Zhou L, Dong P, **Ma ZS*** (2014) Soil bacterial communities of different natural forest types in China. Plant and Soil 383:203-216.

6. Ma, ZS, Liexun Yang, Ronald P. Neilson, Andrew Hess, Richard Millar. 2014. A Survivability-Centered Research Agenda for Cloud Computing Supported Emergency Response and Management Systems. 17pp. The 35th IEEE-AIAA Aerospace Conference (Aerospace 2014), Big Sky, Montana, USA, March 7-15th, 2014.

7. Guan Q & Ma ZS* (2014). Ecological analysis of the human milk microbiome. Chinese Science Bulletin 59(22): 2205-2212.

8. Ma ZS, Guan Q, et al. 2015. Network analysis reveals a potentially 'evil' alliance of opportunistic pathogens inhibited by a cooperative network in human milk bacterial communities. Scientific Reports, srep08275

9. 获"生物信息计算／GPU 高性能计算"领域"软件著作权"**授权**两项。

10. 申请"生物信息计算／GPU 高性能计算"领域专利受理两项。

第三代基因测序软件国际合作研发取得重大突破

基因（DNA）测序技术是现代生物科技的基础。自上世纪 70 年代起，历经三代技术后，目前已发展成为一项相对成熟的生物产业。测序技术的应用也扩展到了生物、医学、制药、健康、食品、农林、园艺、花卉、环保、法医等许多领域，并成为一项与我们衣食住行密切相关的高技术产业。 基因测序也是一些新兴医疗产业，例如遗传疾病基因诊断治疗、 癌症个性化医疗等领域的核心技术。另外，基因测序也是国家安全保障（例如突发流行病、转基因食品安全、生物武器研制等）所无法忽视的基础技术。 如果我们将 DNA 测序仪比作计算机，则基因组装软件就好比微软的 Windows、苹果 OS X， Linux 等操作系统软件。因此，基因组装软件重要性不言而喻！

第三代测序技术的研发已有近十年时间，商业化的第三代测序仪上市也有三年。但目前测序市场仍为二代测序技术所垄断。这一现状背后的深层原因之一非常有趣：人们对三代测序技术似乎"又恨又爱"。例如今年年初，我国顶级科研机构和商业公司所拥有的三代测序仪可能仅有数十台。"爱"自然来之于三代技术的先进性：三代测序技术产生的读段更长，测序成本更低，成本的迅速下降意味着更广泛的应用前景和广阔的市场。因此，新一代测序技术未来取代二代技术是测序技术发展的必然趋势。"恨"则更多是"恨铁不成钢"，目前三代技术的"致命"缺陷是测序错误率高，而且错误的分布模式与前两代测序技术非常不同。

类似于信息技术（IT）领域信号处理、传送中发生的错误，基因测序错误（生物信息技术领域）同样不可避免。二战前后开始研发的数字通讯之所以在 20 世纪末叶才能起飞、人手一部手机在 21 世纪才得以成为现实并非偶然。 而这些数字革命背后的核心技术应该首推电子计算机所支撑的软件技术。 用比较专业的词汇描述，计算机软件除了使得"高速"通讯成为可能，或许更重要的贡献之一是：计算机软件所实现的错误检测和纠错能力极大的提高了数字通讯的"可靠性"。无法"可靠"传输数据的高速网络注定无法获得实用推广。今天的大众心理基本都能接受银行电子转账和支付；但就在 10 年前，许多人对使用电子银行会非常犹豫。因此可以说，如果没有与高速网络相匹配的可靠数字通讯，电子银行时代可能仍在期待中。同样道理，如果没有能与高通量测序配套的计算机软件纠错技术，则高通量技术的优势就难以发挥！

高新技术的产业化，包括改变了现代社会和经济生活的 IT 信息技术，除了技术的先进性和实用性之外，生产制造成本必须与当下社会、经济承受能力相匹配。数字通讯和网络发展的历史告诉我们：硬件技术固然关键，但要依赖硬件技术生产制造出能在激烈的市场竞争中胜出的大众通讯产品则极其困难。如果没有电子计算机软件的支撑，今天我们所能享受到的远程快速通讯手段很可能还停留在上世纪 70 年代或更早的水平：例如已被我们多数人所遗忘的邮局"电报"和固定电话，而不是今天的电子邮件、无线手机、或微博微信。

今天的三代测序技术研发商当然非常了解以上这些历史的经验和教训。 测序技术是生物信息的核心技术，所谓生物信息技术可以简单的理解为生物技术和信息技术的结合。事实上，三代测序技术比目前占垄断地位的二代测序技术更依赖于计算机软件技术。问题是，三代测序技术在将测序通量（类似于电子通讯硬件的速度和通讯容量）推向前所未有的"高通量"的同时，也将测序错误检测和纠错，以及最终的基因组装问题的难度推向了极致。而遗传资源与进化国家重点实验室马占山研究员与美国马里兰大学 Chengxi Ye，James Yorke 等科学家的合作研究正是解决了这一领域的最大技术难题。 在解决测序错误检测和纠正的同时，他们的算法同时大幅度降低了基因组装所需要的计算时间和对计算机内存的需求。原本只有在大型超级计算机才能完成的基因组装任务，现在甚至可能在普通 PC 上完成。这些突破不仅攻克了目前向三代测序技术进行产业升级的最大技术障碍，更是大幅度降低了基因测序所需超级计算设施的投资、以及相应的测序成本。 合作团队相继推出了一种全新的针对三代测序技术特点的基因组装算法、并将其算法开发成一款软件（DBG2OLC）；软件连接 https://sites.google.com/site/dbg2olc/ 论文链接 http://adsabs.harvard.edu/cgi-bin/bib_query?arXiv:1410.2801。多组测序数据的测试表明：与目前用于三代测序最优秀的基因组装软件（PacBio2CA、HGAP、ECTools）相比 DBG2OLC 在计算时间和内存空间的消耗通常仅为其它软件的 1/10。 理论上，DBG2OLC 在时间和空间的使用上相对其它同类软件可减少达 1000 倍。 例如组装关键步骤之一的"两两比对"计算，采用一组由美国"太平洋生命科学公司"（Pacific BioSciences） 提供的人类基因组数据，DBG2OLC 使用一台普通 PC 电脑用了 6 小时完成。而同样计算，"太平洋生命科学公司" 所报道的时间为 405000 CPU 小时，而且是在谷歌公司的超级计算机集群上完成。另外，针对目前占市场垄断地位的二代测序技术，该合作团队曾于 2011 年发布 SparseDBG 算法和 SparseAssembler 软件，曾经比当时主流的基因组装软件节省 90% 的内存空间，而其计算时间和组装质量却毫不逊色。 目前华大基因最广泛应用的基因组装软件 SOAPdenovo2 即采用了 SparseAssembler 中的算法。这次合作团队中还包括了多名世界优秀计算机科学家、数学家和物理学家：例如，物理学家 James Yorke 教授正是数学非线性混沌理论中"混沌"一词的创造人。而马占山研究员在工程和网络可靠性领域的长期研究对于纠错算法研发也起到了关键作用。

Computational Biology and Medical Ecology Lab

Biography of the lab Principal Investigator: **Zhanshan (Sam) Ma** received his double PhDs in Computer Science, and Entomology in 2008, and 1997, respectively, both from the University of Idaho (UI), USA. In November 2010, he was retained as a Professor and Principal Investigator by Kunming Institute of Zoology (KIZ), the Chinese Academy of Sciences (CAS) through "The Elite 100 Scientists Program" of the CAS.

Prior to joining in KIZ, he was a Research Scientist (in Computational Biology & Computer Science) at UI. He was a senior network and software engineer from 1998 to 2006 in the computer industry in Silicon Valley, USA. Dr. Ma has been keeping dual track publishing in both Computer Science and Biology with more than 70 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".

Email: ma@vandals.uidaho.edu or ma@mail.kiz.ac.cn

DBG2OLC—an ultra-efficient genome assembler for large genomes expected to significantly boost the adoptions of single molecule DNA sequencing technologies

The Human Genome Project, the biggest biomedical project humans have ever endeavored to the date, greatly accelerated the advancement of DNA sequencing technologies. Three generations of DNA sequencing technologies have been developed in the last three decades, and we are at the crossroads of the second and third generations. The upgrade to the third-generation single molecule sequencing technology from the currently prevalent second-generation technology is expected to further lower the sequencing cost and expand its applications in biomedical research and biotechnology development. Nevertheless, arguably the biggest roadblock preventing the transition to the third generation technology has been the computational problem of the genome assembly. Specifically the error detection and correction 'curse' returns when we pursue the high throughput long reads which is a best selling point of the third generation technology.

In recently released software, dubbed DBG2OLC (http://sites.google.com/site/dbg2olc/), by a team of scientists including Prof. Sam Ma at the Computational Biology and Medical Ecology Lab of the Chinese Academy of Sciences, and Profs. Chengxi Ye, James Yorke, Aleksey Zimin from the University of Maryland, a novel de novo assembly algorithm was proposed and demonstrated to be ultra-efficient in assembling highly erroneous long reads produced by the third generation of DNA sequencers, in terms of both computational time and memory. The DBG2OLC converts the de novo genome assembly problem from the de Bruijn graph (DBG) to the overlap layout consensus (OLC) framework. For each sequence read, DBG2OLC compresses the regions that lie inside de Bruijn graph contigs, which greatly lowers the complexity of the assembly problem. The compression transforms previously prohibitive tasks such as pair-wise alignment into jobs that require small amounts of time. A compressed overlap graph that preserves all necessary information is constructed with the compressed reads to enable the final-stage assembly. Experiments with the third generation sequencing data produced by PacBio and Oxford Nanopore technologies show that DBG2OLC was able to assemble large genomes two orders of magnitude more efficient than existing 3rd-generation genome assemblers in terms of computational time and memory space usages. The final assembly results are also two orders of magnitude more contiguous than using the prevalent second generation Illumina sequencing technology. For example, on a large PacBio human genome dataset, it took DBG2OLC only 6 CPU hours to calculate the pair-wise alignment of 54x erroneous long reads and 2000 CPU hours to complete the final assembly on a desktop PC, compared to the 405,000 CPU hours previously reported by Pacific Biosciences on a Google cluster. On a Nanopore dataset, DBG2OLC was able to obtain high quality results (identity rate 99.5%) even the sequencing error rate was over 30%.

With the powerful error detection and correction capabilities, and far more parsimonious resource consumptions (two orders of magnitude improvement over the existing techniques), and the lower to moderate requirement for the sequencing coverage (DBG2OLC was able to get decent assembly quality with only 10x sequencing coverage), it is possible to assemble large genome with DGB2OLC efficiently on an office workstation, rather than using expensive supercomputers or clusters. This breakthrough should significantly accelerate the adoptions of the third generation sequencing technologies in large-scale genomic research and biotechnology development.

Network analysis reveals a potentially 'evil' alliance of opportunistic pathogens Inhibited by a cooperative network in human milk bacterial communities

The critical importance of human milk to infants and even human civilization has been well established. Yet our understanding of the milk microbiome has been limited to cataloguing OTUs and computation of community diversity. To the best of our knowledge, there has been no report on the bacterial interactions within the milk microbiome. To bridge this gap, we reconstructed a milk bacterial community network based on Hunt et al1. Our analysis revealed that the milk microbiome network consists of two disconnected sub-networks. One sub-network is a fully connected complete graph consisting of seven genera as nodes and all of its pair-wise interactions among the bacteria are facilitative or cooperative. In contrast, the interactions in the other sub-network of eight nodes are mixed but dominantly cooperative. Somewhat surprisingly, the only 'non-cooperative' nodes in the second sub-network are mutually cooperative Staphylococcus and Corynebacterium that include some opportunistic pathogens. This potentially 'evil' alliance between Staphylococcus and Corynebacterium could be inhibited by the remaining nodes that cooperate with one another in the second sub-network. We postulate that the 'confrontation' between the 'evil' alliance and 'benign' alliance and the shifting balance between them may be responsible for dysbiosis of the milk microbiome that permits mastitis. Ma et al. 2015 Scientific Reports, http://www.nature.com/srep/2015/150205/srep08275/full/srep08275.html

员工简介 Lab Staff

工作人员 Staff

李　明　研究实习员
叶承曦　客座助理研究员
Ming Li & Chengxi Ye
Research Associates

研究生 Graduate Students

关　琼　Qiong Guan，2011
樊萌萌　Mengmeng Fan，2012
李连伟　Lianwei Li，2012
王娅丽　Yali Wang, 2013

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、非洲爪蟾和文昌鱼为动物模型研究神经系统的早期发育机制及其演化。

重要成果（Highlights）

论著（Publications）

1. **Zhang Z**, Shi Y, Zhao S, Li J, Li C, **Mao B***. Xenopus Nkx6.3 is a neural plate border specifier required for neural crest development. *PLoS ONE*, 2014, 9: e115165.

2. **Ma P**, Yang X, Kong Q, Li C, Yang S, Li Y, **Mao B***. The ubiquitin ligase RNF220 enhances canonical Wnt signaling through USP7 mediated deubiquitination of β-catenin, *Mol. Cell. Biol.*, 2014, 34: 4355-4366.

3. **Mao B***, Wu W. More or less is fine:an undercover work of DKK1 in anthrax toxin uptake. *SCIENCE CHINA Life Sciences*, 2014, 57: 735-736.

