



中国科学院动物研究所
INSTITUTE OF ZOOLOGY, CHINESE ACADEMY OF SCIENCES

首届“全国生物系统学学术论坛”

12月9日-12月11日 2016·北京



主办单位：中国昆虫学会青年工作委员会
中国科学院青年创新促进会

承办单位：中国科学院动物进化与系统学重点实验室

赞助单位：北京源宜基因（ORI-GENE）科技股份有限公司

首届“全国生物系统学学术论坛”通知

为了促进和探讨我国生物系统学发展战略、学术交流和青年人才培养，首届“全国生物系统学学术论坛”将于2016年12月9-11日在北京胜利饭店召开。此次会议由中国昆虫学会青年工作委员会、中国科学院青年创新促进会联合主办，中国科学院动物进化与系统学重点实验室承办。

1. 会议内容

学术交流：古生物学、昆虫学、动物学、植物学、微生物学、病毒学等不同学科方向系统学研究进展。

学术研讨：中国生物系统学发展战略、学术交流和青年人才培养思路。

2. 会议时间

2016年12月9日报到；10-11日学术交流、研讨；12日离会。

3. 会议日程：

2016年12月9日

13:30-17:00 到会代表报到、注册（北京胜利饭店）

2016年12月10日

08:00-12:30 现场报到、注册

08:30-08:40 介绍参会来宾与论坛背景

08:40-09:00 中国昆虫学会等领导致辞

09:00-09:10 合影、茶歇

09:10-12:10 学术报告

12:10-13:30 自助餐（胜利饭店）

13:30-16:00 学术报告

16:00-18:00 茶歇，专家发言、自由研讨

18:00 自助餐（胜利饭店）

2016年12月11日

08:30-10:00 学术报告

10:00-10:15 茶歇

10:15-12:15 学术报告

12:15-13:30 自助餐（胜利饭店）

13:30-15:30 学术报告

15:30-15:45 茶歇

15:45-17:45 学术报告

17:45-18:10 小结并闭幕

2016年12月12日

代表离会

4. 会议地点

北京胜利饭店，中国北京市朝阳区昌平路德胜门外北沙滩3号
(<http://www.shenglihotel.com/>)。

5. 主办单位

中国昆虫学会青年工作委员会、中国科学院青年创新促进会。

6. 承办单位

中国科学院动物研究所动物进化与系统学重点实验室。

7. 会议注册费

会议注册费为800元/人(学生600元/人)，会议发票由中国昆虫学会开具。因学会无POS机，无法刷卡，请于现场缴纳现金注册。

本次论坛参会人员交通及住宿费用自理，大会按照规定提供工作餐。敬请理解支持。

8. 会议联系人

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承办: 中国科学院动物进化与系统学重点实验室

主办: 中国昆虫学会青年工作委员会

中国科学院青年创新促进会

2016年12月1日

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首届“全国生物系统学学术论坛”日程安排

会议地点：二楼会议中心

用餐地点：一楼餐厅

开幕式

主持人	时间	报告人	单位	题目
朱江	8:30-8:35	朱江处长	中国科学院动物研究所	介绍来宾
	8:35-8:40	魏辅文副所长	中国科学院动物研究所	致辞
	8:40-8:45	乔格侠副理事长	中国昆虫学会 / 组委会	介绍论坛背景
	8:45-9:00	陈宜瑜院士	专家代表	致辞

2016年12月10日学术报告

主持人	时间	报告人	单位	题目
朱朝东	9:00-9:25	张润志	中国科学院动物研究所	昆虫分类学 Insect Taxonomy
	9:25-9:50	白明	中国科学院动物研究所	现代形态学的历史使命 The Historical Mission of the Modern Morphology
	9:50-10:15	蔡磊	中国科学院微生物研究所	植物病原胶锈菌的物种形成与协同进化 Speciation and Co-evolution of Phytopathogenic Gymnosporangium species
茶歇	10:15-10:30	赞助商“源宜基因”广告片		
周欣	10:30-10:55	Douglas Chesters	中国科学院动物研究所	Increasing Scale and Species-Richness in Phylogenetic analyses
	10:55-11:20	侯仲娥	中国科学院动物研究所	古地中海变迁与钩虾多样性形成机制 The Tethyan Regression Shaped Amphipod Diversification
	11:20-11:45	黄英	中国科学院微生物研究所	链霉菌分子系统学与物种演化 Molecular Systematics for Understanding the Evolution and speciation in streptomycetes
	11:45-12:10	孔宏智	中国科学院植物研究所	毛茛科与花的进化发育 Ranunculaceae and the Evo-Devo of the Flower
午餐	12:10-13:30	自助餐		

孔宏智	13:30-13:55	屈延华	中国科学院动物研究所	谱系地理解析鸟类的遗传特有性 Genetic Endemism– Implication for Current Avian Endemic Centers of China by Comparative Phylogeography
	13:55-14:20	张鹏	中山大学	脊椎动物与鞘翅目昆虫高通用性核基因分子标记的大规模开发与应用 Large-scale Development of Novel Nuclear Markers for Phylogenomics of Vertebrates and Beetles
	14:20-14:45	张勇	中国科学院动物研究所	基因型 - 表型映射关系的进化规律初探
	14:45-15:10	张峰	南京农业大学	跳虫的整合分类思考 Integrative Taxonomy on Collembola
茶歇	15:10-15:30	赞助商“源宜基因”广告片		
张鹏	15:30-15:55	周欣	中国农业大学	5000 Species vs. 5000 genes: 构建全阶元系统发育关系的方法探索
	15:55-16:20	朱天琪	中国科学院应用数学研究所	基于多物种隔离移民模型的基因流检测方法 Maximum Likelihood Implementation of an Isolation-with-Migration Model for Testing Gene Flow
陈宜瑜	16:20-18:00	专家研讨		
晚餐	18:00-	自助餐		

2016年12月11日学术报告

主持人	时间	报告人	单位	题目
江建平	8:30-8:55	缪炜	中国科学院水生生物研究所	纤毛类原生动动物系统发育基因组学研究 Phylogenomics of Ciliates
	8:55-9:20	于黎	云南大学	食肉目犬型超科和灵长目疣猴亚科分子系统学研究
	9:20-9:45	钟伯坚	南京师范大学	The Progress and Limitation of Plant Phylogenomics
	9:45-10:10	高芳奎	福建农林大学植物病毒研究所	马铃薯 Y 病毒的遗传多样性及其分子进化 Genetic Diversity and Molecular Evolution of Potato Virus Y
茶歇	10:10-10:30	赞助商“源宜基因”广告片		
缪炜	10:30-10:55	刘翟	中国科学院微生物研究所	病毒基因组学与进化 - 禽流感为例 Pathogen Genomics and Evolution
	10:55-11:20	郭宝成	中国科学院动物研究所	基于基因组学方法研究鱼类适应辐射 Taking Genomic Approaches to Understand Adaptive Radiation in Fish
	11:20-11:45	江建平	中国科学院成都生物研究所	隆肛蛙属 (<i>Feirana</i>) 物种及种群分化研究 Species and Population Differentiation in the Genus <i>Feirana</i>
	11:45-12:10	刘晓光	南开大学	MrBayes 的 GPU 优化算法进展 The Advance of GPU Based Algorithms for MrBayes
午餐	12:10-13:30	自助餐		
张爱兵	13:30-13:55	刘星月	中国农业大学	脉翅类昆虫的系统分类与宏演化 Systematics and Macroevolution of Neuropterida
	13:55-14:20	毛建丰	北京林业大学	杂交、生态选择和青藏高原适应性起源的进化遗传学：高山松同倍性杂交物种形成研究进展 Hybridization, Ecological Selection, and the Adaptation to Tibetan Plateau: What We Learned from the Homoploid Hybrid Speciation Studies of <i>Pinus densata</i>
	14:20-14:45	齐晓光	西北大学	繁殖机会的博弈促进非人灵长类重层社会系统的进化 Kin-bonds of Bachelor Males Contributes to the Evolution of Primates Multilevel Society

张爱兵	14:45-15:10	史卫峰	泰山医学院	从基因组进化到病毒传播、宿主内变异以及感染方式：以埃博拉病毒为例 From Genome Evolution to Virus Transmission, Intra-host Variation and Infection Mode: an EBOV Perspective
	15:10-15:35	孙红英	南京师范大学	华溪蟹属多样性发生与物种分类界定 Diversification of <i>Sinopotamon</i> Crabs, Taxonomy and Species Delimitation
茶歇	15:35-15:55	赞助商“源宜基因”广告片		
白明	15:55-16:20	吴东辉	中国科学院东北地理与生态研究所	土壤动物多样性维持及其在生态系统中的功能 Soil Animal Biodiversity Assemblage and Its Function in Ecosystem
	16:20-16:45	吴琦	中国科学院动物研究所	非序列联配方法在基因组进化中的理论与应用 Theoretical Basis and Applications of Sequence-Alignment-free Method on Genome Evolution
	16:45-17:10	张爱兵	首都师范大学	From DNA Barcoding to Biodiversity
	17:10-17:35	章张	中国科学院基因组所	The BIG Data Center: from Deposition to Integration to Translation
	17:35-18:00	周长发	南京师范大学	选择的特征与特征的选择（以我国蜉蝣研究为例） To Choose the Natural Selected Characters: Some Examples in Chinese Mayfly Research
朱朝东	18:00-18:15	总结闭幕		
晚餐	18:00-			

全国生物系统学学术论坛

为保障论坛科学、有序推进，建议成立组织委员会：

主任： 中国科学院动物研究所，乔格侠研究员

副主任： 中国科学院动物研究所，朱朝东研究员
中国科学院植物研究所，孔宏智研究员
中国科学院微生物研究所，黄英研究员

委员：

中国科学院动物研究所，张润志研究员	中国科学院植生生态研究所，栾云霞研究员
中国科学院动物研究所，雷富民研究员	中国科学院东北地理与农业生态研究所，吴东辉研究员
中国科学院动物研究所，梁爱萍研究员	中国科学院应用数学研究所，朱天琪博士
中国科学院动物研究所，郭宝成研究员	中国农业大学，周欣教授
中国科学院动物研究所，葛斯琴研究员	南开大学，谢强研究员
中国科学院动物研究所，屈延华研究员	云南大学，于黎教授
中国科学院动物研究所，侯仲娥研究员	陕西师范大学，黄原教授
中国科学院植物研究所，周世良研究员	南京师范大学，孙红英教授
中国科学院昆明动物研究所，车静研究员	南京师范大学，周长发教授
中国科学院水生生物研究所，缪炜研究员	南京师范大学，钟伯坚教授
中国科学院水生生物研究所，李涛研究员	河北大学，张峰教授
中国科学院微生物所，刘翟研究员	首都师范大学，张爱兵教授
中国科学院成都生物研究所，江建平研究员	泰山医学院，史卫峰教授
中国科学院西双版纳热带植物园，彭艳琼研究员	中山大学，张鹏教授
中国科学院基因组研究所，章张研究员	福建农林大学，黄晓磊教授
中国科学院海洋研究所，沙忠利研究员	

秘书：

罗阿蓉、张峰、吴琦、白明

中国科学院动物进化与系统学重点实验室简介

Key Laboratory of Zoological Systematics and Evolution, Chinese Academy of Sciences

动物进化与系统学研究是动物研究所历史最悠久、基础最雄厚、积累最丰富的学科方向之一，在国家、中国科学院及动物研究所层面上都具有鲜明的学科特色和优势，在国内和国际上都具有不可替代性。

本实验室的历史可追溯到 1860 年由法国传教士韩伯禄 (P. M. Heude) 在上海创建的中国第一家自然历史博物馆——徐家汇博物馆 (Musée de Zi-Ka-wei , 1930 年改称震旦大学博物馆 (Musée de Heude) ，本实验室的动物标本馆是在该馆馆藏标本的基础之上建设而成的 (震旦大学博物馆的绝大多数动物标本在上世纪 50 年代初期被移至中国科学院动物研究所) 。上世纪 60 年代，动物研究所下设昆虫分类区系、无脊椎动物分类区系和脊椎动物分类区系三个研究室，这三个研究室在 1996 年被整合为动物进化与系统学研究中心暨标本馆，2007 年更名为动物进化与系统学所级重点实验室。2008 年 12 月，中国科学院正式批准成立中国科学院动物进化与系统学重点实验室，并在 2010 年 7 月以及 2015 年 8 月的中国科学院重点实验室中期评估中获得优秀。

实验室以解决动物系统学及进化生物学领域的关键基础科学问题及面向国家需求为目标，通过宏观与微观生物学手段相结合，综合形态与分子等多层次数据，研究和描述动物物种的多样性，重建物种及种上阶元的系统发育关系，探讨物种及物类的起源与演化，研究协同进化及生态适应的过程与机制；解析物种的地理分布格局及其形成机制，探讨全球环境变化对物种分布及演化的影响；研究动物扩散规律以及入侵生物和重要疫病媒介动物的防控策略；为我国生物多样性资源的可持续利用与保护、为国家的经济建设和生态安全提供科学理论依据和技术支撑。

现代形态学的历史使命

白明

中国科学院动物研究所

生物结构在不同尺度上、不同维度上和不同部位的观察与形态分析，为科学研究结果提供最直接的证据，在众多学科领域扮演了不可或缺的角色。目前生物结构的二维形态观察手段和定性分析已非常成熟，能够为科学研究提供一定地支撑，但三维技术手段和定量分析方法却明显滞后且应用范围不广。而且已有的三维成像技术无法同时解决复杂突变样本的形态信息缺失、成像速度慢、真实纹理难以还原等问题。报告人致力于开拓并且实践“现代形态学”的新学科研究领域，即通过显微 CT、计算机三维重建等已知仪器来获取形态数据，同时还与西安光机所共同提出一种基于结构照明显微术的针对微小动物的高分辨率三维层析成像的新仪器（D-SIM）来快速获取三维形态数据。接着利用几何形态学、支序系统学、有限元等定量形态分析方法，进而可对进化与系统学问题进行全新解读和革命性探索，例如，我们评估了连续性性状的分类学意义（未发表数据），确立了昆虫纲化石新目——奇翅目（Alienoptera）（Bai et al. 2016, Gondwana Research），首次在琥珀中发现反鸟类（Xing et al. 2016, Nature Comm.），缅甸琥珀中发现的带蚕支持冈瓦纳起源生物通过“欧洲扩散”假说扩散到劳亚古陆（Oliveira et al. 2016, Current Biology），首次在缅甸琥珀中发现恐龙（Xing et al. 2016, Current Biology）等。通过与 CLSM、Micro-CT、FIB-SEM、MRI 等当今流行的三维成像技术进行对比发现，D-SIM 技术在成像的单一指标方面虽未必全部占优，但是综合成像质量、成像速度、样本制备方法等要素，其在微小动物精微三维结构成像方面的整体优势确实比较明显。另外，D-SIM 技术与传统光学显微镜具有良好兼容性，并且在设备成本方面也存在巨大优势，因此有望在实验室大规模普及，成为常用成像设备（Ruan et al., 2016, Frontiers in Zoology）。“现代形态学”学科体系涵盖形态数据的获取、形态特征的模拟和对比分析等流程，未来有望为科学研究提供新的解决方案与视角。

The historical mission of the modern morphology

Ming BAI

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The observation of biological structure in different scales, different dimensions and different parts and the morphological analysis approaches provide the most direct evidence and play the indispensable roles in many disciplines. At present, the two-dimensional morphological observation means and qualitative analysis of biological structure are very mature and can provide some supports for the scientific research. But the three-dimensional technology and quantitative analysis methods are

lagging behind and the scope of application is not wide. Additionally the existing three-dimensional imaging technology cannot solve the problems on the morphological information collecting from the complex samples, the missing on the shape information, slow imaging speed, the real texture difficult to restore and so on. We are developing and practicing the new disciplinary research field of "modern morphology", that is, obtaining morphological data through known instruments such as micro CT, computer three-dimensional reconstruction and so on. Furthermore, together with Xi'an Institute of Optics and Precision Mechanics, Chinese Academy of Sciences, we developed a new machine (D-SIM) for high-resolution three-dimensional tomography of small animals to rapidly obtain 3D morphological data. Then we can make new interpretations and revolutionary explorations of evolutionary and systemic problems using quantitative morphological methods such as Geometric Morphometrics, cladistics, and finite element analysis, etc. For example, we evaluated the taxonomic significance of continuous traits (unpublished), erect a new insect order (Alienoptera) from Burmese amber (Bai et al. 2016, Gondwana Research), first discovery of bird from Burmese amber (Xing et al., 2016, Nature Comm.), earliest Onychophoran in amber reveals Gondwanan migration patterns (Oliveira et al. 2016, Current Biology), first discovery of dinosaurs from Burmese amber (Xing et al., 2016, Current Biology). Compared with the popular three-dimensional imaging techniques such as CLSM, Micro-CT, FIB-SEM and MRI, D-SIM technology is not necessarily dominant in single imaging criteria, but it has many advantages such as imaging quality, imaging speed, simple preparation methods, etc. Especially the overall advantage on small animals in three-dimensional imaging is indeed very obvious. In addition, D-SIM technology has good compatibility with traditional optical microscopes, and also has great advantages in equipment cost. It is expected to become a popular imaging equipment in the laboratory (Ruan et al., 2016, Frontiers in Zoology). The discipline system on "modern morphology" covers morphological data acquisition, the simulation of morphological characteristics and comparison analysis process. The future of "modern morphology" is expected to provide a new scientific research solutions and perspective.