Nkx6.3 调控神经板边界与神经嵴发生

神经板边界形成于脊椎动物原肠胚神经板和表皮的交界处，发育为脊椎动物特有的神经嵴和基板。以非洲爪蛙为模型，我们鉴定了一个新的神经板边界特化基因 −Nkx6.3。由于 Nkx6.3 mRNA 的丰度很低，我们将实时定量 PCR 技术与爪蛙胚胎的精细切割结合起来确定了 Nkx6.3 的表达模式：Nkx6.3 表达于表皮、基板和神经嵴，在神经板中几乎没有表达。通过显微注射针对 Nkx6.3 的反义 Morpholino 敲低 Nkx6.3 的蛋白质合成，神经板边界特化基因 Zic1、Pax3 和 Msx1 的表达受到抑制，同时神经嵴的发育也受到严重影响；过表达 Nkx6.3，神经板边界的特化基因除了 Pax3，都在一定程度上受到了 Nkx6.3 的诱导，而神经嵴和基板的发育都受到了抑制，同样受到 Nkx6.3 过表达诱导的基因还有调控神经嵴发育的上游信号 Wnt8。在动物帽中研究人员发现 Nkx6.3 可以诱导神经嵴、神经板边界特化基因以及 Wnt8 mRNA 的转录，这种诱导能力受到转录因子 Dlx3 的拮抗，而 Dlx3 的转录受到 Nkx6.3 的抑制。我们推测 Nkx6.3 和 Dlx3 在神经板边界的相互作用影响了神经板边界及神经嵴的发育。
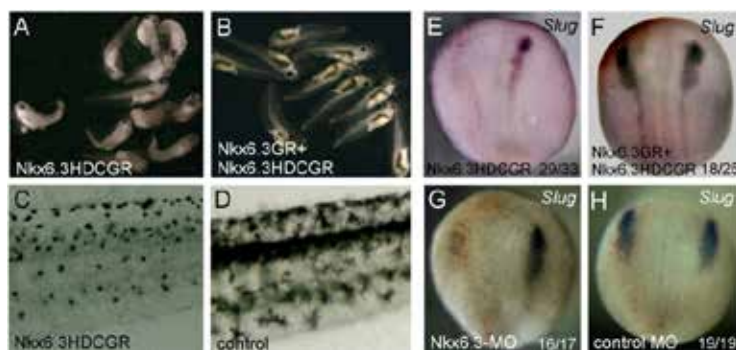

图 1 阻断 Nkx6.3 的功能会抑制胚胎色素细胞的形成（A–D)和神经嵴标记基因 Slug 的表达（E–H），提示神经嵴的发育发生了缺陷。

Figure 1. Nkx6.3 is required for neural crest development in Xenopus. Blocking the fuction of Nkx6.3 induced pigmentation defects at tadpole stages (A–D) and inhibited the expression of the neural crest marker Slug.

Mechanisms of neural patterning and evolution

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

Email:mao@mail.kiz.ac.cn
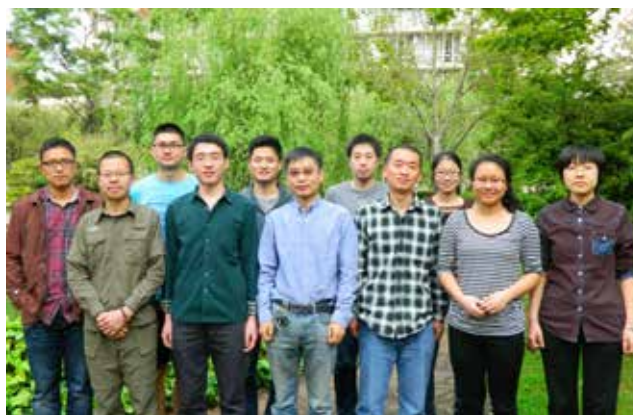
Xenopus Nkx6.3 is a neural plate border specifier

In vertebrates, the neural plate border (NPB) is established by a group of transcription factors including Dlx3, Msx1 and Zic1. Understanding the mechanisms of NPB formation and NC development is critical for our knowledge of related human diseases. We identified Nkx6.3, a transcription factor of the Nkx family, as a new NPB specifier required for neural crest development in Xenopus embryos. XNkx6.3 is expressed in the ectoderm of the neural plate border region at neurula stages, covering the epidermis, placode and neural crest territories, but not the neural plate. Inhibition of Nkx6.3 by dominant negative construct or specific morpholino leads to neural crest defects, while overexpression of Nkx6.3 induces ectopic neural crest in the anterior neural fold. In animal caps, Nkx6.3 alone is able to initiate the whole neural crest regulatory network and induces neural crest fate robustly. Overexpression of Nkx6.3 affects multiple signaling pathways, creating a high-Wnt, low-BMP environment required for neural crest development. Gain- and loss-of-function of Nkx6.3 have compound effects on the expression of known NPB genes which is largely opposite to that of Dlx3. Overexpression of Dlx3 blocks the NC inducing activity of Nkx6.3. The crosstalk between Nkx6.3, Dlx3 and Msx1 is likely crucial for proper NPB formation and neural crest development in Xenopus.

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）
张祖明 Zuming Zhang, 2008
江世友 Shiyou Jiang，2009
孙　健 Jian Sun，2009
杨相彩 Xiangcai Yang, 2010
王晓磊 Xiaolei Wang，2011
刘晓亮 Xiaoliang Liu，2011
谢建新 Jianxin Xie，2012
李永鑫 Yongxin Li，2013
杜家诚 Jiacheng Du，2014

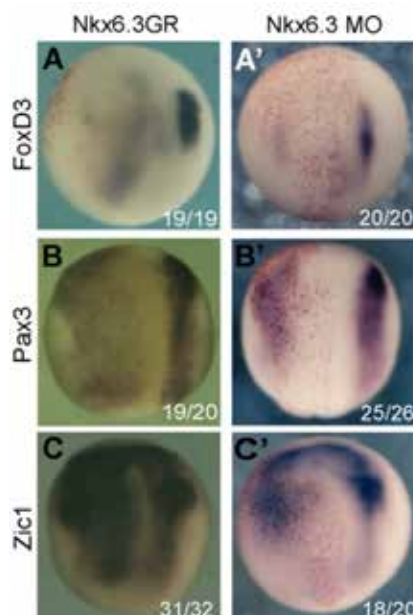图 2. 过表达（A–C)或敲低（A'–C'）Nkx6.3 对神经嵴标记基因 FoxD3 和神经板边界基因 Pax3 和 Zic1 的影响。

Figure 2. The effects of Nkx6.3 overexpression (A–C) or knockdown (A'–C') on the expression of neural crest marker FoxD3 and the neural plate border genes Pax3 and Zic1.

哺乳动物胚胎发育

　　郑 萍，博士，研究员，研究组长，以灵长类（猕猴）和小鼠为动物模型，研究哺乳类卵母细胞及着床前胚胎发育调控。2009 年 6 月通过中科院项目"百人计划"引进昆明动物研究所，加入遗传资源与进化国家重点实验室，并组建哺乳动物胚胎发育课题组。研究方向为配子发育生物学和早期胚胎发育调控。

重要成果（Highlights）
论著（Publications）

1. **Bo Zhao**, **Wei-dao Zhang**, Ying，liang Duan, Yong-qing Lu, Yi-xian Cun, Chao-hui Li, **Kun Guo**, Wen-hui Nie, Lei Li, Rugang Zhang, **Ping Zheng*** , Filia is an ESC-specific regulator of DNA damage response and safeguards genomic stability. *Cell Stem Cell* , in press (2015)

2. Yuqi Zhao，Shuang Ji，Jinkai Wang，Jingfei Huang*，**Ping Zheng***，mRNA-Seq and microRNA-Seq whole-transcriptome analyses of rhesus monkey embryonic stem cell neural differentiation revealed the potential regulators of rosette neural stem cells. *DNA research*, 2014, 21, 541–554.

3. Tao Tan, Yanfeng Zhang, Weizhi Ji* and **Ping Zheng***，miRNA signature in mouse spermatogonial stem cells revealed by high-throughput sequencing，*BioMed Research International*，2014, 154251.

1. 胚胎干细胞维持遗传物质稳定性的分子调控机制

　　多能干细胞在细胞替代治疗中有着广阔的应用前景，认识多能干细胞遗传物质稳定性维持机制可促进多能干细胞的安全应用，并有助于理解早期胚胎如何维持遗传物质的稳定性。我们在小鼠胚胎干细胞(ESC)中鉴定了一个 ESC 特异表达的基因 Filia，并阐明它在 ESC 遗传物质的稳定维持中起关键调控作用。Filia 缺失使 ESC 遗传物质迅速发生变异，并产生高致瘤性。Filia 表达受 DNA 损伤诱导，调控 DNA 损伤反应的多个环节（包括损伤信号传导、细胞周期停滞、DNA 损伤修复以及损伤细胞的凋亡清除）。进一步的机制研究发现，Filia 结合 DNA 损伤反应的另一个多能调控因子 PARP1，并通过激活 PARP1 酶活性调控 DNA 损伤反应。另外，Filia 还以不依赖于 PARP1 的途径作用。Filia 定位于中心体并调控其正常功能。DNA 受损时 Filia 进入细胞核并定位于损伤位点参与损伤修复。在凋亡诱导条件下，Filia 还能转移至线粒体调控细胞凋亡。该研究论文已被 Cell Stem Cell 接收。

2. 哺乳动物雌性生殖干细胞再生现象的研究

　　出生后哺乳动物卵巢中是否存在生殖干细胞及雌性配子的再生是长期争议的重要科学问题。我们采用 in vivo lineage tracing 手段对这一科学问题进行了探讨。通过对表达 Oct4 的卵泡前生殖细胞进行长达 4 个月的示踪研究，发现成年卵巢内存在活跃的生殖干细胞，它们能进行持续的 DNA 复制和有丝分裂，能分化进入减数分裂，并发育形成原始卵泡。这些结果支持出生后哺乳动物卵巢中存在生殖干细胞及雌性配子的再生。该研究论文已投稿。

Mammalian Embryonic Development

Group leader: **Ping Zheng**, Ph.D, joined in Kunming Institute of Zoology, Chinese Academy of Sciences in 2009. Dr. Zheng's lab is interested in female germ cell biology and early embryonic development.

E-mail: zhengp@mail.kiz.ac.cn
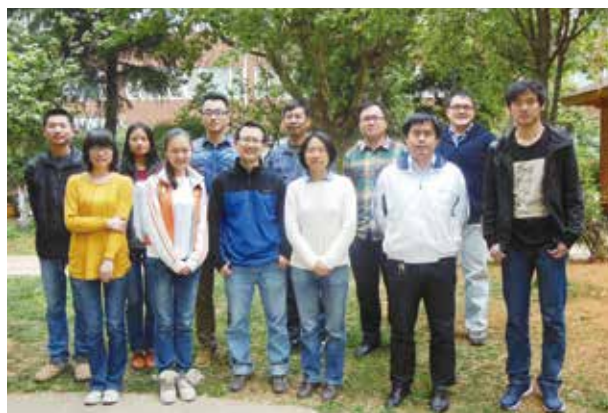
1. Preserving genetic integrity of embryonic stem cells

Pluripotent stem cells (PSCs) possess great promise in cell-based therapy. However, genomic instability observed in them represents a major challenge for their potential applications. Unique factors by which PSCs regulate their genomic stability remain elusive. Herein we report the identification of Filia as a unique master regulator of genomic stability in mouse embryonic stem cells (ESCs). Filia expression is induced by genotoxic stress. It ensures centrosome integrity and regulates DNA damage response (DDR) at multiple levels. These include DDR signaling, cell cycle checkpoints and damage repair, ESC differentiation and apoptosis. Consequently, Filia depletion causes ESC genomic instability, induces resistance to apoptosis and promotes malignant transformation. Filia interacts with PARP1 and stimulates its enzymatic activity, which amplifies Filia's roles on DDR. Moreover, Filia constitutively resides on centrosomes and translocates onto DNA damage sites or mitochondria to perform its regulations on centrosome integrity, damage repair or apoptosis induction. This paper has been accepted by *Cell Stem Cell*.

2. Germ stem cells are active in postnatal mouse ovary under physiological conditions

In female mammals, whether there is postnatal neo-oogenesis has been vigorously debated for more than six decades. Recent in vitro studies suggested the existence of germ stem cells in postnatal ovaries of mouse, pig and human. However, it is unclear whether such germ stem cells are active under physiological conditions and play essential roles in sustaining normal ovarian function. Herein we utilize tamoxifen inducible Cre-loxP genetic marking approach to investigate whether there are active germ stem cells in postnatal mouse ovaries under physiological conditions. Oct4-Cre-ERT2 mice were crossed with Rosa26-Stop-eYFP mice to establish a tamoxifen inducible tracing system. By labeling Oct4-expressing germ cells with YFP in adult mice ovaries (5-6 Weeks old) and tracing them for one day, three days, two months and four months, we document the persistent YFP+ germ cell proliferation and mitotic division through 5-bromodeoxyuridine triphosphate (BrdU) incorporation assay. Some YFP labeled non-follicular germ cells continuously entered into meiosis as indicated by the expression of meiosis markers Sycp3 and Stra8. Moreover, new primordial follicles retaining Sycp3 or Stra8 signal were persistently generated from YFP+ labeled germ cells. Together, our data support the notion that active germ stem cells exist and function in vivo to replenish primordial follicle pool in postnatal mouse ovaries under physiological conditions.

员工简介（Lab Staff）
工作人员（Staff）

和协超　高级实验师
He, Xiechao: Senior technician
赵　博　助理研究员
Zhao, Bo: Research associate
吕永青　研究实习员
Lu, Yongqing: Research assistant
张锦娟　研究实习员
Zhang, Jinjuan：Research assistant
陈忠良　研究实习员
Chen, Zhongliang: Research assistant

博士后 （Post-doc)

段莹亮 Duan, Yingliang， 2013

研究生（Graduate Students）

李朝晖 Li, Chaohui 2011
王鑫轶 Wang, Xinyi 2012
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
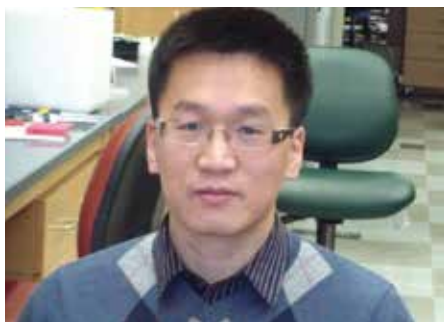
发育的印迹调控与进化

焦保卫，博士，研究员，博士生导师。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）

JongDae Shin, Mary C. Wallingford, Judith Gallant, Chelsea Marcho, **Baowei Jiao**, Meg Byron, Michael Bossenz, Jeanne B. Lawrence, Stephen N. Jones, Jesse Mager, Ingolf Bach. RLIM is dispensable for X-chromosome inactivation in the mouse embryonic epiblast. *Nature*. 2014 511(7507):86-89.

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（intralocus 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。

Imprinting in Development and Evolution

Dr. Baowei Jiao, Principal Investigator, joined inKunming 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.

Email: jiaobaowei@mail.kiz.ac.cn

Research Interests:

1. 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 modication, 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 an 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.

2. 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.

3. 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.

4. 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）

杨　钦　助理实验师
Qin Yang, Assistant Experimentalist
邹　丽　助理实验师
Zou Li, Assistant Experimentalist
徐海波　研究实习员
Xu Haibo, Research Assistant
张洪磊　博士后
Zhang Honglei, Postdoctor

研究生（Graduate Students）
柯　浩　Ke Hao 2013 博士
赵丽敏　Zhao Limin 2013 硕士
赵丽娜　Zhao Lina 2014 博士
杨　星　Yang Xing 2014 硕士
冯　旭　Feng Xu 2014 硕士
吴　瑜　Wu Yu 2014 客座

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：1207 万（2013−2014 年经费）。

The Genetic and Genomic Mechanisms of Important Domesticated Plants and Animals in China during the Evolution of Artificial Selection. National Basic Research Program (973) project, Period: 2013-2017; Head of project, Wen Wang; Amount: RMB 12.07 million for 2013-2014.

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.

羊和猪的转基因调控元件及转基因载体，农业转基因重大专项子课题；执行年限：2014−2015；项目负责人：王文；金额：146 万。

Regulatory Elements and Vectors for Transgenic Sheep and Pig. Major Projects on Transgenic Agricultural Organisms, Period, 2014-2015; Head of project, Wen Wang; Amount: RMB 1.46 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：2014−2016；项目负责人：王文；金额：600 万元。

Evolutionary Origins of New Genetic Structure in Genome and Animals' Adaptive Evolution. Innovation team project of National Science Foundation of China, Period, 2014-2016; Head of project, Wen Wang; Amount: RMB 6.0 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：200 万元。

Genetic mechanisms of adaptive evolution in mammals. National Science Fund for Distinguished Young Scholars, Period, 2014-2017; Head of project, Peng Shi; Amount: RMB2.0 million.

进化生态学与进化博弈论，国家杰出青年基金，执行年限：2014−2017；项目负责人：王瑞武；金额：200 万元。

Evolutionary Ecology and Evolutionary Game Theory. National Science Fund for Distinguished Young Scholars, Period, 2014-2017; Head of project, Ruiwu Wang; Amount: RMB2.0 million.

适应性进化的分子机制研究，国家自然科学基金优秀重点实验室项目；执行年限：2012−2015；项目负责人：黄京飞；金额：300 万

Molecular Mechanisms of Adaptive Evolution, Excellent State Key Laboratory project from the National Science Foundation of China, Period, 2012-2015; Head of project, JingFei Huang; Amount: RMB 3.0 million.

动物 DNA 条形码标准基因及高通量条形码新方法的研究，国家自然科学基金重大项目；执行年限：2011−2014；项目负责人：张亚平；金额：516 万元（云南省额外匹配 200 万元）。

Standard Gene and High-throughput Methods for Animal DNA Barcoding, Major project of National Science Foundation of China, Period: 2011-2014; Head of project, Yaping Zhang; Amount: RMB 5.16 million（Yunnan Province additionally matched RMB 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 National 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.

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. Joint Funds of National Science Foundation 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。
Found and Nechanism Research of Anti-tumor Compound Based on the Hedgehog Signaling Pathway and Cilia Formation. Joint Funds of National Science Foundation of China-Yunnan Province; Period, 2014-2017; Head of project, Bingyu Mao; Amount: RMB 2.0 million.

榕树−榕小蜂合作系统中的非对称性与不确定性选择；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：王瑞武；金额：200 万。
Research the asymmetry and uncertainty choice of Banyan - fig wasps cooperation system. Joint Funds of National Science Foundation of China-Yunnan Province; Period, 2014-2017; Head of project, Ruiwu Wang; 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 Youth Science Foundation; Period, 2014-2016; Head of project, Qingpeng Kong; Amount: RMB 1.0 million.

动物复杂性状的进化解析与调控；中国科学院战略性先导科技专项（B 类）；执行年限：2014−2019；项目负责人：王文、施鹏；金额：2.226 亿元。
Evolutionary analysis and functional regulation of animal complex traits；Strategic Priority Research Programs (B) of Chinese Academy of Sciences (CAS), Period, 2014-2019; Head of project, Wen Wang, Peng Shi; Amount: RMB222.6 million.

猪脂肪沉积等优质高产分子模块解析；中科院分子模块设计育种创新体系战略性先导科技专项子课题；执行年

限：2013-2014；项目负责人：张亚平；金额：937 万元。
Analyse on Pig Fat Deposition and Other High-yield Molecular Module .The Pilot Special Project on Molecular Module Design of Breeding Innovation System of Chinese Academy of Sciences, Period, 2013-2014; Head of project, Yaping Zhang; Amount: RMB9.37 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创新体系战略性先导科技专项子课题；执行年限：2013-2014；项目负责人：高云；金额：658 万元。
Improvement and Capacity Building of Molecular Breeding Base in Southwest. The Pilot Special Project on Molecular Module Design of Breeding Innovation System of Chinese Academy of Sciences, Period,2013-2014; Head of project, Yun Gao; Amount:RMB6.58million.

猕猴胚胎干细胞向神经终末细胞分化谱系的研究；中科院干细胞先导专项子课题；执行年限：2011-2015；项目负责人：郑萍；金额：600 万元。
Induced differentiation of Macaque embryonic stem cell into nerve cell, The Pilot Special Project on Stem Cell of Chinese Academy of Sciences, Period, 2011-2015; Head of project, Ping Zheng; Amount:RMB6.0 million

动物复杂性状的进化解析与调控；中科院前沿科学重大突破择优支持项目；执行年限：2014-2015；项目负责人：王文、施鹏；金额：4000 万元。
Evolutionary analysis and functional regulation of animal complex traits；Merit support Project for Major breakthrough in Frontier Sciences(CAS), Period, 2014-2015; Head of project, Wen Wang, Peng Shi; Amount: RMB40million.

东非脊椎动物多样性格局及形成机制，中国科学院国际合作课题；执行年限：2013-2015；项目负责人：蒋学龙；金额：140 万元。
East African vertebrate diversity and formation mechanism, International Cooperation Project of Chinese Academy of Sciences. Period, 2013-2015; Head of project, Xuelong Jiang; Amount: RMB1.40 million.

非洲家禽的分子进化与基因组多样性研究，中国科学院国际合作课题；执行年限：2013-2015；项目负责人：彭 晟；金额：120 万元。
Molecular Evolution and Diversity of African Poultry Genome. International Cooperation Project of Chinese Academy of Sciences. Period, 2013-2015; Head of project, Minsheng Peng; Amount: RMB1.40 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.

研发面向"整合计算生物信息学和个性化医学（疗）"的"GP-GPU 微型超算技术系统"，云南省高端科技人才引进计划；执行年限：2012-2014；项目负责人：马占山；金额：200 万。
Research on "GP-GPU Micro-Supercomputer Technology System" for "Integration of Computing Bioinformatics and Personalized Medicine (Therapy)"; Projects for Recruited Top Talent of Sciences and Technology of Yunnan Province, Period: 2012-2014; Head of project, Zhanshan Ma; Amount: RMB 2.0 million.

滇池海菜花－金线鱼复合生态系统重建及持续利用扩大示范研究，2012 年省级九湖水污染防治专项资金；执行年限：2012-2014；项目负责人：杨君兴；金额：580 万。
Reconstruction and Continued Usage of the Ottelia - Nemipterus Complex Ecosystem in Dianchi Lake; The Special

Funds for Prevention and Control of Nine Lake Water Pollution in Yunnan Province. Period: 2012-2014; Head of project, Junxing Yang; Amount: RMB 5.8 million.

云南珍稀特有优质鱼类滇池金线　人工繁殖扩大试验研究，云南省环保厅生物多样性保护战略与行动计划；执行年限：2013-2014；项目负责人：杨君兴；金额：260 万。
Expand Experimental Research on Artificial Propagation of Sinocyclocheilus Grahami; Biodiversity Conservation Strategy and Action Plan of Yunnan Province Environment Department; Period: 2013-2014; Head of project, Junxing Yang; Amount: RMB 2.6 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.

石斛基因组技术开发，企业委托；执行年限：2012-2014；项目负责人：王文；金额：420 万。
Genomic Technology Development of Dendrobium. Company Supported, Period, 2012-2014; Head of project, Wen Wang; Amount: RMB 4.2 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.

云南澜沧江糯扎渡水电工程施工期生态监测项目，企业委托项目；执行年限：2009-2014 项目负责人：杨君兴；金额：135 万元。
Ecological monitoring of Nuozhadu hydro power station in Lancangjiang River, Yunnan, during construction period, Company supported, Period, 2009-2014; Head of project, Junxing Yang; Amount: RMB 1.35 million.

发表论文　Publications

1. Ai WM, Chen SB, Chen X, Shen XJ, **Shen YY***. Parallel evolution of IDH2 gene in cetaceans, primates and bats. FEBS LETT. 2014, 588(3):450-454.

2. Angleby H, Oskarsson M, **Pang JF**, **Zhang YP**, Leitner T, Braham C, Arvestad L, Lundeberg J, Webb KM*, Savolainen P. Forensic Informativity of similar to 3000bp of Coding Sequence of Domestic Dog mtDNA. J FORENSIC SCI.2014, 59(4):898-908.

3. **Bai B**, Zhao WM, Tang BX, Wang YQ, Wang L, Zhang Z, Yang HC, Liu YH, Zhu JW, **Irwin DM**, **Wang GD***, **Zhang YP***. DoGSD: the dog and wolf genome SNP database. NUCLEIC ACIDS RES, 2014,43:777-783.

4. Bayliss J, Schaafsma M, Balmford A, Burgess ND, Green JMH, Madoffe SS, Okayasu S, Peh KSH, Platts PJ, **Yu DW***.The current and future value of nature-based tourism in the Eastern Arc Mountains of Tanzania. Ecosystem Services.2014, 8:75-83.

5. Bohmann K, Evans A, Gilbert MT*, Carvalho GR, Creer S, Knapp M, **Yu DW**, de Bruyn M. Environmental DNA for wildlife biology and biodiversity monitoring. TRENDS ECOL EVOL.2014, 29,358-367.

6. Bryson RJ*, Linkem CW, Dorcas ME, Lathrop A, Jones JM, Alvarado-Díaz J, Grünwald CI, **Murphy RW**. Multilocus species delimitation in the Crotalus triseriatus species group (Serpentes: Viperidae: Crotalinae), with the description of two new species. ZOOTAXA. 2014, 3826(3):475-496.

7. **Cao X**, Irwin DM, Liu YH, Cheng LG, Wang L, **Wang GD***, **Zhang YP***. Balancing Selection on CDH2 May Be Related to the Behavioral Features of the Belgian Malinois. PLOS ONE.2014, 9(10):e110075.

8. **Chen L***, Tang LY, Xiang H, Jin LJ, Li QY, **Dong Y**, **WangW**, **Zhang GJ**. Advances in genome editing technology and its promising application in evolutionary and ecological studie. GigaScience.2014, 30(3):24.

9. Chen SL, Zhang G, Shao C, Huang Q, Liu G, Zhang P, Song W, An N, Chalopin D, Volff JN, Hong Y, Li Q, Sha Z, Zhou H, Xie M, Yu Q, Liu Y, **Xiang H**, Wang N, Wu K, Yang C, Zhou Q, Liao X, Yang L, Hu Q, Zhang J, Meng L, Jin L, Tian Y, Lian J, Yang J, Miao G, Liu S, Liang Z, Yan F, Li Y, Sun B, Zhang H, Zhang J, Zhu Y, Du M, Zhao Y, Schartl M, Tang Q, Wang J*. Whole-genome sequence of a flatfish provides insig hts in to ZW sex chromosome evolution and adaptation to a benthic lifestyle. NAT GENET. 2014, 46 (3):253

10. **Chen SM**, Gao S, **Cheng DQ**, **Huang JF***. The characterization and comparison of amyloidogenic segments and non-amyloidogenic segments shed light on amyloid formation. BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS. 2014, 447 (2):255-262.

11. Chen X*, **Jiang K**, Guo P, Huang S, **Rao DQ**, Ding L, Takeuchi H, **Che J**, **Zhang YP**, Myers EA, Burbrink FT. Assessing species boundaries and the phylogenetic position of the rare Szechwan ratsnake, Euprepiophis perlaceus (Serpentes: Colubridae), using coalescent-based methods. MOL PHYLOGENET EVOL.2014, 70:130-136.

12. **Cheng DQ**, **Li Y**, **Huang JF***.Molecular Evolution of the Primate alpha-/theta- Defensin Multigene Family. PLOS ONE.2014, 9 (5):10.1371.

13. Cheng QQ*, Zhu YX, **Chen XY***.High polymorphism and moderate differentiation of chub mackerel, Scomber japonicus (Perciformes: Scombridae), along the coast of China revealed by fifteen novel microsatellite markers. CONSERV GENET.2014, 15 (5):1021-1035.

14. Choi SK, Lee JE, Kim YJ, Min MS, Voloshina I, Myslenkov A, Oh JG, Kim TH*, Markov N, Seryodkin I, Ishiguro N, Yu L, **Zhang YP**, Lee H, Kim KS. Genetic structure of wild boar (Sus scrofa) populations from East Asia based on microsatellite loci analyses. BMC GENET.2014, 15:85.

15. **Dong F**, Li SH, Zou FS, Lei FM, Liang W, **Yang JX***, **Yang XJ***.Molecular systematics and plumage coloration evolution of an enigmatic babbler (Pomatorhinus ruficollis) in East Asia. MOL PHYLOGENET EVOL.2014, 70:76-83.

16. **Dong F**, Zou FS, Lei FM, Liang W, Li SH, **Yang XJ***.Testing hypotheses of mitochondrial gene-tree paraphyly: unravelling mitochondrial capture of the Streak-breasted Scimitar Babbler (Pomatorhinus ruficollis) by the Taiwan Scimitar Babbler (Pomatorhinus musicus). MOL ECOL.2014, 23(23):5855-5867.

17. Du XY, Servin B, Womack JE, Cao J, Yu M, **Dong Y**, **Wang W***, Zhao S*. An update of the goat genome assembly using dense radiation hybrid maps allows detailed analysis of evolutionary rearrangements in Bovidae. BMC GENOMICS.2014, 23;15:625.

18. Edwards DP*, Magrach A, Woodcock P, Ji YQ,Lim NT, Edwards FA, LarsenTH, Hsu WW, Benedick S, Khen CV, Chung AYC, Hamer KC, Wilcove DS, **Yu DW**. Selective-logging and oil palm: multitaxon impacts, biodiversity indicators, and trade-offs for conservation planning. ECOL APPL.2014, 24(8), 2029-2049.

19. Feng XM, **Yang CL**, Zheng WY, **Wen JF***.Structural and evolutionary characteristics of pyruvate phosphate dikinase in Giardia lamblia and other amitochondriate protozoa. CHINESE MEDICAL JOURNAL.2014, 127(23):4097-4103.

20. Gao H, Grueschow S, Barke J, Seipke RF, Hill LM, Orivel J, **Yu DW**, Hutchings MG, Pierson TW, Yan F, Wang Y, Papenfuss TGoss RJM*. Filipins: the first antifungal "weed killers" identified from bacteria isolated from the trap-ant. RSC ADV.2014, 4(100):57267- 270

21. Gao JJ, Pan XR, Hu J, Ma L, Wu JM, Shao YL, Ai SM, Liu SQ, Barton SA, Woodruff RC, **Zhang YP**, Fu YX*. Pattern of Mutation Rates in the Germline of Drosophila melanogaster Males from a Large-Scale Mutation Screening Experiment. G3-GENES GENOM GENET. 2014, 4(8):1503-1514.