植物病原胶锈菌的物种形成与协同进化

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Speciation and coevolution of *Gymnosporangium* species

Abstract: *Gymnosporangium* species (Pucciniaceae, Pucciniales) cause serious diseases and significant economic losses to apple cultivars. Most of the reported species are heteroecious and complete their life cycles on two different plant hosts belonging to two unrelated genera, i.e. *Juniperus* and *Malus*. However, the phylogenetic relationships among *Gymnosporangium* species and the evolutionary history of *Gymnosporangium* on its aecial and telial hosts were still undetermined. In this study, we recognized species based on rDNA sequence data by using coalescent method of generalized mixed Yule-coalescent (GMYC) and Poisson Tree Processes (PTP) models. The evolutionary relationships of *Gymnosporangium* species and their hosts were investigated by comparing the cophylogenetic analyses of *Gymnosporangium* species with *Malus* species and *Juniperus* species, respectively. The concordant results of GMYC and PTP analyses recognized 14 species including 12 known species and two undescribed species. In addition, host alternations of 10 *Gymnosporangium* species were uncovered by linking the derived sequences between their aecial and telial stages. This study revealed the evolutionary process of *Gymnosporangium* species, and clarified that the aecial hosts played more important roles than telial hosts in the speciation of *Gymnosporangium* species. Host switch, losses, duplication and failure to divergence all contributed to the speciation of *Gymnosporangium* species.

Increasing Scale and Species-Richness in Phylogenetics

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An artifact of study focused on model organisms and useful genes is a distinct partition between gene-rich (genomic) and species-rich (DNA barcode) sequence data. Both of these data types are informative for phylogenetics. Genomic data are capable of resolving ancient and otherwise obscured divergence events, while DNA-barcodes and related markers hold valuable information on species-level diversity. However, currently there is little integration of these data. This represents an obstruction to building phylogenies which are both broad in taxon and representative in patterns of diversity. Using insects as a case study, I outline an approach for de novo construction of phylogenies which far out-scale current supermatrix-based trees. Further, the requirement for such trees is demonstrated in tree-based profiling of DNA-barcode or metabarcode datasets.

古地中海变迁和钩虾多样性形成机制

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主要以甲壳动物钩虾为研究材料，发现淡水钩虾 1 新属 63 新种，并探讨古地中海消亡过程中钩虾的时空变化格局。研究发现钩虾起源于古地中海，发生了从咸水向淡水生境的迁移，导致物种分化速率增加，验证了生态机遇促进物种分化的理论 (Hou et al., 2011. PNAS)。对全球钩虾科研究中发现古地中海变迁导致姐妹群间不同的分化模式，黑海钩虾最早占据古地中海盆地，为匀速进化；钩虾属在选择压力下开拓了欧亚大陆淡水生境并快速分化，是一种适应性进化；而萨钩虾为子遗进化，物种数量少，分布局限在帕米尔高原和地中海边缘 (Hou et al., 2014. *Cladistics*)。与古地中海消亡相伴随的是青藏高原的隆起、太行山隆起、东亚海侵等地质历史事件对中国钩虾生物多样性起源有重大影响，研究结果阐明了遗传变异与分布格局相吻合的机制。

The Tethyan regression shaped amphipod diversification

The amphipod crustaceans are critically important in marine and freshwater ecosystems. On species delimitation and distribution study, a new genus of *Eurypodogammarus* and 63 new species of *Gammarus* have been discovered in China. Based on Holarctic amphipods, a phylogenetic analysis showed that *Gammarus* originated from the Tethyan region with a habitat shift from marine to freshwater, and underwent a rapid diversification phase with successively occupation across Eurasia. The diversification pattern of *Gammarus* provides an excellent aquatic case supporting the hypothesis that ecological opportunities promote diversification. Furthermore, diversification analysis combined with paleogeological evidence suggested that the Tethyan changes triggered different diversification modes and range expansions for sibling lineages: the pontogammarids firstly occupied the Tethyan basin and maintained stable diversification, the lineage of *Gammarus* underwent an early rapid radiation across Eurasia, whereas sarothrogammarids experienced evolutionary stasis by stranding on the ancient Tethyan margins. Phylogeographical patterns exhibited by local species provided solid evidence that Tethyan regression and tectonic uplift drove the diversification of extant taxa. Moreover, low dispersal ability maintained the high endemism, inferring species clades being geographically defined.

Molecular systematics for understanding the evolution of and speciation in streptomycetes

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The study of genetic variation among prokaryotes is fundamental for understanding their evolution and untangling their ecology and evolutionary theory-based systematics. *Streptomycetes* are a diverse group of bacteria that are widely distributed in nature and a rich source of useful bioactive compounds. We have recently established multilocus sequence analysis (MLSA) as a powerful phylogenetic approach for defining the taxonomic structure and evolutionary history of *streptomycetes*. In this study, the largest sample of *Streptomyces* species to date, consisting of 142 type strains spanning the genus, was collected and subjected to a comprehensive population genetic analysis on the basis of MLSA. The results indicated frequent homologous recombination among *Streptomyces* species, which occurred three times more frequently and was nearly 14 times more important than point mutation in nucleotide sequence divergence. As a result, a facilitating effect on the evolutionary process and confusion in phylogenetic relationships were observed, as well as a number of specific transfer events of the housekeeping gene fragments. A resultant phylogenetic network depicted extensive horizontal genetic exchange which decays clonality in streptomycetes. Nevertheless, seven evolutionary lineage groups were identified in the present sample in the Structure analysis, generally consistent with morphological and physiological data. Furthermore, we performed phylogenetic and population genetic analyses on 41 *Streptomyces albidoflavus* and 35 *Streptomyces olivaceus* strains derived from diverse habitats, mainly insects, sea and soil. The results underpinned the predominance of homologous recombination within *Streptomyces* species and emphasized habitat barriers to homologous recombination in the diversification of streptomycetes. For each species, all three habitat-associated groups, particularly the entomic group, demonstrated significantly reduced levels of gene flow with one another. Finally, a population genomic analysis of *S. albidoflavus* strains unraveled a series of genetic changes between the populations for adapting to different habitats in a microevolution scope and further indicated the role of horizontal gene transfer in the process of speciation in streptomycetes.

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Ranunculaceae and the evo-devo of the flower

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Abstract

Flowers show tremendous diversity in size, color, structure, symmetry, display, and function, etc. The mechanisms that underlie the origin and diversification of the flower, however, remain largely unclear. One of the obstacles that prevent us from knowing more about the underlying mechanisms of flower evolution is the lack of suitable model systems. To solve this problem, we have developed the basal eudicotyledonous family Ranunculaceae into a model system to address the important evolutionary developmental questions that cannot be addressed by using any other existing models. In this talk, I will first introduce the advantages of using the Ranunculaceae as a model and then present our new results on three topics: 1) the molecular mechanism underlying parallel petal losses within the Ranunculaceae; 2) the molecular basis and its flexibility of the floral organ identity determination program in *Nigella damascena*, a species with spiral flower; and 3) the tempo, mode, and mechanisms of character evolution during petal elaboration within the genus *Nigella*.

遗传特有性 — 以谱系地理解析鸟类遗传特有性的形成机制

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第四纪冰期对我国现有鸟类遗传特有性的影响最大，青藏高原在冰期时期退缩到高原东北部边缘的避难地。由于冰后期种群扩张促进了基因交流，一些高原鸟类，如白腰雪雀、棕颈雪雀没有遗传分化；而一些迁徙能力弱的鸟类，如地山雀在冰期时期处于两个独立的避难地。分布在高原腹地的鸟类，它们的栖息地在冰期时期被冰川所覆盖，种群经历了冰期带来的瓶颈效应以及冰后期扩张所带来的种群增长；而分布在边缘地区的鸟类，它们的栖息地在冰期时期没有被冰川所覆盖，因此种群处于稳定状态，逐步积累了遗传分化。在冰期时期这些高原鸟类的避难地都集中在青藏高原东北部边缘地区。这些避难地与现生鸟类的特有分布中心，祁连山地区相一致。“更新世冰期避难地”保存了高原鸟类古老的遗传特有性，并由此促进了祁连山地的鸟类特有化过程。西南山地在地质结构上处于南亚大陆与欧亚大陆镶嵌交界带的东翼，地质构造复杂，山脉、河流南北纵贯，高差很大，山地垂直变化异常明显。复杂的地形与异质的环境可能会阻碍鸟类的扩散，呈现“演化岛”状的隔离分布格局，使得鸟类物种在长期孤立中产生了遗传分化。西南山地的许多山脉海拔高度在 4000 米以上。在第四纪冰期，冰川未曾覆盖 2000 米以下的低海拔地区，因此西南山地低海拔地区提供给鸟类相对稳定的环境。在冰期时期，西南山地鸟类处于稳定状态，没有经历瓶颈效应以及冰后期扩张所带来的遗传混合，在长期稳定环境中进一步积累了遗传分化。可见，西南山地的“演化岛”起着摇篮与博物馆的效应，对鸟类遗传多样性的形成与积累有着极为重要的作用（Cradle and Museum Effect）。台湾岛也是中国鸟类的特有化中心，但该岛屿鸟类遗传特有性的形成机制却与西南山地与祁连山地不同。我们通过比较研究几种鹑类和山雀类鸟类的基因树、种树以及生态位模型，发现台湾岛具有不同的演化历史。在更新世冰期，北半球被冰川所覆盖，但西南山地与祁连山地的低海拔地区没有冰川覆盖，提供给当地鸟类比较稳定的环境，保存了当地鸟类的遗传特有性。而台湾岛在冰期时期海平面下降，通过大陆桥与内陆地区连接，两岸鸟类产生基因交流，因此减少了遗传特有性。因此，同是鸟类的特有化区，但具有不同的特有化历史，从而造成了不同的特有化格局。

Genetic endemism— implication for current avian endemic centers of China by comparative phylogeography

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Pleistocene climate fluctuations have shaped the patterns of genetic diversity observed in extant species. East Asia is known for its exceptionally high biological diversity and endemism. Various geological and climatic events during the Pliocene and Pleistocene have been invoked to explain this high endemism, and these processes have had different impacts on different organisms.