22. Gao YD, **Zhao YQ**, **Huang JF***. Metabolic Modeling of Common Escherichia coli Strains in Human Gut Microbiome. BIOMED RES INT.2014, 2014:694967.

23. Geng JW, Song QF,Tang XD, Liang X, Fan H, Peng HL, Guo Q*, **Zhang ZG***. Co-occurrence of driver and passenger bacteria in human colorectal cancer. GUT PATHOG. 2014, 6:26:00.

24. Grossen C*, Keller L, Biebach I, **International Goat Genome Consortium**, Croll D. Introgression from Domestic Goat Generated Variation at the Major Histocompatibility Complex of Alpine Ibex. PLOS GENET.2014, 10(6):e1004438.

25. **Guan Q**, **Ma ZS***. Ecological analysis of the human milk microbiome. CHINESE SCI BULL.2014, 59(22): 2205-2212.

26. Guo MH, Wu WJ, Fan L, **Peng MS**, **Yang JK**, Zhang W, Hao F, Xie HF, Xiang LH, Zheng M, Guo YN0, Song QH, Tu CX, Zhong H, Fan WG, Shi YJ, Cao P, Feng LY, Na M, Pang Q, Yang XY, Yang C, Zou X, He L, **Zhang YP***. No association between Y chromosomal haplogroups and severe acne in the Han Chinese population. J HUM GENET.2014, 59(8):475-476.

27. **He JZ**, W**ang RW***, Jensen CXJ, Li YT. Evolutionary Stability in the Asymmetric Volunteer's Dilemma. PLOS ONE.2014, 9(8):e103931.

28. **He K**, **Jiang XL***. Sky islands in southwest China. I. an overview of phylogeographic patterns. CHINESE SCI BULL.2014, 59:585-597.

29. **He K**, Shinohara A, **Jiang XL***, Campbell KL*.Burbrink FT. Multilocus phylogeny of talpine moles (Talpini, Talpidae, Eulipotyphla) and its implications for systematics. MOL PHYLOGENET EVOL.2014, 70:513-521.

30. He L*, Wu WJ, **Yang JK**, Cheng H, Zuo XB, Lai W, Gao TW, Ma CL, Luo N, Huang JQ, Lu FY, Liu YQ, Huang YJ, Lu QJ, Zhang HL, Wang L, Wang WZ, Wang MM, Xiao SX, Sun Q, Li CY, Bai YP18, Li H, Zhou ZC, Zhou FS, Chen G, Liang B, Qi J, Yang XY, Yang T Zheng X, Sun LD, Zhang XJ, **Zhang YP***. Two new susceptibility loci 1q24.2 and 11p11.2 confer risk to severe acne. NAT COMMUN.2014, 5:2870.

31. **He YH**, Kong WL, Wang G, Zhao Y, Bi MX, Na LX, Wang MQ, Perry B, Li Y*. The calcium-sensing receptor

R990G polymorphism is associated with increased risk of hypertriglyceridemia in obese Chinese. GENE.2014, 533(1):67-71.

32. **He YH**, Li W, Li Y, Zhang S, Wang Y*, Sun C. Ursolic Acid Increases Glucose Uptake through the PI3K Signaling Pathway in Adipocytes. PLOS ONE.2014, 9(10):e110711.

33. **He YH**, **Lu X**, **Wu H**, Cai WW, **Yang LQ**, Xu LY, Sun HP, **Kong QP***. Mitochondrial DNA content contributes to healthy aging in Chinese: a study from nonagenarians and centenarians. NEUROBIOL AGING. 2014, 35 (7):10.1016.

34. **He YH**, **Lu X**, **Yang LQ**, Xu LY, **Kong QP***. Association of the insulin-like growth factor binding protein 3 (IGFBP-3) polymorphism with longevity in Chinese nonagenarians and centenarians. AGING-US.2014, 6(11):944-56.

35. **He YH**, Zhang YX, **Yang LQ**, **Liao XP**, **Zhang QY**, Cai WW, **Kong QP***. Assessment of the Health Status of Centenarians in the South of China-across-sectional study. J AM GERIATR SOC.2014, 62 (7):1402-1404.

36. **Hu NQ**, **Orkin J**, **Huang B**, **He K**, **Jiang XL***. Isolation and characterization of Thirteen microsatellite loci for the western black crested gibbon (Nomascus concolor) by high-throughput sequencing.CONSERV GENET RESOUR.2014, 6:179-181.

37. Huang YF, **He YH**, Sun XW, He YJ, Li Y, Sun CH*. Maternal High Folic Acid Supplement Promotes Glucose Intolerance and Insulin Resistance in Male Mouse Offspring Fed a High-Fat Diet. INT J MOL SCI.2014, 15(4):6298-6313.

38. **Huang YF**, **Yang JX***, **Chen XY***. Stenorynchoacrum xijiangensis, a new genus and a new species of Labeoninae fish from Guangxi, China (Teleostei: Cyprinidae). ZOOTAXA.2014, 3793 (3): 379-386.

39. **Jiang Y**, Xie M, Chen W, Talbot R, Maddox JF, Faraut T, Wu C, Muzny DM, Li Y, Zhang W, Stanton JA, Brauning R, Barris WC, Hourlier T, Aken BL, Searle SM, Adelson DL, Bian C, Cam GR, Chen Y, Cheng S, DeSilva U, Dixen K, **Dong Y**, Fan G, Franklin IR, Fu S, Fuentes-Utrilla P, Guan R, Highland MA, Holder ME, Huang G, Ingham AB, Jhangiani SN, Kalra D, Kovar CL, Lee SL, Liu W, Liu X, Lu C, Lv T, Mathew T, McWilliam S, Menzies M, Pan S, Robelin D, Servin B, Townley D, Wang W, Wei B, White SN, Yang X, Ye C, Yue Y, Zeng P, Zhou Q, Hansen JB, Kristiansen K, Gibbs RA, Flicek P, Warkup CC, Jones HE, Oddy VH, Nicholas FW, McEwan JC, Kijas JW, Wang J, Worley KC*, Archibald AL, Cockett N*, Xu X*, **Wang W***, Dalrymple BP*. The sheep genome illuminates biology of the rumen and lipid metabolism. SCIENCE.2014, 344 (6188):1168-1173.

40. **Kai Z**, Woan TS, Jie L, Goodale E, Kitajima K, Bagchi R, Harrison RD*. Shifting Baselines on a Tropical Forest Frontier: Extirpations Drive Declines in Local Ecological Knowledge. PLOS ONE.2014, 9(1):e86598.

41. Kraaijenbrink T, van der Gaag KJ, Zuniga SB1, Xue Y, Carvalho-Silva DR, Tyler-Smith C, Jobling MA, Parkin EJ, **Su B, Shi H**, Xiao CJ, Tang WR, Kashyap VK, Trivedi R, Sitalaximi T, Banerjee J, Karma Tshering of Gaselô, Tuladhar NM, Opgenort JR, van Driem GL, Barbujani G, de Knijff P*. A Linguistically Informed Autosomal STR Survey of Human Populations Residing in the Greater Himalayan Region. PLOS ONE.2014, 9(3):e91534.

42. Lei J, Sun XY, **Jiang K**, Vogel G, Booth D, Ding L*. Multilocus Phylogeny of Lycodon and the Taxonomic Revision of Oligodon multizonatum. ASIAN HERPETOL RES.2014, 5(1):26-27.

43. Li AM, Zhang JY*, **Zhou ZY**. PLEK: a tool for predicting long non-coding RNAs and messenger RNAs based on an improved k-mer scheme. BMC BIOINFORMATICS.2014, 15:311.

44. **Li D**, Yan Z, Lu L, Jiang HF*, **Wang W***.Pleiotropy of the de novo-originated gene MDF1. SCI REP-UK.2014, 4:280.

45. **Li GH, Huang JF***. Inferring therapeutic targets from heterogeneous data: HKDC1 is a novel potential therapeutic target for cancer. BIOINFORMATICS.2014, 30 (6):748-752.

46. Li H,**Ye DD**,Wang XG,Settles ML, Wang J, Hao ZQ,Zhou LS,Dong P, Jiang Y, **Ma ZS*** .Soil bacterial communities of different natural forest types in Northeast China. PLANT SOIL.2014, 383:203-216.

47. **Li M**, Luo XJ, Rietschel M, Lewis CM, Mattheisen M, Muller-Myhsok B, Jamain S, Leboyer M, Landen M,

Thompson PM, Cichon S, Nothen MM, Schulze TG, Sullivan PF, Bergen SE, Donohoe G, Morris DW, Hargreaves A, Gill M, Corvin A, Hultman C, Toga AW, **Shi L**, **Lin Q**, **Shi H**, Gan L, Meyer-Lindenberg A, Czamara D, Henry C, Etain B, Bis JC, Ikram MA, Fornage M, Debette S, Launer LJ, Seshadri S, Erk S, Walter H, Heinz A, Bellivier F, Stein JL, Medland SE, Arias Vasquez A, Hibar DP, Franke B, Martin NG, Wright MJ, Moo DSBC, Swedish Bipolar Study G, Alzheimer's Disease Neuroimaging I, Consortium E, Consortium C, **Su B***. Allelic differences between Europeans and Chinese for CREB1 SNPs and their implications in gene expression regulation, hippocampal structure and function, and bipolar disorder susceptibility. Mol Psychiatry.2014, 19(4): 452-461.

48. **Li M**, Ohi K, Chen C, He Q, **Liu JW**, Chen C, Luo XJ, Dong Q, Hashimoto R, **Su B***. Failure of replicating the association between hippocampal volume and 3 single-nucleotide polymorphisms identified from the European genome-wide association study in Asian populations. NEUROBIOL AGING. 2014, 35(12):2883.

49. **Li R**, **Wang H**, Yang L, Zhang B, Li Y, Hu J, **Kong QP***. The whole mitochondrial genome of the Cynomolgus macaque (Macaca fasciularis). MITOCHONDR DNA.2014, doi:10.3109/19401736.2013.825777.

50. **Li S***, Liu SY. Geographic variation of the large-eared field mouse (Apodemus latronum Thomas, 1911) (Rodentia: Muridae) with one new subspecies description verified via cranial morphometric variables and pelage characteristics. ZOOLOGICAL STUDIES.2014,53:1-11.

51. **Li XY**, Buzzard P, **Jiang XL***. Validity of the camera trapping method for abundance estimate and its application to a habitat association analysis for four ungulate species in mountain forests. POPUL ECOL.2014, 56:251–256.

52. **Li XY**, Buzzard P, **Jiang XL***. Habitat associations of four ungulates in mountain forests of southwest China, based on camera trapping and dung counts data. POPUL ECOL.2014, 56(1):251-256.

53. **Li XY**, **Jiang XL***. Implication of musk deer (Moschus spp.) depletion from hunter reports and dung transect data in northwest Yunnan, China. J NAT CONSERV.2014, 22:474-478.

54. Li Y, Huang W, Yu Q, **Cheng YT**, **Kong QP***. Lower mitochondrial DNA content relates to high-altitude adaptation in Tibetans. MITOCHONDR DNA.2014, 20:1-5.

55. **Li Y**, **Wang GD**, **Wang MS**, **Irwin DM**, **Wu DD**, **Zhang YP***. Domestication of the Dog from the Wolf Was Promoted by Enhanced Excitatory Synaptic Plasticity: A Hypothesis. GENOME BIOL EVOL.2014, 6(11):3115–3121.

56. **Wu DD**, Wang X, **Li Y**, **Zeng L**, **Irwin DM**, **Zhang YP***."Out of Pollen" Hypothesis for Origin of New Genes in Flowering Plants: Study from Arabidopsis thaliana. GENOME BIOL EVOL.2014, 6(10):2822–2829.

57. **Li Y**, **Wu DD***, Boyko AR, **Wang GD**, **Wu SF**, Irwin DM, **Zhang YP***. Population Variation Revealed High-Altitude Adaptation of Tibetan Mastiffs. MOL BIOL EVOL.2014, 31(5):1200-1205.

58. Li ZP, **Zhang ZG***, Xu C, Zhao JB, Liu H, Fan ZY, Yang FH, Wright AD, Li GY. Bacteria and Methanogens Differ along the Gastrointestinal Tract of Chinese Roe Deer (Capreolus pygargus). PLOS ONE.2014, 9(12):e114513.

59. **Liu HQ**, **Li Y**, Irwin DM, **Zhang YP***, **Wu DD***. Integrative analysis of young genes, positively selected genes and lncRNAs in the development of Drosophila melanogaster. BMC EVOL BIOL.2014, 14:241.

60. Liu J, Wang XP, Cho S, Lim BK, Irwin DM, Ryder OA, **Zhang YP***, Yu L*. Evolutionary and Functional Novelty of Pancreatic Ribonuclease: a Study of Musteloidea (order Carnivora). SCI REP-UK.2014, 4:5070.

61. **Liu J**, Xu LY,Li RL ,Li EM, **Kong QP***. Evaluating the Susceptibility of Mitochondrial DNA Germline Mutations in Chinese Cancer Patients. CURR MOL MED.2014, 14,1265- 1272.

62. **Liu LN**,Wang CY, **Lu X**, **Xiao FH**, **Wang HW**, **Yang LQ**, Xu LY, **Kong QP***. The MNS16A polymorphism in the TERT gene in peri-centenarians from the Han Chinese population. SCI CHINA LIFE SCI. 2014,57 (10):1024-1027.

63. Liu SJ*, **Zhang YP**. Mitochondria in Human Diseases and Animal Evolution. CURR MOL MED.2014, 14(10):1245-1246.

64. **Liu YW**, **He YH**, Zhang YX, **Cai WW***, **Yang LQ**, Xu LY, **Kong QP***. Absence of A673T variant in APP gene

indicates an alternative protective mechanism contributing to longevity in Chinese individuals. NEUROBIOL AGING.2014, 35 (4):10.1016.

65. **Liu Z***. Codon 104 of p53 is not an adaptively selected site for extreme environments in mammals of the Tibet plateau. P NATL ACAD SCI USA. 2014,111（23）:E2357.

66. **Liu Z**, **Qi FY**, **Zhou X**, **Ren HQ**, **Shi P***. Parallel sites implicate functional convergence of the hearing gene prestin among echolocating mammals. MOL BIOL EVOL.2014, 31(9): 2415–2424.

67. **Liu Z**, **Wang W**, Zhang TZ, **Li GH**, **He K**, **Huang JF**, **Jiang XL**, **Murphy RW**, **Shi P***. Repeated functional convergent effects of NaV1.7 on acid insensitivity in hibernating mammals. Proc. R. Soc. B-Biol. Sci.2014, 281(1776): 20132950.

68. Luo J, **Gao Y**, Ma W, Bi XY, **Wang SY**, Wang J, Wang YQ, Chai J, Du R, **Wu SF**, Meyer A, Zan RG, Xiao H, **Murphy RW**, **Zhang YP***. Tempo and mode of recurrent polyploidization in the Carassius auratus species complex (Cypriniformes, Cyprinidae). HEREDITY.2014, 112(4):415-427.

69. Luo ST, Wu YC, Chang Q, Liu Y, **Yang X**J, Zhang ZW, Zhang M, Zhang Q, Zou FS*. Deep phylogeographic divergence of a migratory passerine in Sino- Himalayan and Siberian forests: the Red- flanked Bluetail (Tarsiger cyanurus) complex. ECOL EVOL.2014, 4(7):977-986.

70. Luo XJ*, Huang L, **Jia P**, **Li M**, **Su B**, Zhao Z, Gan L. Protein-Protein Interaction and Pathway Analyses of Top Schizophrenia Genes Reveal Schizophrenia Susceptibility Genes Converge on Common Molecular Networks and Enrichment of Nucleosome (Chromatin) Assembly Genes in Schizophrenia Susceptibility Loci. SCHIZOPHRENIA BULL. 2014,40(1):39-49.

71. **Luo XJ***, **Li M**, Huang L, Steinberg S, Mattheisen M5, Liang G6, Donohoe G, Shi Y, Chen C, Yue W, Alkelai A, Lerer B, Li Z, Yi Q, Rietschel M, Cichon S, Collier DA, Tosato S, Suvisaari J, Rujescu D, Golimbet V, Silagadze T, Durmishi N, Milovancevic MP, Stefansson H, Schulze TG, Nöthen MM, Chen C, Lyne R, Morris DW, Gill M, Corvin A, Zhang D, Dong Q, Moyzis RK, Stefansson K, Sigurdsson E, Hu F; MooDS SCZ Consortium, Su B, Gan L. Convergent lines of evidence support CAMKK2 as a schizophrenia susceptibility gene. MOL PSYCHIATRY.2014, 19(7):774-783.

72. **Lyu J***, Li B, He W, Zhang S, **Gou ZH**, Zhang J, Meng L, Li X, Tao D, Huang W, Hu F, **Wang W***. A genomic perspective on the important genetic mechanisms of upland adaptation of rice. BMC PLANT BIOL.2014, 11;14:160.

73. Ma L, **Wu DD**, Ma SL, Tan LW, Chen XG, Tang NLS*, Yao YG*. Molecular evolution in the CREB1 signal pathway and a rare haplotype in CREB1 with genetic predisposition to schizophrenia. J PSYCHIATR RES.2014, 57(2014):84-89.

74. Ma LQ, Zou T, Yuan YP, Lv JJ, Dong XQ, Yang G, Zhu YZ, Luo J, **Zhang ZG***, Yang JF*. Duodenal Ferroportin Is Up-Regulated in Patients with Chronic Hepatitis C. PLOS ONE.2014, 9(10):e110658.

75. **Ma PC**, **Yang XC**, **Kong QH**, **Li CC**, **Yang SJ**, Li Y, **Mao BY***. The Ubiquitin Ligase RNF220 Enhances Canonical Wnt Signaling through USP7-Mediated Deubiquitination of -Catenin. MOL CELL BIOL. 2014,34(23):4355-4366.

76. Ma W, Zhu ZH, Bi XY, **Murphy RW**, Wang SY, **Gao Y**, Xiao H, **Zhang YP**, Luo J*. Allopolyploidization is Not So Simple: Evidence from the Origin of the Tribe Cyprinini (Teleostei: Cypriniformes). CURR MOL MED.2014, 14(10):1331-1338.

77. **Ma ZS***, Yang LX, Neilson RP, Hess A, Millar R. A Survivability-Centered Research Agenda for Cloud Computing Supported Emergency Response and Management Systems. The 35th IEEE-AIAA Aerospace Conference.

78. Manriquez-Moran*, Norma L,Mendez-de la Cruz, Fausto R, **Murphy RW**. Genetic Variation and Origin of Parthenogenesis in the Aspidoscelis cozumela Complex: Evidence from Mitochondrial Genes. ZOOL STUD.2014, 31(1):14-19.

79. **Mao BY***, Wu W. More or less is fine：An undercover work of DKK1 in anthrax toxin uptake. SCI CHINA LIFE SCI.2014, 57(7):735-736.

80. Mu D, Yang H, Zhu JW, Liu FL, Tian RR, Zheng HY, Han JB, **Shi P***, Zheng YT*. Independent Birth of a Novel TRIMCyp in Tupaia belangeri with a Divergent Function from Its Paralog TRIM5. MOL BIOL EVOL.2014, 31(11):2985–2997.

81. **Nguyen SN, Yang JX**, Le TN, Nguyen LT, Orlov NL, Hoang CV, Nguyen TQ, **Jin JQ, Rao DQ**, Hoang TN, **Che J**, **Murphy RW***, **Zhang YP**. DNA barcoding of Vietnamese bent-toed geckos (Squamata: Gekkonidae: Cyrtodactylus) and the description of a new species. ZOOTAXA.2014, 3784(1):48-66

82. Hou M, Wu YK, Yang KL, Zheng S, **Yuan ZY**, Li PP*. A missing geographic link in the distribution of the genus Echinotriton (Caudata: Salamandridae) with description of a new species from southern China. ZOOTAXA.2014, 3895(1):89-102.

83. **Ni G**, Li Q*, Kong L, Yu H. Comparative phylogeography in marginal seas of the northwestern Pacific. MOL ECOL.2014, 23(3):534-548.

84. **Ni QY**, **Huang B**, Liang ZL, Wang XW, **Jiang XL*** .Dietary Variability in the Western Black Crested Gibbon (Nomascus concolor) Inhabiting an Isolated and Disturbed Forest Fragment in Southern Yunnan, China. AM J PRIMATOL.2014, 76:217–229.

85. **Ning T**, Li J, Lin K, Xiao H, Wylie S, Hua S, Li H*, **Zhang YP***. Complex Evolutionary Patterns Revealed by Mitochondrial Genomes of the Domestic Horse. CURR MOL MED.2014, 14(10):1286-1298.

86. **Orkin JD***. Landscape genetics of western Black Crested Gibbons (Nomascus concolor) in China. AM J PHYS ANTHROPOL.2014, 153:200-201.

87. Palanichamy MG* ,Mitra B,Debnath M ,Agrawal S ,Chaudhuri TK ,**Zhang YP***. Tamil Merchant in Ancient Mesopotamia. PLOS ONE.2014, 9(10):e109331.

88. Peng LF，Lu CH, **Huang S**, Guo P, **Zhang YP***. A New Species of the Genus Thermophis (Serpentes: Colubridae) from Shangri-La, Northern Yunnan, China, with a Proposal for an Eclectic Rule for Species Delimitation. ASIAN HERPETOL RES.2014, 5(4):228-239.

89. **Peng MS**, **He JD**, Fan L, **Liu J**, **Adeola AC**, **Wu SF**, **Murphy RW**, Yao YG, **Zhang YP***. Retrieving Y chromosomal haplogroup trees using GWAS data. EUR J HUM GENET.2014, 22:1046-1050.

90. Pierson TW*, **Yan F**, Wang Y, Papenfuss T. A survey for the Chinese giant salamander (Andrias davidianus; Blanchard, 1871) in the Qinghai Province.AMPHIBIAN AND REPTILE CONSERVATION. 8(1):1-6.

91. **Qi XB**, Cui C, Ouzhuluobu, Wu T, **Su B***. Prehistoric Colonization and Demographic History of Modern Humans on the Tibetan Plateau. In. eLS: John Wiley & Sons.2014, 30 (8): 1761-1778.

92. Qu JG, Rizak JD, Fan YD, Guo XX, **Li JJ**, Huma T, Ma YY*.Establishment and partial characterization of a human tumor cell line, GBM-HSF, from a glioblastoma multiforme. HUM CELL.2014. 27(3):129-136.

93. **Qu KX**, He ZX, Hao RJ, Zhang JC, Huang BZ, Zan LS, **Zhang YP***. A new high-frequency allele of the BM2113 locus in the Yunnan mithun population. GENET MOL RES.2014, 13(1):2155-2159.

94. Scott IM, Clark AP, Josephson SC, Boyette AH, Cuthill IC, Fried RL, Gibson MA, Hewlett BS, Jamieson M, Jankowiak W, Honey PL, Huang Z, Liebert MA, Purzycki BG, Shaver JH, Snodgrass JJ, Sosis R, Sugiyama LS, Swami V, **Yu DW**, Zhao Y, Penton-Voak IS*. Human preferences for sexually dimorphic faces may be evolutionarily novel. P NATL ACAD SCI USA.2014, 111(40):14388-93..

95. **Shen YY***, Dai K, **Cao X**, **Murphy RW**, Shen XJ, **Zhang YP***. The Updated Phylogenies of the Phasianidae Based on Combined Data of Nuclear and Mitochondrial DNA. PLOS ONE.2014, 9(4):e95786.

96. **Shi L**, **Lin Q**, **Su B***. Human-specific hypomethylation of CENPJ, a key brain size regulator. MOL BIOL EVOL.2014, 31(3): 594-604.

97. **Shi NN**, Fan L, Yao YG, **Peng MS***, **Zhang YP***. Mitochondrial Genomes of Domestic Animals Need Scrutiny. MOL ECOL.2014, 23:5393-5397.

98. Su RR, Wang A, Hou ST, Gao P, Zhu GP*, **Wang W***. Identification of a novel fumarase C from Streptomyces lividans TK54 as a good candidate for malate production. MOL BIOL REP.2014, 41 (1):497-504.

99. Sun HY, Qian Q, Wu K, Luo J, Wang S, Zhang C, Ma Y, Liu Q, Huang X, Yuan Q, Han R, Zhao M, Dong G, Guo L, Zhu X, **Gou ZH**, **Wang W**, Wu Y, Lin H, Fu XD*. Heterotrimeric G proteins regulate nitrogen-use efficiency in rice. NAT GENET.2014, 46 (6):652-656.

100. Sun SJ*, Jiang P, **Su WT**, Xiang Y, Li J, Zeng L, **Yang SJ**. Wild chrysanthemum extract prevents UVB radiationinduced acute cell death and photoaging. CYTOTECHONOLOGY. 2014, 64:95–105.

101. **Tan T**, Zhang YF, Ji WZ*, **Zheng P***. miRNA Signature in Mouse Spermatogonial Stem Cells Revealed by High-Throughput Sequencing. BIOMED RESEARCH INTERN ATIONAL. 2014, 154251.

102. Tang XS, Chen JM, **Huang S***.Mitochondrial genome of the Chung-an ground lizard Takydromus sylvaticus (Reptilia: Lacertidae). MITOCHONDR DNA.2014, 25(4):319-320.

103. Tosser-Klopp G*, Bardou P, Bouchez O, Cabau C, Crooijmans R, **Dong Y**, Donnadieu-Tonon C, Eggen A, Heuven HC, Jamli S, Jiken AJ, Klopp C, Lawley CT, McEwan J, Martin P, Moreno CR, Mulsant P, Nabihoudine , Pailhoux E, Palhière I Rupp R, Sarry J Sayre BL, Tircazes A, Jun Wang, Wang W, Zhang W; International Goat Genome Consortium. Design and Characterization of a 52K SNP Chip for Goats. PLOS ONE.2014, 9 (1):10.1371.

104. **Wang B**, Geng XZ, Ma LB, Cook JM, **Wang RW***.A trophic cascade induced by predatory ants in a fig-fig wasp mutualism. J ANIM ECOL.2014, 83(5):1149-1157.

105. **Wang GD**, Fan RX, Zhai W, **Liu F**, Wang L, Zhong L, Wu H, **Yang HC**, **Wu SF**, **Zhu CL**, Li Y, **Gao Y**, Ge RL, Wu CI, **Zhang YP***. Genetic Convergence in the Adaptation of Dogs and Humans to the High-Altitude Environment of the Tibetan Plateau. GENOME BIOL EVOL.2014, 6(8):2122-2128.

106. **Wang GD**, **Xie HB**, **Peng MS**, Irwin D, **Zhang YP***.Domestication Genomics: Evidence from Animals. ANNUAL REVIEW OF ANIMAL BIOSCIENCES.2014, 2(2):65-84.

107. Wang RR, Yang QH, Luo RH, Peng YM, Dai SX, Zhang XJ, Chen H, **Cui XQ**, Liu YJ, Huang JF, Chang JB*, Zheng YT. Azvudine, A Novel Nucleoside Reverse Transcriptase Inhibitor Showed Good Drug Combination Features and Better Inhibition on Drug-Resistant Strains than Lamivudine In Vitro. PLOS ONE.2014, 9(8): e105617.

108. **Wang RW***, **Yang Y**. Wiggins NL. Asymmetric or diffusive co-evolution generate meta-populations in fig-fig wasp mutualisms. SCI CHINA LIFE SCI.2014, 57(6): 596-602.

109. **Wang RW***, Dunn DW, Sun BF. Discriminative host sanctions in a fig-wasp mutualism. ECOLOGY.2014, 95(5):1384-1393.

110. Wang SQ, Zhao H*, **Zhang YP**. Advances in research on Shadoo, shadow of prion protein. CHINESE SCI BULL.2014, 59(9):821-827.

111. Wang WJ, Dai CY, Alström P, Zhang CL, Qu YH, Li SH, **Yang XJ**, Zhao N, Song G, Lei FM*.Past hybridization between two East Asian long-tailed tits (Aegithalos bonvaloti and A. fuliginosus). FRONT ZOOL.2014, 11:40.

112. Wang YJ, Guo XL, Li SA, **Zhao YQ**, Liu ZC, Lee WH, Xiang Y*, Zhang Y*. Prohibitin is involved in the activated internalization and degradation of protease-activated receptor 1. BBA-MOL CELL RES.2014, 1843(7):1393-1401.

113. **Wang YQ**, Li YT, **Wang RW***. The optimal sex ratio in cooperatively breeding populations. CHINESE SCI BULL.2014, 59(35):5047-5079.

114. **Xiao J**, Zhong H, Zhou Y, Yu F, **Gao Y**, Luo Y, Tang Z, Guo ZB, Guo EY, Gan X*, Zhang M*, **Zhang YP**. Identification and Characterization of MicroRNAs in Ovary and Testis of Nile Tilapia (Oreochromis niloticus) by Using Solexa Sequencing Technology. PLOS ONE.2014, 9(1):e86821.