We compared the phylogeographical patterns of five avian species on the Tibetan plateau using three species of the snow finches (*Montifringilla* complex), Ground tit (*Parus humilis*), the horned lark (*Eremophila alpestris*), the twite (*Carduelis flavirostris*) and the black redstart (*Phoenicurus ochruros*). A single refugium was identified in a restricted semi-continuous area around the eastern margin of the plateau. For the other two species distributed on the edges of the plateau (the twite and black redstart), populations were maintained at stable levels. Edge areas are located on the eastern margin, which might have had little or no ice cover during the glaciation period. Thus, milder climate may have mitigated demographic stresses for edge species relative to the extremes experienced by platform counterparts, the present day ranges of which were heavily ice covered during the glaciation period. Finally, various behavioural and ecological characteristics, including dispersal capacities, habitat preference and altitude specificity along with evolutionary history might have helped to shape different phylogeographical structures appearing in these five species. The dramatic topography of the Southwest Mountainous Region resulting from the tectonic uplift during the late Pliocene leads to dramatic ecological stratification, which creates physical barriers to migration and isolates organisms into different subregions and mountain systems. This agrees with the observation that the phylogeographical patterns found in four species of birds (*Alcippe morrisonia*, *Stachyridopsis ruficeps*, *Parus monticolus* and *Aegithalos concinnus*) distributed in this region are characterized by deep splits between lineages that coalesce between 0.8 and 2.1 Ma. Unlike other regions at this latitude, the Southwest Mountainous Region was largely unaffected by the Pleistocene glaciations. Genetically isolated populations of these birds could thus be maintained throughout the Pleistocene in these rather stable montane environments. In comparison, we found radically different phylogeographical patterns in populations of the same four species distributed in the adjacent lowland, the Central China region. This region has a distinctly different geological history with dramatic, climate-induced shifts in vegetation during the Pleistocene. Here, we found a considerably less geographical structure in the genetic variation and a much younger coalescence time (0.3–0.7 Ma). We also found evidence of genetic bottlenecks during the glacial periods and gene flow during the interglacial expansions. We conclude that the high genetic diversity in the Southwest Mountainous Region results from a long-term in situ diversification within these evolutionary isolated

and environment stable montane habitats. Taiwan Island is another endemic center of birds in China. We investigate the relative role of these historical processes in the genetic evidence for endemism of intraspecific lineages of two East Asian species: the grey-cheeked fulvetta (*Alcippe morrisonia*) and the red-headed tree babbler (*Stachyridopsis ruficeps*). The genetic structure analysis and species tree estimation revealed three deeply divergent lineages within both species. One lineage is endemic to the mountains of Southwest China and the other to Taiwan. Coalescent simulations suggested that lineage diversification mostly occurred during the late Pliocene. Within this time frame, uplift of the mountains of Southwest China and formation of the island of Taiwan are geological events consistent with the geographical isolation and ecological niche divergence of these phylogeographic lineages. Our results suggest that the main driver of avian endemism in East Asia was the formation of new montane and island habitats following the uplift of the mountains of Southwest China and formation of the island of Taiwan in the Pliocene. However, the populations in the two regions were affected differently by the climatic oscillations during the Pleistocene. The mountains of Southwest China were climatically stable during glaciations, allowing populations to persist throughout the Pleistocene and maintain their genetic uniqueness. In contrast, glaciations resulted in lowered sea levels, allowing dispersal between the island of Taiwan and mainland China, thus obscuring the genetic endemism of the Taiwanese populations.

脊椎动物与鞘翅目昆虫高通用性核基因分子标记的大规模 开发与应用

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在分子系统学研究中，解析一些困难的进化节点往往需要分析大量的分子标记，然而分子标记的开发数量在不同生物类群中是很不一样的。对于一些特定生物类群的研究者来说，缺少数量足够而又适用于其所研究生物类群的分子标记，往往是其研究的主要瓶颈。近年来大量模式生物基因组数据的积累，为分子标记的开发提供了良好的数据基础。通过对脊椎动物与鞘翅目昆虫现有基因组数据的深入挖掘，我们提出了一套可以在基因组水平上对候选分子标记座位进行筛选的生物信息学分析方案，可以快速寻找到大量类群通用性的基因座位（包括编码区与非编码区）用于分子标记的开发。同时，我们提出了一种基于巢式 PCR 技术的分子标记引物设计策略，能够将核分子标记的扩增成功率从不足 50%，提高到 90% 左右。以此为基础，我们为脊椎动物开发了 102 个蛋白编码基因的核分子标记，能在任何脊椎动物类群中应用，其实验成功率超过了 95%；为鞘翅目昆虫开发了 95 个蛋白编码基因的核分子标记，能在任何甲虫分类单元中应用，其实验成功率超过了 90%；为蛇类开发了 96 个基于内含子序列的核分子标记，能在任何所有蛇类物种中应用，其实验成功率超过了 90%。此外，我们还建立了一套基于 Illumina HiSeq 测序平台的 PCR 产物快速测序技术，可以同时测定大小不同、丰度不同、甚至有杂带的上万个 PCR 产物的全序列，而时间成本与经济成本还不到常规 Sanger 测序的 1/10。基于这些实验技术，我们对有尾两栖类的科级关系、无尾两栖类的科级关系、鞘翅目科级关系、无肺螈科内部关系、瓢虫科内部关系、亚洲蝮蛇属下的物种关系等不同进化深度的系统学问题进行了研究，均得到了较好的效果。我们希望这些新的分子标记与高通量测序方法能够在推进脊椎动物与甲虫生命树的最终解析上发挥作用。

Large-scale Development of Novel Nuclear Markers for Phylogenomics of Vertebrates and Beetles

Resolving difficult nodes for any part of the tree of life often requires analyzing a large number of markers. Lacking of molecular markers that are workable for the groups of interest is often a bottleneck in phylogenetic research. During the past five years, we developed a series of data mining strategy to search for genomic loci that are suitable for marker development. These strategies are workable for animal groups with substantial genome data (such as vertebrates) or animal groups with less genome data available (such as beetles). We also used nested PCR strategy to increase the amplification of nuclear markers from 50% to 90%. Based on these methods, we successfully developed 102 nuclear

protein-coding markers that can be universally used across vertebrates (success > 95%), 95 nuclear protein-coding markers that can be universally used across beetles (success > 90%), and 96 intronic markers that can be universally used across snakes (success > 90%). We also developed a high throughput method that can simultaneously sequence tens of thousand of PCR products, based on Illumina Hiseq platform, which is much more cost-effective than the conventional Sanger sequencing. Based on these novel markers and sequencing method, we resolved the phylogeny of salamanders (family-level), the phylogeny of beetles (family-level), the phylogeny of ladybird beetles (species-level), the phylogeny of lungless salamanders (species-level), and the phylogeny of Gloydius snakes (intra species-level). We hope our work can help to accelerate the completion of many parts of the tree of life of vertebrates and beetles.