115. Xu HF, **Liu YW**, Wang F, Yuan L, Wang YC, Ma SY, Benes H, Xia QY*. Overexpression and functional characterization of an Aspergillus niger phytase in the fat body of transgenic silkworm, Bombyx mori. TRANSGENIC RES.2014, 23, (4):669-677.

116. **Yang CX**, **Wang XY**, Miller JA, de Blécourt M, **Ji YQ**, **Yang CY**, Harrison RD, **Yu DW***. Using metabarcoding to ask if easily collected soil and leaf-litter fauna can be used as a general biodiversity indicator. ECOL INDIC.2014, 46, 379-389.

117. Yang JK, **Gong YY**, **Xie L**, Yang Y, Xu LY, **Zhang YP***. Association study of promoter polymorphisms in the CETP gene with longevity in the Han Chinese population. MOL BIOL REP.2014, 41(1):325-329.

118. Yang JK, Wu WJ, He L*, **Zhang YP***. Genotype-Phenotype Correlations in Severe Acne in a Han Chinese Population. DERMATOLOGY.2014, 229(3):210-214.

119. Yang JK, Wu WJ, Qi J, He L, **Zhang YP***. TNF-308 G/A Polymorphism and Risk of Acne Vulgaris: A Meta-Analysis. PLOS ONE.2014, 9(2):e87806.

120. **Yang LX**, Zhang R, **Li M**, Wu X, Wang J, Huang L, Shi X, Li QB, **Su B***. A Functional MiR-124 Binding-Site Polymorphism in IQGAP1 Affects Human Cognitive Performance. PLOS ONE.2014, 9 (9):e107065.

121. Yu XJ, Yi Z, Gao Z, Qin D, Zhai Y, Chen X, Ou-Yang Y, Wang ZB, **Zheng P**, Zhu MS, Wang H, Sun QY, Dean J*, Li L. The subcortical maternal complex controls symmetric division of mouse zygotes by regulating F-actin dynamics. NAT COMMUN.2014, 5,4887.

122. **Yuan ZY**, Zhao HP, **Jiang K**, Hou M, He LZ, **Murphy RW**, **Che J*** .Phylogenetic Relationships of the Genus Paramesotriton (Caudata: Salamandridae) with the Description of a New Species from Qixiling Nature Reserve, Jiangxi, Southeastern China and a Key to the species. ASIAN HERPETOL RES.2014, 5(2):67–79.

123. Zhang D, Qi J, Yue J, Huang J, Sun T, Li S, **Wen JF**, Hettenhausen C, Wu J, Wang L, Zhuang H, Wu J, Sun GL*. Root parasitic plant Orobanche aegyptiaca and shoot parasitic plant Cuscuta australis obtained Brassicaceae-specific strictosidine synthase-like genes by horizontal gene transfer. BMC PLANT BIOL.2014, 14:19.

124. Zhang HQ, Teng JH, Li Y, Li XX, **He YH**, He X, Sun CH*. Vitamin D status and its association with adiposity and oxidative stress in schoolchildren. NUTRITION.2014, 30(9): 1040-1044.

125. Zhang Q, **Su B***. Evolutionary origin and human-specific expansion of a cancer/testis antigen gene family. MOL BIOL EVOL.2014, 31(9): 2365-2375.

126. Zhang W, Tang J, Zhang AM, **Peng MS**, **Xie HB**, Tan L, Xu L, **Zhang YP**, Chen XG*, Yao YG. A Matrilineal Genetic Legacy from the Last Glacial Maximum Confers Susceptibility to Schizophrenia in Han Chinese. J GENET GENOMICS.2014, 41(7): 397-407.

127. Zhang W, Xiao MS, **Ji S**, Tang J, Xu L, Li X, Li M, Wang HZ, Jiang HY, Zhang DF, Wang J, Zhang S, Xu XF, Yu L, **Zheng P**, Chen X, Yao YG*. Promoter variant rs2301228 on the neural cell adhesionmolecule 1 gene confers risk of schizophrenia in Han Chinese. SCHIZOPHR RES.2014, 160(1): 88-96.

128. **Zhang XM**, Kampuansai J, **Qi XB**, Yan S, **Yang ZH**, Serey B, Sovannary T, Bunnath L, Aun HS, Samnom H, Kutanan W, Luo XJ, Liao S, Kangwanpong D, Jin L, **Shi H***, **Su B***. An updated phylogeny of the human Y-chromosome lineage O2a-M95 with novel SNPs. PLOS ONE.2014, 9 (6): 0101020.

129. Zhang XO, Yin QF, Wang HB, Zhang Y, Chen T, **Zheng P**, Lu X, Chen LL*, Yang L. Species-specific alternative splicing leads to unique expression of sno-lncRNAs. BMC GENOMICS.2014, 15;287.

130. **Zhang YJ**, Yang CL, Hao YJ, Li Y, Chen B, **Wen JF***. Macroevolutionary trends of atomic composition and related functional group proportion in eukaryotic and prokaryotic proteins. GENE.2014, 534 (2): 163-168

131. **Zhang ZG**, Geng J, Tang X, Fan H, Xu J, Wen X, **Ma ZS***, **Shi P***. Spatial heterogeneity and co-occurrence patternsof human mucosal-associated intestinal microbiota. The ISME Journal.2014, 8, 881–893.

132. **Zhang ZM**, Shi Y, **Zhao SH**, **Li JJ**, **Li CC**, **Mao BY***. Xenopus Nkx6.3 is a neural plate border specifier required for neural crest development. PLOS ONE.2014, 9(12): e115165.

133. Zhao HP, Kong XH, **Zhou CJ***. The mitogenome of Pangasius sutchi (Teleostei, Siluriformes: Pangasiidae). MITOCHONDR DNA.2014, 25(5):342-344.

134. **Zhao YJ**, Zeng Y, **Chen L**, **Dong Y**, **Wang W***. Analysis of transcriptomes of three orb-web spider species reveals gene profiles involved in silk and toxin. INSECT SCI.2014, 21(6): 687-698.

135. **Zhao YQ**, Ji S, Wang J, **Huang JF***, **Zheng P***. mRNA-Seq and MicroRNA-Seq Whole-Transcriptome Analyses of Rhesus Monkey Embryonic Stem Cell Neural Differentiation Revealed the Potential Regulators of Rosette Neural Stem Cells. DNA Res.2014, 21(5):541-54.

136. **Zhong L**, Tang J, **Kong QP***, Sun C, **Zhou WP**, Yang M, Yao YG, **Zhang YP***. Reappraising the Relationship Between Mitochondrial DNA Variant m.16189T > C and Type 2 Diabetes Mellitus in East Asian Populations. CURR MOL MED.2014, 14(10): 1273-1278.

137. **Zhou CJ**, Wang X, Wang D, He SP*. The complete mitochondrial genome of Leiocassis crassilabris (Teleostei, Siluriformes: Bagridae). MITOCHONDR DNA.2014, 25(3):183-184.

138. Zhou HY, **Wang HW**, Tan SN, Chen Y, Wang WL, Tao HX, Yin ZC, Zou YH, Ouyang SM, Ni B*. Genetic affinities of central China populations. GENET MOL RES.2014, 13(1): 616-625.

139. **Zhou TC**, Shen X, **Irwin DM**, **Shen YY***, **Zhang YP***. Mitogenomic analyses propose positive selection in mitochondrial genes for high-altitude adaptation in galliform birds. MITOCHONDRION.2014, 18:70-75.

140. **Zhou WW**, **Zhang BL**, **Chen HM**, **Jin JQ**, **Yang JX**, **Wang YY**, **Jiang K**, **Murphy RW**, **Zhang YP***, **Che J***. DNA barcodes and species distribution models evaluate threats of global climate changes to genetic diversity: a case study from Nanorana parkeri (Anura: Dicroglossidae). PLOS ONE.2014, 9(8):e103899.

141. **Zhou ZY**, Li AM, **Adeola AC**, Liu YH, **Irwin DM**, **Xie HB**, **Zhang YP***. Genome-Wide Identification of Long Intergenic Noncoding RNA Genes and Their Potential Association with Domestication in Pigs. GENOME BIOL EVOL.2014, 6(6):1387-1392.

142. Zou T, **Zhang ZG**, Zou C, Chen K, Dai Y, Tong J, Yu X, Liu J, Chen D, Xu H, Shi H, Wang Z, Wu S, Sun C, Cui W, Chen H, Yu J, Yang JF*. Subclinical infections of cardiac implantable electronic devices: Insights into the host-bacteria dialog from blood and pocket tissue with pyrosequencing. INT J CARDIOL.2014, 174（3）：545-549.

143. **陈兵，文建凡** *. 血吸虫的寄生适应性研究及其应用价值．中国血吸虫病防治杂志 .2014, 26（1）：84-89.

144. **陈鹏，王应祥，林苏，蒋学龙** *. 中国兽类新纪录—耐氏大鼠 Leopoldamys neilli. 四川动物 .2014, 33:858-864.

145. 刘铁，许金山，李田，潘国庆，何强，**李学燕** *，周泽扬．从金凤蝶分离的一株微孢子虫的全基因组 MITEs 转座子鉴定与系统进化分析．蚕业科学．2014，400(1):0052-0058

获奖 Awards

2014 张亚平，孔庆鹏，吴东东，彭旻晟，孙昌。国家自然科学奖二等奖（基因组多样性与亚洲人群的演化）

2014 Yaping Zhang, Qingpeng Kong, Dongdong Wu, Mingsheng Peng, Cang Sun. The second prize for State Natural Science Award.(Genomic Diversity and Evolution of Asian Populations.)

该成果以基因组多样性的分布格局及形成机制为视角，以亚洲人群为对象，紧紧围绕"亚洲人群源流历 史和演化"这一核心目标，取得一系列重要研究成果：证明亚洲人群源自"走出非洲"后沿亚洲海岸线的快速迁移扩散事件，证实东亚人群起源于非洲且无当地直立人的母系遗传贡献，揭示早期人群迁移及文化扩散是亚洲民族人群形成的重要原因，并诠释人群对新环境适应的遗传学机制。 以第一单位发表高影响 SCI 论文 20 篇，被 Nature、Science 等国际著名 SCI 刊物正面他引 602 次，国际影响广泛。

2014 宿兵研究员入选云南省首批"云岭学者"人才培养工程

2014 Prof. Bing Su was selected into the first "Yunling Scholar" talent Training Project in Yunnan Province.

2014 孔庆鹏研究员荣列科技部中青年科技创新领军人才入选名单

2014 Prof. Qingpeng Kong was selected as "Young and middle-aged leading talent in Science and Technology " of MOST.

2014 施鹏研究员荣获王宽诚西部学者突出贡献奖，吴东东副研究员荣获王宽诚卢嘉锡青年人才奖

2014 Prof. Peng Shi was awarded as "The outstanding contribution prize in Wang kuancheng western scholars, Chinese academy of sciences (CAS)". Dr. Dongdong Wu was awarded as "Lu Jiaxi Youth Talent Award".

2014 王国栋和石磊入选 2015 年度中国科学院青年创新促进会会员

2014 Guodong Wang and Lei Shi were selected as members of the Young Innovators Association of CAS.

2014 王国栋入选第十七批省中青年学术和技术带头人后备人才培养对象

2014 Guodong Wang was selected into the Seventeenth Installment of Young Academic and Technical Leader Reserve Personnel Training Project.

2014 宿兵研究员、王文研究员被评为中国科学院优秀研究生指导教师，车静研究员获朱李月华优秀教师奖。

2014 Profs. Bing Su and Wen Wang were awarded Outstanding Graduate Student's Instructor of CAS. Prof. Jing Che was awarded "Zhu Li Yuehua Outstanding Instructor of CAS".

昆明野生动物细胞库

昆明野生动物细胞库成立于 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 323 种动物的细胞系 1777 株 10000 余份。大多数为哺乳动物的细胞系，其中包括 59 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、中国科学院野生生物资源库、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. Sun SJ, Jiang P, **Su WT**, Xiang Y, Li J, Zeng L, Yang SJ. Wild chrysanthemum extract prevents UVB radiationinduced acute cell death and photoaging. Cytotechnology 2014, 64: 95–105.

2. Li SB, Li B, Chang C, Xiong ZJ, Liu QB, Lai JH, Carey HV, Zhang Q, Zheng HB, Wei SG, Zhang HB, Chang L, Liu SP, Zhang SX, Yu B, Zeng XF, Hou Y, **Nie WH**, Guo YM et al. Genomic signatures of near-extinction and rebirth of the crested ibis and other endangered bird species. *Genome Biology* 2014 15:557.

2014 年主要工作进展

2014 年度，野生动物细胞库利用从野外采集以及从其他途径获得的动物材料，共新建各类动物细胞系 88 株，其中包括非洲狮、马来熊、高原鼢鼠、鼠兔、弓鱼、箭鱼、巨须裂腹鱼、双须裂腹鱼、沙蜥等 9 种野生动物的细胞系 23 株，9 种家养动物和实验动物的细胞系 39 株，EBV 转化的人淋巴细胞系 11 株以及人和动物的肿瘤细胞系 15 株；复苏和扩增各类动物细胞系 374 株；为遗传资源与进化国家重点实验室及全国各地的研究人员提供细胞服务 370 株次；提供核型分析、支原体检测和荧光检测等技术服务 14 次。

在今年的工作中，我们重点进行了鱼类稳定传代细胞培养体系的建立。培养的鱼类细胞已被广泛应用于许多生物学研究，特别是用于病毒的检测。由于鱼类细胞培养温度低于哺乳动物细胞，生长缓慢，建系周期长，目前在我们野生动物细胞库中已成功建系的鱼类细胞系并不多，与其丰富的种类资源相比，差距巨大。为了收集和保藏更多的鱼类细胞系，野生动物细胞库，在去年成功建立了一株能在体外稳定传代的斑马鱼细胞系的基础上，进一步优化了鱼类稳定细胞系建立的取材方法、培养条件等，今年成功建立了五种鱼类不同组织（尾鳍、鳃和吻）的细胞系 10 株，并用培养的细胞进行了不同鱼类的核型分析。为今后开展鱼类的研究奠定了基础。

巨须裂腹鱼 (Schizothorax macropogon)

培养的巨须裂腹鱼细胞

另外，我们再次为大额牛的基因组测序提供三个个体的大额牛皮肤成纤维细胞，同时通过微创取样后进行细胞培养为课题组完成了三个已取样大额牛个体的核型分析，满足了课题组的研究需求。

Kunming Wild Animal Cell Bank

In order to conserve genetic resource and genetic diversity of animals, Kunming wild animal cell bank was established in Kunming Institute of Zoology, Chinese Academy of Science in 1986. Up to now 1777 cell lines belonging to 323 species have been preserved in our cell bank. Most cell lines are derived from mammals. Among the species, 59 are national protected wildlife in China. Now it is one branch of National Platform of Experimental Cell Resources for Sci-Tech, Wildlife Resource Bank of CAS, China Germplasm Bank of Wild Species, and State Key Laboratory of Genetic Resources and Evolution.

The main work in 2014

In 2014, We have established and frozen 88 cell lines from various wild and domestic animals. Among these cell lines, 23 cell lines are derived from 9 species of wild animals such as African lion, sun bear, plateau zokor, pika etc; 39 cell lines are established from 9 species of domestic animals and experimental animals; 11 cell lines are obtained by EBV-transferred human lymphocytes; and 15 cell lines are tumor cell lines from human and other animals. Three hundred and seventy-four of frozen-stored cell lines were also resuscitated and subcultured. In this year, the cell bank provided 370 cell lines and 14 times of technical service such as karyotype analysis, mycoplasma contamination test and Fluorescence detection for the researchers not only at State key laboratory of genetic resources and evolution, but also at other Chinese universities and scientific research institutions.
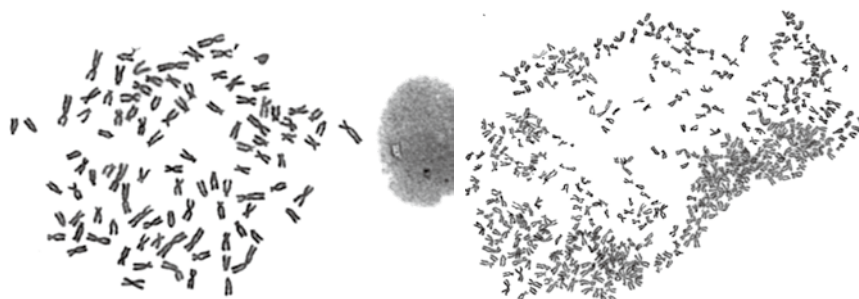
The metaphase of S. macropogon

The metaphase of Ptychobarbus dipogon

In the work of this year, an important work that we have done is establishing the stable cell culture system for various fish species. Cultured fish cells have been application in many fields of biological research, such as being used for viral diagnostic purposes. Unlike mammalian cell cultures, the fish cells survive and thrive with infrequent subculture (7-14 days or more) and require changes of the culture temperature and the salt concentration in various of fish species. In our cell bank, there are few fish cell lines. There are large gaps between the abundance fish species resource and the amount of established fish cell lines. In order to collect more fish cell lines, we further optimized the fish cell culture system including the method for taking the tissue and the culture conditions based on the method for establishing the cell line of zebra fish, and successfully established ten cell lines from different tissues (fin, gill and lip) of five fish species. Karyotype analyses were done in various fish species using cultured cells. The establishment of these cell lines would lay the foundation for future studies on fish.

In addition, after 2013, we provided cell lines from three gayal individuals for the research group to do the gayal genome sequencing again. We also finished the karyotype analyses of another three gayal individuals that they had taken the tissues by primary cell culturing. This work made sure that the sequencing species were right, and met their requirements.

员工简介（Lab Staff）
工作人员（Staff）

佴文惠　正高级工程师
Wenhui Nie
Senior Engineer
whnie@mail.kiz.ac.cn

王金焕　高级实验师
Jinhuan Wang
Senior Experimentalist
wangjing315@163.com

苏伟婷　实验师
Weiting Su
Experimentalist
weitingsu@126.com

胡　怡　技术员
Yu Hu
Technician
524140624@qq.com

生命条形码南方中心

生命条形码南方中心于 2011 年成立，专门从事 DNA 条形码相关的科学研究、技术革新和应用推广。日常支撑工作包括：服务于国内外科研人员，开展 DNA 条形码测序实验；针对国内外的学员开展 DNA 条形码技术培训；DNA 条形码的数据提交和管理；动物遗传资源采集；管理种质资源库动物分库；开展利用 DNA 条形码技术的司法鉴定；与国家重点实验室的课题组合作，进行相关的科学研究等。

论著 Publications

Wei-wei Zhou, Bao-lin Zhang, Hong-man Chen, Jie-qiong Jin, Jun-xiao Yang, Yun-yu Wang, Ke Jiang, Robert W. Murphy, Ya-ping Zhang, Jing Che, 2014. DNA Barcodes and Species Distribution Models Evaluate Threats of Global Climate Changes to Genetic Diversity: A Case Study from Nanorana parkeri (Anura: Dicroglossidae). Plos one. Aug 5;9(8):e103899.

1.DNA 条形码技术在肉制品鉴别中的应用

2014 年 10 月 9 日上午，由中科院昆明动物所生命条形码南方中心主持召开"DNA 条形码技术在肉制品鉴别中的应用"项目启动会。正式启动了中科院与地方科学院合作，以 DNA 条码技术为核心，应用于食品鉴定的开创性项目。

食品安全是国家安全战略的一部分，DNA 条形码技术实现了鱼肉和主要畜禽肉类来源快速检测的关键技术。2014 年围绕该项目，部门已经检测贵州科学院送检市场肉类样品 144 份，取得一批示范性应用成果，获得社会的广泛赞誉。并对贵州省分析测试院的技术人员进行了两次 DNA 条形码标准试验培训。

2. 基于自然保护区的 DNA 条形码

SCDBC 和生态与环境保护中心合作的科技基础性工作专项"基于自然保护区的 DNA 条形码"于 2012 年正式启动，该项目将 DNA 条形码工作同自然保护区生物多样性考察结合起来。

项目组 2014 年召开了第二次年度会议，项目组成员着眼于自然保护区，进一步推进保护区在生物多样性保护中的作用，基于项目产生的大量数据为保护区今后的工作提供支持和建议，并探索南北两个保护区生物多样性分布的异同点、梯度变化形成的原因等。

根据会议要求，生命条形码南方中心开展了三次高黎贡山的无脊椎动物样品采集，设置了 2 个梯度 6 块马氏网监测样地开展周期性定点采集，并对不同梯度的样品进行标记和统计。2014 年度一共采集得无脊椎动物超过 40000 份。

Southern China DNA Barcoding Center

In the year of 2014, the SCDBC collected over 40K specimens in wild field, got over 10K standard DNA barcodes, and uploaded 4716 standard data to Chinese DNA barcoding database and/or Barcoding of Life System.

The SCDBC promoted the mitogenomics technologies which was based on the next generation Ion Torrent platform, and shed lights on food species traceability, and co-hosted the fifth international barcode of life conference in Kunming

3. SCDBC moved to new building

SCDBC moved to the new southwest biodiversity laboratory building in August 2014. With the high equipped facility, including two Hamilton ML STAR workstations, ABI 3730xl sequencer, Eppendorf thermo cycler array and high performed computer, SCDBC enhanced the barcoding ability to 500 specimens per day.

4. A universal and effective NGS mitogenomics solution utilizing the long PCR fragments.

工作人员 Staff

王文智 助理研究员
Wen-zhi Wang
Assistant Research Fellow

王运宇 实验师
Yun-yu Wang
Engineer
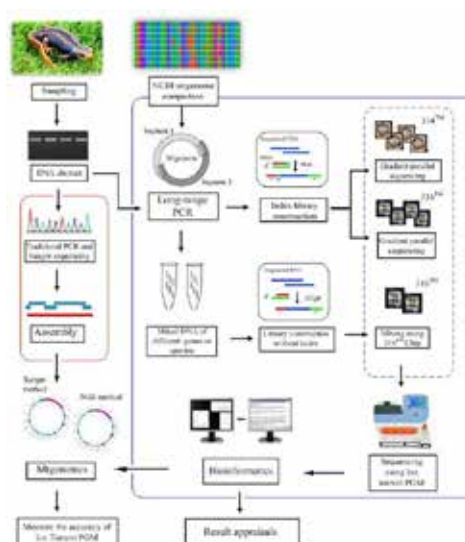
李宗煦 研究实习员
Zong-xv Lee
Fellow

陈 兴 研究实习员
Xing Chen
Fellow

王玉水 助理实验师
Yu-shui Wang
Technician

刘 浏 助理实验员
Liu Liu
Technician

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/

工作人员 （Staff）

许绍斌　工程师
Mr. Shaobin Xu
Engineer
xushao@mail.kiz.ac.cn

唐　嘉　工程师
Mrs. Jia Tang
Engineer
tangj@mail.kiz.ac.cn

李桂梅　实验师
Mrs. Guimei Li
Experimentalist
liguimei246@mail.kiz.ac.cn

杨双娟　助理实验师
Ms. Shuangjuan Yang
Assistant Experimentalist
yangsj@mail.kiz.ac.cn

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．高性能计算平台

该平台是采用曙光 4000A 为基础的 Linux 高性能计算机群，机群由 39 个曙光 620 机架服务器和 1 个 DELL R910 服务器（512 GB 内存胖节点）组成。机群具有每秒 2.929 万亿次的峰值速度。在线存储采用具有 40GB 缓存 20TB 总容量的 Panasas 8 系列并行存储，可以支持高吞吐率的并行 IO。系统使用 Torque2.4.8 和 maui3.3 作为机群作业调度管理软件，可以支持 288 个计算核的并行计算作业。

Core Facility

The Core Facility of the State Key Laboratory of Genetic Resources and Evolution is established in November 2008. Currently, the center contains three major technology platforms: Genomic Analysis Platform, Proteomic Analysis Platform, and High Performance Computing Platform. Each platform is supported by professional technicians, from the experimental design, instrument operation, to data analysis.
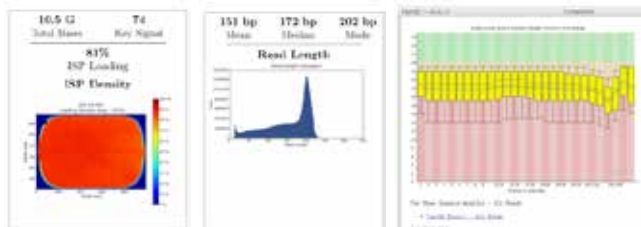
http://www.kiz.cas.cn/gre/gre6/gre61/

The Three Technical Platforms

I. Genomic Analysis Platform

1. Ion Torrent Sequencers

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


2. Miseq Sequencer

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

### 3. QuantStudio 12K Flex Real-Time PCR System

QuantStudio 12K Flex Real-Time PCR System is new level for qPCR, designed for maximum throughput, flexibility, and scalability. You can choose not only OpenArray®, 384-well, 96-well blocks for your experiments, but also digital PCR for high accuracy and sensitivity.
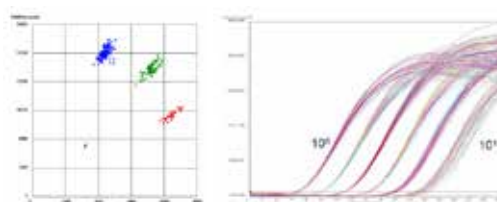
### 4. Roche LightCycler 480

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.
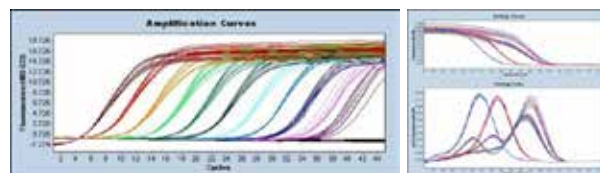
II. Proteomic Analysis Platform

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.
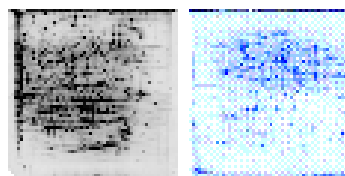
III. High Performance Computing Platform

The HPC is a 2.929 TFlops linux cluster consists of 39 servers from dawning (now Sugon) and one huge memory(512GB RAM) R910 server from DELL.A set of 20TB raw volume size high performance PAS8 from Panasas serves as the online storage. Torque and Maui were used to manage the job scheduling system, thus it can support parallel computing jobs scale up to 288 CPU cores. Now we have more than 95 users from KIZ and some other partners such as Yunnan University. The accumulated used walltime is over 1million CPU hours. At the end of 2011 there were more than 60 bioinformatics software such as Qiime ,RaxML installed.
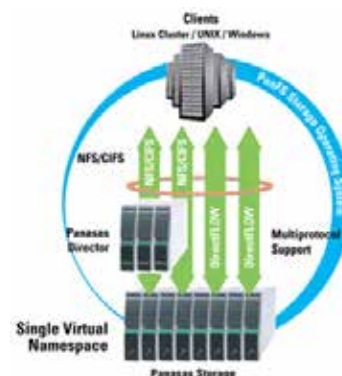
参加学术会议（Attended Scientific Meetings）

序号	报告名称	报告人	会议名称	地点	会议时间
1	发育的印迹调控	焦保卫	云南省"六学会"2014 年新春联谊会暨学术交流会	丽 江	2014.1.23–24
2	Sex–specific epigenetic regulation of mammary gland by the RLIM/Rnf12 in mice	焦保卫	遗传学与表观遗传学前沿暨第三届中国青年遗传学家论坛	镇 江	2014.4.11–14
3	Genetic Evidence of Paleolithic Colonization and Neolithic Expansion of Modern Humans on the Tibetan Plateau	祁学斌	第十届国际高原医生生理学与高山急救大会	意大利 Bolzano	2014.5.24–6.2
4	藏族人群对高原低氧的遗传适应机制	宿 兵	第十届国际高原医生生理学与高山急救大会	意大利 Bolzano	2014.5.24–6.2
5	Secreted and full length EphA7 regulates pronephors development through modulating claudin6 level and apical actin accumulation in Xenopus	毛炳宇	第二届全国发育生物学大会	兰 州	2014.10.16
6	Detecting mammals and counting bees with DNA	Douglas W Yu	中国动物学会第十七届全国会员代表大会暨学术讨论会	中 山	2014.11.19
7	贾第虫兼具原始性和寄生适应性的奇特甘油磷脂合成途径及其对该生物特殊进化地位的提示	叶青青	中国动物学会第十七届全国会员代表大会暨学术讨论会	广 州	2014.11.17–11.20
8	藏族人群对高原低氧的遗传适应机制	宿 兵	中德高原肺动脉高压的致病机理与高原低氧适应的遗传基础双边研讨会	德国吉森大学	2014.11.24–11.29
9	青藏高原史前人类定居与群体动态变化历史的遗传学证据	祁学斌	中德高原肺动脉高压的致病机理与高原低氧适应的遗传基础双边研讨会	德国吉森大学	2014.11.24–11.29
10	面向三代测序技术的新一代基因组装演算法及其医学生态学进展	马占山	中科院／"中研院"第二届"海峡两岸生命科学论坛"	台 湾	2014.11.29–12.4