基因型－表型映射关系的进化规律初探

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近年来，基因组学、分子生物学等多学科交叉使得若干推动表型进化的遗传变异得以鉴定；然则基因型-表型映射关系(GPM)的进化是否有其内在规律鲜有人提。我们的工作发现动物体的突变、发育和调控有其自身的特点，而这些特点会影响GPM的进化。具体说来，1)不同物种的突变机制差别较大，可以预期基因型空间组成差别显著；作为证据，与哺乳动物相比，非哺乳动物体系多通过LTR转座子介导RNA水平的基因复制，后者所产生的复制基因拥有新的嵌合结构，因而在表型空间更有可能扮演新的角色(Genome Research 2016)。2)新的基因型经过发育程序映射为某种表型，只对少数发育阶段或器官产生影响即多效性较低的基因型更容易固定；与此相符，基因丢失突变富集于器官特异表达的基因(Molecular Biology & Evolution 2015)。3)不同表型可能共享类似的调控机制，因而征召同一基因型，表现为多效性乃至演化的成本。例如，睾丸精子发生后期的全局去甲基化导致了宽松的转录环境，从而使得新基因易于在该器官起源；癌症与睾丸共享类似的表观调控，这些基因同样易于上调(Current Opinion Genetics & Development 2014)，促进癌症进程。

Preliminary explorations of rules in the evolution of genotype-phenotype map (GPM) In recent years, the integrative efforts across genomics, molecular biology and developmental biology identified numerous mutations underlying phenotypic evolution. However, whether there are some intrinsic rules governing the evolution of genotype-phenotype map (GPM) is seldom studied. Our efforts revealed several rules seemingly caused by mechanistic bias on developmental, regulatory and mutational levels. First, compared to mammals, non-mammal animals often adopt a LTR-mediated RNA-duplication mechanism, which leads to a complex gene structure presumably playing a radically novel function in phenotypic evolution. Thus, different species may have radically different genotypic space. Second, as advocated by the Evo-Devo school, mutations minimizing negative pleiotropic effects between tissues or developmental stages is more likely fixed as supported by an excess of new genes in human brain or frequent loss of midgut-specific genes. Finally, the regulatory similarity between spermatogenesis and tumorigenesis facilitates that the latter can often hitchhike testis-specific young genes, which could be viewed as a cost of new gene origination.

跳虫的整合分类思考

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跳虫（弹尾纲）广泛分布于全世界的各种陆生环境，是三大土壤动物（线虫、螨、跳虫）之一。传统上跳虫分类主要依赖于外部形态特征，如体色、毛序、口器等，但仍有很多物种或类群极为保守，形态上难以区分。多数据来源的整合分类思路为跳虫分类提供了便利，同时也产生了不少实际操作问题，如匹配跳虫的物种概念、数据来源类型及分析方法、物种界定标准。泛物种（separately evolving metapopulation lineage, de Queiroz, 2007）概念为分类实践提供了可操作性的理论基础。适合于跳虫的分类数据主要来自于形态学、核基因、线粒体基因、生态/地理等领域；为了确保可靠的跳虫物种单元，界定策略倾向于分类单元保守地兼容所有的数据类型及分析方法。对于具体的分类数据而言，形态学仍需拓展更多的新特征以满足形态差异的发现，分子分类较合适的分析策略为距离法 ABGD、进化模型法 PTP 及多基因溯祖贝斯法 BPP，种间地理距离阈值约 100 公里。

Integrative taxonomy in Collembola

Springtails (Collembola), one of the three major soil animals (nematodes, acariformes, collembolans), are widely distributed in all kinds of terrestrial ecosystems. Traditional taxonomy of Collembola relies on external morphological characters, such as pigmentation, chaetotaxy, mouth parts etc. However, many species or complexes are difficult to discriminate because of their stasis in morphology. Multisource integrative taxonomy provides powerful tools for collembolan taxonomy although there are some practical problems in available species concepts, selection of data disciplines and analytical methods, and delimitation criteria. Unified species concept (separately evolving metapopulation lineage, de Queiroz, 2007) provides theoretical groundwork for operational taxonomical practices. Taxonomical data for Collembola is easier to obtain from morphology, nuclear DNA, mitochondrial DNA, ecology/geography etc. To recognize the reliable collembolan species, operational taxonomical units should be congruent across data and delimitations. Among disciplines used in collembolan taxonomy, morphology requires more new characters to discover diagnostic differences between species; robust analytical methods for DNA taxonomy are distance-based ABGD, evolutionary model-based PTP, and multilocus Bayesian delimitation BPP; inter-specific threshold of geographical distance is approximate 100 km.

5000 species vs. 5000 genes: Tree of Life from root to tips

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Molecular phylogenomics has seen significant progress over the past few years. Genome-wide DNA sequences have been employed in reconstruction of Tree of Lives for major taxon groups, e.g., insects, plants, fishes. In particular, a robust phylogeny has been built for Insecta, the most diverse eukaryotes, using a set of 1,478 single-copy orthologous genes obtained from full transcriptomes for 144 arthropods. Much larger transcriptomic datasets are being coordinated in reconstructing phylogenies for sub-lineages of insects. At the same time, other large data sources from anchored enrichment or ultraconservative element approaches will fill in gaps where fresh RNA materials are not available. These vast amounts of genomic data will solidify the backbone phylogeny for major insect lineages. However, the Tree of Life also needs insights at the tip-level, where COI barcodes and a few nuclear genes may play major roles in recovering species-level phylogeny. In this presentation, I propose an approach to integrating -omics data and barcodes to construct a TOL from root to tips, using Trichoptera as an example.

基于多物种隔离移民模型的基因流检测方法

朱天琪

我们建立了基于极大似然方法的用于估计基因组数据中物种（群体）间移民率的方法。假设物种树已知，两个近缘物种中存在移民，但与外群无基因交流。通过用马氏链刻画系谱过程，并通过数值积分实现似然函数的计算。该方法现在可用于分析每个位点上有两条或者三条序列的数据，并允许非对称的基因流。该方法可迅速分析上万个位点的数据，因此可用于分析基因组数据是否存在基因流信息。通过基因树后验概率的计算，可以识别基因组中发生基因流的位点和区域。通过对多组数据的计算机模拟，我们测试了似然比检验的统计特性。模拟结果显示，外群的使用极大地提高了估计的精度和检验的功效。最后，我们用该方法分析了一个果蝇数据，分析结果显示，两个近缘物种间存在单向的基因流，强度大致为 0.02 个个体 / 代。

Maximum likelihood implementation of an isolation-with-migration model for testing gene flow

We develop a maximum likelihood (ML) method for estimating migration rates between species using genomic sequence data. A species tree is used to accommodate the phylogenetic relationships among three species, allowing for migration between the two sister species, while the third species is used as an out-group. A Markov chain characterization of the genealogical process of coalescence and migration is used to integrate out the migration histories at each locus analytically, whereas Gaussian quadrature is used to integrate over the coalescent times on each genealogical tree numerically. This is an extension of our early implementation of the symmetrical isolation-with-migration model for three species to accommodate arbitrary loci with two or three sequences per locus and to allow asymmetrical migration rates. Our implementation can accommodate tens of thousands of loci, making it feasible to analyze genome-scale data sets to test for gene flow. We calculate the posterior probabilities of gene trees at individual loci to identify genomic regions that are likely to have been transferred between species due to gene flow. We conduct a simulation study to examine the statistical properties of the likelihood ratio test for gene flow between the two in-group species and of the ML estimates of model parameters such as the migration rate. Inclusion of data from a third out-group species is found to increase dramatically the power of the test and the precision of parameter estimation. We compiled and analyzed several genomic data sets from the *Drosophila* fruit flies. Our analyses suggest no migration from *D. melanogaster* to *D. simulans*, and a significant amount of gene flow from *D. simulans* to *D. melanogaster*, at the rate of ~ 0.02 migrant individuals per generation.

纤毛类原生动物系统发育基因组学研究

熊杰 姜传奇 杨文涛 缪炜

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纤毛类原生动物（纤毛虫）具有丰富的物种多样性，纤毛门包括了 2 亚门 11 纲 57 目 300 科，有超过 8000 多个形态描述种，然而彼此间的系统发育关系依然存在许多争论。随着基因组测序技术的迅猛发展，我们对 10 种膜口类、2 种盾纤类和 14 种缘毛类纤毛虫进行了基因组 / 转录组测序，基于这些高通量数据在组学水平上探讨了它们的系统发育问题。

Phylogenomics of ciliates

The ciliated protozoa (ciliates) possess abundant diversity, the Phylum Ciliophora are now divided into two major subphyla, including 11 classes, 57 orders and 300 families, more than 8,000 species. And yet there are ambiguous phylogenetic relationships of these taxon which are not well supported by both molecules and morphology. With the development of the genome sequencing techniques, we sequenced genomes/transcriptomes of 10 representatives of hymenostomes, 2 representatives of scuticociliates and 14 representatives of peritrichs, and then discussed the phylogenetic relationships within them based on these omic data.

食肉目犬型超科和灵长目疣猴亚科分子系统学研究

于 黎

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以喜马拉雅 - 横断山区为中心的中国西南部因其特殊的地形地貌以及复杂多样的生境成为研究生物多样性演变机制的天然实验室。以这一生物多样性关键区域中的两个重要动物类群—食肉目犬型超科 (Caniformia) 和灵长目疣猴亚科 (Colobinae) 为研究模型系统, 开展分子系统发育研究。通过不断发展和完善有效, 高分辨率的遗传标记系统, 针对这两个类群的不同分类阶元中长期争论不休, 备受关注的系统发育难题开展研究, 研究结果进一步揭示了食肉目犬型超科物种形成和演化历史, 为一些长期争论不休, 备受关注的系统发育难题提供了重要信息, 并为这两个重要类群的适应性进化遗传机制研究奠定基础。

The Promise and Limitation of Plant Phylogenomics

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Abstract:

Phylogenomics based on chloroplast genomes and nuclear genes has shown great achievements in plant phylogenetic research in recent years. However, there are some errors/bias in plant phylogenomic reconstruction causing the poor fitness between molecular data and evolutionary model. Inaccurate phylogenetic relationships are often inferred when the data poorly fit to the substitution model. In this presentation, I will present our recent progress in plant phylogenomics focusing on resolving ancient phylogenetic relationships, discuss potential errors limiting the resolution of phylogenomic inference, and provide some approaches to improve the goodness of fit between the model and data.

Genetic diversity and molecular evolution of Potato Virus Y in China

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Potato virus Y (PVY) is one of the most destructive pathogens constraining sustainable development of potato industry. Currently, knowledge of the population genetic structure and evolutionary biology of the pathogen is limited, but it is vital in developing sustainable management schemes. In this study, the population genetic structure and molecular of PVY were studied using 181 *P1*, 248 *P3*, 184 *CI*, 182 *VPg* and 305 *CP* gene sequences of viral isolates collected from four potato cropping areas in China, including northern single-cropping area (NSA), central double-cropping area (CDA), southern winter cropping area (SWA) and southwestern mixed cropping area (SMA). Sequence analyses showed that haplotype diversity and nucleotide diversity in the PVY populations from four cropping areas were all higher than 0.50 and 0.50×10^{-2} , respectively, indicating that a high genetic diversity in these areas. The genetic differentiation between PVY populations from SMA and other areas were all significant (all *FST* values > 0.15), indicating a great spatial structure of the pathogen. An extended Bayesian skyline plot (EBSBP) revealed a relatively explicit demographic history for population expansion by showing that the same derived four populations experienced a demographic expansion recently. Pairwise nucleotide sequence identities in respective *P1*, *P3*, *CI*, *VPg* and *CP* genes varied, but were higher than 72%, in which *P1* and *P3* had 52.06% and 49.23% polymorphic sites, respectively, suggesting the two genes were highly variable. Intragenic recombination signals were detected in *P1*, *VPg* and *CP* genes but not *P3* and *CI* genes in the four cropping populations. A majority of polymorphic sites in the five genes were under purifying selection using FEL, IFEL and MEME, suggesting that many of the mutations in the five genes are harmful and consequently eliminated by natural selection. However, some polymorphic sites in *P3*, *CI* and *CP* genes were under positive selection, suggesting that these mutations were beneficial for PVY survival. Significant population subdivision was detected in the viral populations originated from different geographic regions by Bayesian Tip-Association Significance (BaTS) testing, demonstrating local environment also plays an important role in the adaptation of the pathogen. In addition, high levels of genetic flow occurred among the cropping areas except between NSA and SMA, CDA and SMA, which indicated gene flow was also one of the important factors that shape the structure of PVY populations in China. Taken together, mutation, recombination, natural selection and gene flow all contribute to the genetic diversity and population dynamic of the virus. This study extends our understanding in the population genetic structure and evolutionary processes of PVY.

基于基因组学方法研究鱼类适应辐射

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适应辐射是指由于环境变化而出现生态机遇时，某一生物支系由此快速演变产生多种多样、各自适应于独特生态位的物种或者群体的过程；导致不同生态位物种或群体间的趋异进化和相似生态位物种间的趋同进化或群体间的平行进化；是产生生物多样性的重要方式。尽管自然界中不乏适应辐射的例子，但适应辐射仅发生在某些特定的生物类群中。因为适应辐射的发生，不仅需要生态机遇而且需要相应的遗传基础，即生物面对生态机遇时需要迅速地产生可遗传的表型改变及遗传创新从而与环境相互作用以利用生态机遇。适应辐射发生于辐鳍鱼类这一种类最丰富的脊椎动物的多个类群中，如鲷鱼、刺鱼，极大的丰富了辐鳍鱼类物种的多样性。因此，鱼类适应辐射发生的遗传基础一直是进化生物学的热点研究之一。本报告旨在结合已有研究和本人的个人研究总结讨论目前用于研究鱼类适应辐射遗传基础的基因组学方法。

Taking genomic approaches to understand adaptive radiation in fish

Adaptive radiation refers to the process that certain organismal lineage has exhibited an exceptional extent of adaptive diversification into a variety of ecological niches when environmental changes result in ecological opportunity, with such divergence often occurring extremely rapidly. Adaptive radiation generates both disparities – divergent evolution among species and/or among populations within species in different ecological niches, and similarities – convergent evolution among species and parallel evolution among populations within species in geographically independent but ecologically similar niches. Adaptive radiations play key roles in the generation of biodiversity. Although adaptive radiation is not rare in wild, it occurs in only certain organismal lineages. It is due to that adaptive radiation is not only is triggered by accessing to novel ecological opportunity, but also requires underlying genetic basis that can relatively rapidly generate phenotypic modifications and innovations to utilize ecological opportunity. Adaptive radiation occurred in several lineages of ray-finned fish—the most diverse and species-rich group of vertebrates, e.g., in cichlids and in sticklebacks, which contributed the ray-finned fish species richness. Therefore, understanding the genetic basis that drive adaptive radiation in fish has long been the hotspot topic of evolutionary biology. In this presentation, I will summarize the current genomic approaches used to uncover genetic basis of adaptive radiation in fish by including my own studies.

隆肛蛙属 (*Feirana*) 物种及种群分化研究

(Amphibia: Anura: Dicroglossidae)

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隆肛蛙属 *Feirana* 是中国特有的两栖动物类群, 因其独特的特征(肛部隆起)和繁殖行为方式(无抱对)而广受关注。本文系统地介绍了我们在属的建立与物种组成, 形态、遗传分化与物种种群组成, 谱系的地理分化与发展过程, 物种同域分布区分布型、遗传隔离, 种间竞争和局地适应对表型进化中的作用等方面取得的研究进展。发表 3 新种, 建立 1 新属, 界定了各物种的种群组成。发现隆肛蛙和太行隆肛蛙在秦岭地区有大范围的重叠分布区, 并存在 5 个型, 未检测到物种间基因交流, 这两个物种在同域分布时资源利用相关的特征(头体长、头长)趋异, 而与视觉相关的特征(眼径、眼间距)趋同。该属物种在末次大冰期存在多个避难所, 隆肛蛙的秦岭和米仓山-西秦岭支系在距今 2 万年后开始种群快速扩张, 结果导致了他们形成现今的二次接触区。

关键词: 隆肛蛙属、分类、谱系地理、分布格局、基因流、适应进化、功能性状、资源竞争、同域分布

Species and population differentiation in the genus *Feirana* (Amphibia: Anura: Dicroglossidae)

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The genus *Feirana* is endemic to China and has been widely followed with interests since their anal bulged and reproduction without amplexus behavior. Here we introduce our work on genus establishment and species composition of *Feirana*, morphological and genetic differentiations and population composition, lineages differentiation of each species, geographical distribution patterns and their genetic flow within sympatric region, inter-specific competition and local adaptation shaping the phenetic evolution of characters. Three new species were discovered and one new genus was established. *Feirana quadranus* and *F. taihangnica* occupy a large range as the overlapped region, with five types of the pattern, within their geographical distribution, and gene flow was not testified between the two species while characters e.g. the head length and head wide with resources use trend to

divergent but those related to visual ability trend to convergent. Multiple refugia existed for them during the last glacial maximum, populations of *F. quadranusthat* originated in the Daba Mountains colonized the Main Qinling Mountains after the LGM, recent sharp expansion of the Micang–Western Qinling and Main Qinling lineages probably contribute to their present-day secondary contact.

Key words: Feirana, Taxonomy, Phylogeography, Distribution pattern, Gene flow, Adaptation evolution, Functional trait, Resource completion, Sympatry

Pathogen genomics and evolution

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Infectious diseases are of the most pivotal concerns to the public health, as there are about 15 million of people died from them in each year. The emergence and re-emergence of pathogens, such as influenza virus, MERS-corona virus, Ebola viruses, yellow fever virus, have occasionally caused outbreaks worldwide in recent years and thus led to great losses. Owing to the development of sequencing techniques, applying the views of genomics to dissect genetic diversity and evolutionary dynamics of pathogens are becoming the mainstream. In this talk, I will present applications of using pathogen genomics and bioinformatics to address the issues of origin, transmission and evolution of pathogens. **Origin and transmission of H7N9 influenza virus.** The H7N9 avian influenza virus is a kind of segmented RNA viruses with eight distinct genes, and genetic reassortment is one of the key features. Applying phylogenetics and coalescence analyses, we discerned that the origination of H7N9 influenza virus was from at least four different lineages of influenza viruses; and during rapid transmission, its genetic diversity increased dramatically through the exchange of internal genes with poultry H9N2 influenza viruses. This mechanism is different from H1N1 and H5N1 influenza viruses.