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）
GREKF14-01	Nikolay A. Poyarkov	讲 师	Lomonosov Moscow State University	蛙属（Ranidae Rana）系统发育与全北区物种多样性差异形成机制研究	10
GREKF14-02	胡继宏	讲 师	武汉大学	云南涛源水稻超高产的表观遗传调控研究	10
GREKF14-03	李 英	研究员	四川农业大学	人群长寿机制研究：肠道微生物视角	10
GREKF14-04	于 黎	教 授	云南大学	滇金丝猴高海拔适应分子机制的基因组学研究	10
GREKF14-05	苏晓三	副研究员	昆明市第一人民医院	遗传印迹对乳腺发育的调控机制研究	10
GREKF14-06	温秀军	教 授	华南农业大学	人体宏基因组与疾病健康关系的生物信息学研究	10
GREKF14-07	王 波	助理研究员	中国科学院西双版纳热带植物园	捕食性蚂蚁与榕－蜂共生系统直接、间接效应的化学通讯机制	10
GREKF14-08	王震波	副 研	中国科学院动物研究所	人类大脑进化关键基因 MCPH1 和 FOXP2 的转基因动物研究	10
GREKF14-09	崔超英	教 授	西藏大学	藏族人群对高原低氧环境长期适应的多基因互作机制研究	10
GREKF14-10	李 艳	研究员	中国科学院昆明植物研究所	几个小分子 Wnt 信号抑制剂的作用机制研究	10
GREKF14-11	秦 燕	讲 师	莱芜职业技术学院	贾第虫基因转换机制的研究	10
GREKF14-12	庄会富	工程师	中国科学院昆明植物研究所	自由生活的六鞭毛虫与贾第虫的比较基因组学研究	10
GREKF14-13	耿宇鹏	副教授	云南大学生态学与地植物学研究所	eDNA 技术在入侵物种小龙虾监测中的应用	10
GREKF14-14	李志鹏	助理研究员	中国农业科学院特产研究所	梅花鹿瘤胃细菌与代谢表型的共发生关系研究	10
GREKF14-15	管振华	助理研究员	西南林业大学生物多样性研究院	西黑冠长臂猿营养生态研究	10
GREKF14-16	阚显照	教 授	安徽师范大学	基于 RNA-Seq 技术的燕雀小目比较基因组学研究	10

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	陈　华	Temple University, USA	2014.2.27	Computationally Efficient Methods for Population Genetic Inference in the Era of Genomic Sequencing
2	程　乐	中国国家基因库	2014.3.6	基因测序技术最新进展及其在医学、农业研究领域的应用
3	Derek W. Dunn	University of Nottingham, UK	2014.3.18	Fig trees and fig wasps – the importance of being cooperative
4	顾正龙	Cornell University , USA	2014.4.24	Evolution of Metabolism in Model Organism and Human
5	陆　剑	北京大学	2014.4.24	Function and Evolution of small RNA targeting
6	张云武	厦门大学	2014.5.16	参与阿尔茨海默病的新基因的鉴定及功能研究
7	黄锦岭	East Carolina University, USA	2014.5.22	多细胞真核生物中的水平基因转移
8	李国红	中科院生物物理研究所	2014.5.26	Chromatin fiber: a left-handed double helix
9	刘　江	中科院北京基因组研究所	2014.6.5	Inheritance and programming of parental DNA methylomes in vertebrates
10	Ingolf Bach	University of Massachusetts,USA	2014.6.16	Sex-specific epigenetic regulation of female nurturing tissues by the X chromosome in mice
11	康　乐	中科院动物研究所	2014.6.30	动物群聚的分子机制：多巴胺还是五羟色胺？
12	张克勤	云南大学	2014.6.30	细菌招募真菌杀线虫的分子机制
13	石　琼	深圳华大基因研究院	2014.7.17	海洋基因科技及其产业化应用
14	张惠文	中国科学院沈阳应用生态研究所	2014.7.18	土壤微生物分子生态机理研究方法进展
15	宋　旭	四川大学	2014.8.6	The Functional Role of Long ncRNA-Protein Interaction in Cell
16	Viorel Dan Popescu	Simon Fraser University, Canada	2014.8.13	Wildlife conservation in a changing world: from autecology to large scale conservation planning
17	Andrey Dmitrievich Poyarkov	Institute of Ecology and Evolution, Russian Academy of Sciences	2014.9.12	Snow Leopard Research Program and Conservation in Russia
18	张志谦	北京大学	2014.11.17	α2δ1 阳性肝癌干细胞恶性特性的分子调控和靶向干预
19	John James Wilson	University of Malaya, Malaysia	2014.11.28	DNA barcoding and biodiversity in Malaysia
20	汪香婷	中国科学技术大学	2014.12.9	Long noncoding RNAs: "dark matter" of human cancer diagnosis and treatment resistance
21	宋晓元	中国科学技术大学	2014.12.9	脑衰老相关的长链非编码 RNA 功能及机理研究
22	Weligalle Wedarallage Dewar AsokaGunawardena	University of Ruhuna, Sri Lanka	2014.12.22	An23imal Genetic studies in Sri Lanka
23	秦　楠	浙江大学	2014.12.29	高通量测序技术在人类微生物组研究中的应用

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	姚 瑶，史妮妮，王运梅，吕梦蝶 霍永霞，沈全宽，汪 轩，芦方茹	尹婷婷，曾 琳，叶凌群，杨军校，Adeola Adeniyi Charles，Otecko Newton Otieno，杨贺川，曹 雪，刘 杰，袁智勇，徐 丹，周中银，刘鹤群，王明山，杨 阳，邵 永，柴 静，白 冰，周太成	李艳，倪 刚，Lee Mu-Yeong
2	彭旻晟	宋娇娇		
3	杨君兴	赵婷怡，程 城，张源伟，郑 秋	杨坤凤	
4	陈小勇	秦 涛，陈枳颖		
5	车 静	高 伟，付婷婷	黄翠萍	Chatmongkon Suwannapoom
6	焦保卫	赵丽敏，杨 星	柯 浩，赵丽娜	张洪磊
7	孔庆鹏	余 琴，吴 焕，夏王晓，程乐华	王晓雄，肖富辉，刘耀文，李玉春胡菀钊，田娇阳	
8	毛炳宇	谢建新，李永鑫，杜加诚	王晓磊，杨相彩，孙 健，江世友，刘晓亮	
9	宿 兵	何一博，罗 鑫，廖世玉，虎恩志 和耀喜，李 敏，张栋秦	张 煦，sushil，向 坤，杨德英，刘杰伟，杨晏冬，林 强	
10	王 文	奎 玲，苟志恒，王 筱，任彦栋 赵颖俊，张 如，生承晔，曾 严 陈海涛	徐 讯，张 田，刘 晖，张业胜 沈文菁，陈 垒，向志丹，刘力源	刘 斌，吴江鸿，苏 蕊
11	文建凡	姚友旭，黄海波，薛敏，吕章夏	叶青青，李毓劲，刘 芳	
12	郑 萍	张伟道，班文赞，李竞争	何大健，王鑫轶，李朝晖，郭 琨	段莹亮
13	王瑞武	罗天逊，黄 俊	文晓岚，李肇天	Riccardo Pansini，陈 春，黄 强
14	马占山	李连伟，王娅丽	樊萌萌	
15	施 鹏	郭雨龙，李 芸，张 涛，张 佳	罗 杰，郑智中，许东明，王 维	
16	黄京飞	张 琳，廉 婷，安三琪，李文兴	韩菲菲，郭义成，郑俊娟，郑俊娟	
17	蒋学龙	黄 程，赵启龙，杜宜青，程 峰	万 韬，张 斌，陈中正，胡 清，李 权，宁文鹤	陈顺德
18	饶定齐	宋心强		
19	Douglas W Yu	王晓阳	张 凯	
20	杨晓君	胡菀钊	董好岩，王荣兴，卢光义	

毕业研究生
Students Graduated

序号	姓　名	学　位	导师姓名	毕业时间
1	Nguyen Ngoc Sang	博　士	张亚平	2014–03
2	王　茉	博　士	杨君兴	2014–11
3	王晓爱	博　士	杨君兴	2014–06
4	杨立新	博　士	宿　兵	2014–12
5	杨召辉	博　士	宿　兵	2014–12
6	杨晨雪	博　士	Douglas Yu	2014–12
7	张祖明	博　士	毛炳宇	2014–11
8	张晓明	博　士	宿　兵	2014–06
9	张爱娣	博　士	黄京飞	2014–05
10	陈舜梅	博　士	黄京飞	2014–05
11	曹　雪	博　士	张亚平	2014–11
12	程东强	博　士	黄京飞	2014–05
13	程耀霆	博　士	孔庆鹏	2014–06
14	王文敏	硕　士	文建凡	2014–07
15	卢光义	硕　士	杨晓君	2014–05
16	关　琼	硕　士	马占山	2014–07
17	祁飞燕	硕　士	施　鹏	2014–06
18	李立立	硕　士	王瑞武	2014–12
19	杨松霖	硕　士	施　鹏	2014–01
20	张锦娟	硕　士	郑　萍	2014–05
21	罗　军	硕　士	王瑞武	2014–06
22	夏　季	硕　士	杨晓君	2014–05
23	徐海波	硕　士	张亚平	2014–05
24	涂小龙	硕　士	车　静	2014–07
25	韩徐曼	硕　士	张亚平	2014–05
26	谢钢琴	硕　士	文建凡	2014–11
27	王文敏	硕　士	文建凡	2014–07
28	卢光义	硕　士	杨晓君	2014–05

研究生获奖 (Awards to Graduate Students)

李明博士论文、姜雨博士论文获中科院优秀博士学位论文。
The doctoral theses of Ming Li and Yu Jiang were selected as " Outstanding Doctoral Dissertations of CAS".

张晓明、吕俊获 2014 年院长奖学金。
Xiaoming Zhang and Jun Lv won "the President Scholarship of CAS".

徐雯雯、刘耀文、杨召辉获朱李月华优秀博士生奖。
Wenwen Xu, Yaowen Liu and Zhaohui Yang won "Zhu Li Yuehua Outstanding PhD Graduate Scholarship of CAS".

林强获地奥奖学金一等奖；
Qiang Lin won the First Prize of "Di'ao Scholarship of CAS".

刘耀文获保罗生物科技奖特别奖。
Yaowen Liu won " Special Award of Paul biotechnology student award."

重点实验室优秀论文奖
Outstanding Paper Awards for Graduate Students from SKLGRE

二等奖 (The Second prize):
史妮妮 Nini Shi

三等奖 (The third prize)：
王　维 Wei Wang
张晓明 Xiaoming Zhang
杨立新 Lixin Yang
曹　雪 Xue Cao

大事记　Major Events

（1）2014 年 5 月 17 日，实验室参与举办昆明动物所第十届"公众科学日"活动。活动中，实验室 2 位科技人员作了科普报告，部分研究组对外开放参观。

The key lab participated in the Tenth "Public Science Day" of Kunming Institute of Zoology on May17,2014. Two staff scientists gave talks and some groups of the lab were open to the public to visit.

（2）2014 年 6 月 3–4 日，实验室主持的中国科学院战略性先导科技专项（B 类）"动物复杂性状的进化解析与调控"项目启动会在昆明召开。

The start meeting of Strategic Priority Research Programs (B) of CAS titled Evolutionary analysis and functional regulation of animal complex traits, held by the key lab, was held in Kunming on June 3-4, 2014.

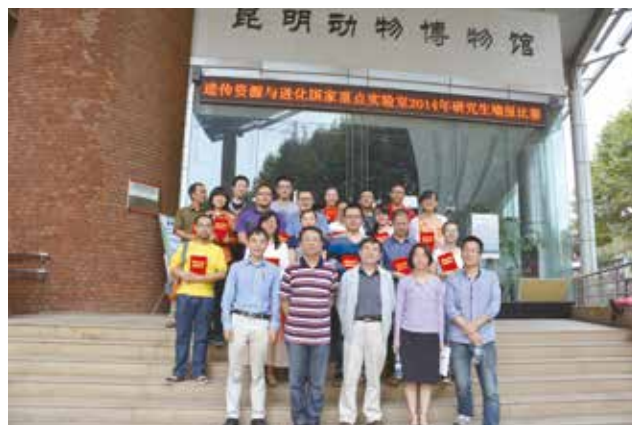（3）2014 年 6 月 30 日，实验室第二届学术委员会第三次会议在昆明召开。

The third meeting of the second academic committee of the key lab was held in Kunming on June 30, 2014.

（4）2014 年 8 月 15 日，实验室举办了 2014 年研究生墙报比赛。

The 2014 Graduates' Poster Competition of the key lab was held on August 15, 2014.

（5）2014 年 8 月 11–17 日，实验室与所研究生部合作在昆明主办"2014 年进化生物学暑期班"

On August 11-17, 2014, the Evolutionary Biology Summer Course was held in Kunming organized by the key lab and the Office of Postgraduate Affairs of KIZ .

（6）2014 年 10 月 28 日，实验室在昆明召开了 2014 年学术交流年会。

The 2014 Annual Meeting of the key lab was held in Kunming, on Oct.28,2014.

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
王瑞武	车　静	张亚平	杨君兴	杨晓君	俎文惠
郑　萍	施　鹏	宿　兵	黄京飞	焦保卫	蒋学龙

其他工作人员

马云飞	马鹏程	王文智	王运宇	王　林	王国栋
王金焕	王晓爱	石　宏	石　磊	叶志强	代绍兴
吕永青	朱春玲	任国鹏	任海清	刘　佳	刘贵春
刘　振	刘淑伟	刘　衡	祁飞燕	祁学斌	许绍斌
孙艳波	苏伟婷	李功华	李其刚	李学友	李学燕
李宗煦	李桂梅	李朝翠	李媛媛	杨双娟	杨利琴
杨春燕	杨　钦	杨　晖	杨　爽	杨敏敏	时晓菲
吴　飞	吴世芳	吴东东	吴春莹	何永捍	何　静
何　锴	余国华	余　蕊	邹　丽	闵　锐	张志刚
张栋儒	张晓明	张　慧	陈小勇	陈小琼	陈　兴
陈　兵	陈宏满	陈忠良	邵静茹	岩　道	季吟秋
金洁琼	周炜帏	周　鑫	郑兰平	赵玉琪	赵若苹
赵　博	郝军军	相　辉	饶定齐	徐海波	高　云
高建云	唐　嘉	浦绍艳	黄　蓓	彭　忆	彭旻晟
董　锋	蒋万胜	韩树标	韩徐曼	程耀霆	舒树森
谢海兵	廖爱文	颜　芳	潘晓赋		