MrBayes 的 GPU 优化算法进展

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MrBayes 是最流行的基于贝叶斯推断的种系发生学软件之一。它的核心是名为 Metropolis-coupled Markov chain Monte Carlo (MCMCMC or $(MC)^3$) 的算法。它可以通过物种已知的 DNA 序列推断物种间的演化关系树。但是，遗憾的是， $(MC)^3$ 算法的计算速度非常慢，特别是在基因测序进入大数据时代后。MrBayes 的计算速度远不能满足生物学家的需要。

在这个报告中，我们将介绍在使用 GPU 加速 MrBayes 方面取得的一些进展和最新的工作情况。这一工作起步于 2011 年 (Bioinformatics)。在 2013 年发布的版本中，取得了 170 倍的加速。2015 年，面向蛋白质领域研究，设计了针对蛋白质数据的优化算法。目前，正在完善针对 MrBayes3.2 的 GPU 优化版本。

软件下载地址：<https://sourceforge.net/projects/mrbayes-gpu>

The advance of GPU based algorithms for MrBayes

MrBayes, using Metropolis-coupled Markov chain Monte Carlo (MCMCMC or $(MC)^3$), is a popular software package for Bayesian phylogenetic inference, which uses an iterative approach to derive an evolutionary tree for a collection of species whose DNA sequences are known. The $(MC)^3$ Bayesian algorithm and its improved and parallel versions are now not fast enough for biologists to analyze massive real-world DNA data. Recently, graphics processor unit (GPU) has shown its power as a coprocessor (or rather, an accelerator) in many fields.

In this report, a GPU based MrBayes is introduced, its first version is released in 2011 (Bioinformatics). In 2013 (MBE), the speedup for DNA improved to up 170. In 2015 (MBE), a special version for protein data is released. Now, some new optimized algorithms are doing for next release version.

Download: <https://sourceforge.net/projects/mrbayes-gpu>

脉翅类昆虫的系统分类与宏演化

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脉翅类（脉翅总目）是完全变态类昆虫中具有关键系统地位及生态功能的重要类群，具有高度多样化的适应性特征及独特的地理分布格局，并具有一定的生防应用价值。近年来，对亚洲广翅目、东亚蛇蛉目、白垩纪缅甸琥珀脉翅类等昆虫进行了大量分类修订研究，系统记述 500 余个物种，建立 2 新科、3 新亚科，发现 20 新属、185 新种。在此基础上，综合形态、分子、化石等多方面数据，对脉翅类科间系统发育以及泥蛉科、齿蛉亚科、螳蛉科等类群的系统发育进行了研究，初步探讨了以下关于脉翅类演化方面的科学问题：1) 脉翅目捕捉足的演化格局；2) 脉翅目食性的早期演化；3) 泥蛉科的系统发育与地理分布格局的形成；4) 齿蛉亚科性选择特征的演化；5) 脉翅目科间系统发育及幼虫栖境的演化格局。

Systematics and macroevolution of Neuropterida

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The superorder Neuropterida is one of the holometabolous insect groups with significant systematic and ecological status. This group possesses highly diversified adaptive traits and remarkable distribution patterns, while some species of Neuroptera can be also used as natural enemies for biological control. In recent years, we studied the systematics of many groups of Neuropterida, including Megaloptera from Asia, Raphidioptera from East Asia, Neuropterida from the Cretaceous amber of Myanmar. Approximately 500 species were described, with establishment of 2 new families and 3 new subfamilies, and description of 20 new genera and 185 new species. Accordingly, we reconstructed the phylogenetic relationships among the families of Neuropterida as well as the phylogeny within Sialidae, Corydalinae, Mantispidae, etc., by using combined dataset from morphology, molecule and fossils. A number of interesting questions concerning the evolution of Neuropterida were discussed, including 1) the evolution of raptorial leg in Neuroptera, 2) the early evolution of feeding habits of Neuroptera, 3) the phylogeny and biogeography of Sialidae, 4) the evolution of sexually selected traits in Corydalinae, and 5) the familial relationships of Neuroptera and the evolutionary pattern of the larval life-style.

杂交、生态选择和青藏高原适应性起源的进化遗传学：高山松同倍性杂交物种形成研究进展

Hybridization, ecological selection, and the adaptation to Tibetan Plateau: what we learned from the homoploid hybrid speciation studies of *Pinus densata*

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Abstract: Genetic exchange (hybridization, lateral gene transfer and symbiosis) has been highlighted the main driving forces for generating innovation and genomic complexity, and the important process shaping biodiversity. Evidences of interspecific hybridization are accumulated in almost all pro-/eukaryotic lineages, including human and Neandertal, mice, butterflies, Darwin finches, cichlids mosquito and most of plant taxa. Reticulate evolution (Web of Life), process incorporating genetic exchange and conflict with traditional Tree of Life, has already been used to approximately depict the formation and evolution of biodiversity. Evolutionary processes and genetic components underpinning the genetic exchange among diverged lineages remain unclear, especially for cases featured with long divergence history, broad geographic range and complex ecological shift. In our study, we used *Pinus densata* (高山松), an evidenced homoploid hybrid pine tree living across the high mountains of southeast of Tibetan Plateau, and its two putative parental pines, *P. yunnanensis* (云南松, from Yun-Gui Plateau) and *P. tabuliformis* (油松, from the northern China) as research system. We tackled questions: (1) population genetic divergence of the pine species complex; (2) fitness of the hybrid lineage and its isolation with the parental; (3) genetic and ecological components of the origin of unique adaptation to Tibetan Plateau in the hybrid lineage. We found: (1) the ancient hybrid zone may be in the east edge of the southeast part of Tibetan Plateau; (2) the hybrid lineage experienced extensive introgression from both the parental pines and runs of genetic bottleneck events in its colonization of the high mountains of Tibetan Plateau; (3) the formation (speciation) of the hybrid lineage featured with distinguished ecological transition and ecological selection (with elevation as an agent) is the key factor in maintaining the isolation among the taxa but not any factors of internal genomic mechanisms; (4) the unique high-elevation adaptation of the hybrid was correlated to gene expression pathways and genes of environmental signaling and adaptation. Our study provide fascinating case of hybrid speciation and ecological speciation, and contribute to our understanding of the evolution of Tibetan vegetation.

Kin–bonds of bachelor males contributes to the evolution of primates multilevel society

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In contrast to most mammalian social systems, a small number of primates, including early humans, live in multilevel societies (MLS) in which multiple family units co-exist to forming breeding band of several hundred of individuals and an associated all-male bands (AMB). Although primate MLS has importance for the understanding the origin of human sociality, previous knowledge mainly focused on the African Papionins, and revealed that MLS evolved from internal fissioning process from large multi-male/multi-female group. Based on a combination of social network analysis, satellite telemetry, and genetic investigation, we estimated the dynamic of interactions between bachelor males to restructure their affiliation patterns, cooperative and tolerance behavior to form and maintain a larger AMB in golden snub-nosed monkeys (*Rhinopithecus roxellana*). The results show bachelor males forming stronger alliance when they approaching to breeding females, using a novel HPMT mathematic model, we demonstrate that the kinship was the most important factor facilitating alliance formation among AMB, followed by age and dominance rank. We suggest that an 'arms race' between breeding males collective defense against the attempted usurpation of bachelor males, and bachelor males aggregative offense for reproductive opportunities selected for larger groups on both sides. This provides further support for the *R. roxellana* MLS having evolved from a fusion of a network of small, isolated family groups in an ancestral Asian colobine, as well as implicates understanding of the human social evolution, because male-male affiliations are trademarks of small- and large-scale human societies.

Keyword: all-male group; multilevel society; social network analysis; kinship; fusion hypothesis; Cliquishness

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From genome evolution to virus transmission, intra-host variation and infection mode: an EBOV perspective

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Abstract:

The 2013-2016 epidemic of Ebola virus disease (EVD) in Western Africa was unprecedented, with 28,616 confirmed, probable and suspected cases and 11,310 deaths as of June 10, 2016. The timely Next Generation Sequencing (NGS) of plenty of Ebola virus (EBOV) genomes provides an opportunity to trace the origin, evolution and spread during the epidemic. In the present study, we show that how the EBOV sequence data was used to reconstruct the transmission network in West Sierra Leone and to study the intra-host nucleotide variation of the virus. In addition, we have also correlated the molecular evolution with different infection modes. To conclude, this outbreak marked the beginning of large-scale real-time molecular epidemiology, which would be crucially important in our attempts to track and control future infectious disease outbreaks.

华溪蟹属的物种多样性发生与分类界定*

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中国特有的淡水蟹类——华溪蟹属 (*Sinopotamon Bott*, 1967) 或广义华溪蟹属 (*Sinopotamon s. lat.*) 是全球溪蟹科 (*Potamidae Ortmann*, 1896) 物种多样性最丰富、地理分布最广的一个类群。它为我们深刻认识内陆淡水生态系统生物多样性的进化历史和驱动机制提供了理想的模型。本文基于深入的全分布区标本采集 (覆盖 75% 以上的已知华溪蟹物种), 联合线粒体和核 DNA 标记, 对华溪蟹多样性的发生与驱动机制进行了研究, 并就华溪蟹的分类和物种界定进行了探讨。研究发现, 现生华溪蟹属的物种多样性经历了时空及支系间的异质性变化; 分布在中西部地区的华溪蟹 (分支 II) 经历了更新世近期 (0.7 百万年前) 的加速多样化, 这促使华溪蟹物种多样性的快速辐射。进一步联合线粒体和核 DNA 条形码标记重建的华溪蟹及溪蟹科近缘属种的系统发生关系提示, 现有的广义华溪蟹属 (即经典的华溪蟹属)、狭义华溪蟹属 (*Sinopotamon s. str.*) 和龙溪蟹属 (*Longpotamon Shit*, Huang & Ng, 2016) 均非单系类群。综合 4 种物种界定方法对华溪蟹分支 (包括华溪蟹及 6 个近缘属) 中全部 68 种华溪蟹分析显示: 约 50% 的物种 (35 种) 得到至少 1 条标记和两种以上界定方法的支持; 在其余的 24 种华溪蟹中, 无论使用何种标记 (除 CO I 外) 或何种界定方法分析, 光泽华溪蟹 (*S. davidi*)、灌县华溪蟹 (*S. kwanhsiense*)、复兴华溪蟹 (*S. fuxingense*) 和峨眉华溪蟹 (*S. emeiense*) 共同形成一个种组 (或物种复合体), 类似的情况还见于长江华溪蟹 (*S. yangtsekiense*)、河南华溪蟹 (*S. honanense*) 和陕西华溪蟹 (*S. shensiense*) 等, 然而这些物种彼此之间在雄性第 1 腹肢和雌性生殖孔等特征上均可以明显区分; 有必要综合分子分类、形态特征、地理分布和生活史等数据信息的整合分类学方法对华溪蟹的分类和物种界定进行全面分析。

Diversification of *Sinopotamon* crabs, taxonomy and species delimitation*

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土壤动物多样性维持及其在生态系统中的功能

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“土壤动物多样性及其在生态系统中的功能”是近年来学科前沿与热点。本报告以东北黑土农田为例，介绍近年来在该地区开展长期人类活动影响下农田土壤动物多样性如何维持这一科学问题的一些结果，同时探讨不同体长土壤动物在农田生态系统中功能作用，认识“农田耕作影响-土壤动物响应-生物多样性维持及功能实现”的过程与机制。

Soil Animal Biodiversity Assemblage and its Function in Ecosystem

“Soil animal biodiversity and its function in ecosystem” is a hotspot in soil animal ecology in recent years, and scientists pay more and more attention in this field. Soil environmental degradation is a key ecological problem in farmland, and it would be harmful to soil animal biodiversity. This research in farmland is one of most important and significant work to national ecological safety in the world. In this report, we show soil animal biodiversity in black soil region of Northeast China to discuss how to keep, protect and utilize them in the farmland degeneration environment. Basing on profoundly knowing the process and the mechanism of “the farmland cultivation influence - soil animal response - biodiversity maintenance” in the multi-scale farmland field, we hope to understand the mechanism of soil animal biodiversity assemblage in the farmland, and simultaneously appraise the different body length soil animal's ecological function to the farmland ecosystem in the long-term cultivation farmland.

非序列联配方法在基因组进化中的理论与应用

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不依赖于序列联配方法，通过对序列中所有可能出现的 Kmer 的统计特征的比对和分析来实现系统发育的构建。这类方法对获取基因组总体特征上有独到的优势，但是目前仍没有一个基于 kmer 频率的进化模型，这限制了这类方法只能使用 NJ 类的距离树来得到系统发育关系。这限制了这类方法的应用。本文使用成熟的 CVTree 方法针对哺乳动物纲建立了系统发育树并进行了深入分析。同时，我们探讨了一个基于 *kmer* 频率的进化模型。并尝试在模型中引入信息理论中交互信息量的概念，来得到一个基因组遗传信息随进化逐步增加的进化图景。

The theoretical basis and application of sequential alignment free method in genome evolution

The sequential-alignment-free method were used to construct phylogenic tree via extracting statistical feature of genome sequences and feature alignment approaches. These methods took advantages on obtaining over-all feature of the whole genome, but the lack of an undergoing evolutionary model limited the application of these methods. In this work, an NJ tree for mammal class were constructed with a intensive studied program CVTree. At the same time, an evolutionary model based on *kmer* frequency were made in this work. The concept of mutual information were attempted to introduce to obtained an evolutionary insight that the genetic information of the whole genome tends to increasing during the life history.

The BIG Data Center: from deposition to integration to translation

Zhang Zhang on Behalf of BIG Data Center Members

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Biological data are generated at unprecedentedly exponential rates, posing considerable challenges in big data deposition, integration and translation. China has become a powerhouse in generating vast quantities of biological data, but is in the embarrassing situation of lacking a centralized data center that is committed to opening data in this big data world and to making data well-organized and publicly accessible to worldwide scientific communities. The BIG Data Center, established at Beijing Institute of Genomics (BIG), Chinese Academy of Sciences, provides a suite of database resources, including (i) Genome Sequence Archive, a data repository specialized for archiving raw sequence reads, (ii) Gene Expression Nebulas, a data portal of gene expression profiles based entirely on RNA-Seq data, (iii) Genome Variation Map, a comprehensive collection of genome variations for featured species, (iv) Genome Warehouse, a centralized resource housing genome-scale data with particular focus on economically important animals and plants, (v) Methylation Bank, an integrated database of whole-genome single-base resolution methylomes and (vi) Science Wikis, a central access point for biological wikis developed for community annotations. The BIG Data Center is dedicated to constructing and maintaining biological databases through big data integration and value-added curation, conducting basic research to translate big data into big knowledge and providing freely open access to a variety of data resources in support of worldwide research activities in both academia and industry. All of these resources are publicly available and can be found at <http://bigd.big.ac.cn>.

从 DNA 条形码到生物多样性

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DNA 条形码自 2003 年提出以来 (Hebert et al. 2003), 主要作为物种识别的方法和手段, 被认为是经典形态分类的重要补充。条形码技术和理念极大地促进了人们对全球生物多样性认知的广度、深度和速度, 目前 DNA 条形码的应用已经向进化、生态学的多个研究领域延伸, 从最初单纯的物种识别、隐存种发现, 到海关检疫、外来入侵种检测、药材检测, 到生态系统食物链、食物网构建, 到物种多样性的评估、描述和监测, 再到生物多样性维持机制的研究。本文主要回顾 DNA 条形码研究方法及算法的进展, 包括基于人工智能的 DNA 条码识别方法 (Zhang et al. 2008a)、基于机器学习 (Zhang et al. 2012a)、模糊数学理论 (Zhang et al. 2012b) 等 DNA 条形码的方法, 及相关软件的开发 (Zhang et al. 2008b, Zhang et al. 2016), 同时简单回顾 DNA 条码技术的最新发展, 包括宏条形码 (metabarcoding), eDNA, 及条码技术在生物多样性维持机制方面的潜在应用。

From DNA barcoding to biodiversity

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DNA barcoding was initially proposed to serve as a tool for species identification basically. However, it has largely improved our understanding of global biodiversity. Currently, DNA barcoding has extended its application to many research fields, including monitoring of invasive species in the customs and quarantine, species identification of traditional Chinese medicine, construction of food web, measurement of biodiversity, mechanisms of biodiversity maintenance. We review the main advances of DNA barcoding methodology, BP-based species identification approach (Zhang et al. 2008), machine-learning based approach (Zhang et al. 2012a), fuzzy-set based approach (Zhang et al. 2012b), and the latest program BarcodingR (Zhang et al. 2016), and its potential applications.

选择的特征与特征的选择

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由于进化历史无法再现,在物种分类、定义与系统发育关系重建时必须使用生物所具有的特征。然而,由于异源同形、特征进化不同步等原因,选择不同特征可能产生极为不同的结果。无论是进化论、支序系统学原义都要求使用同源的、在自然选择作用下不断改进完善和分异的特征。我国蜉蝣近年来的研究显示,如果更多考虑特征的功能,使用多维特征特别是生态学、生物学特征在系统学中,也许能得到更有说服力的结果。

Choosing and Using the Characters favored by Natural Selection

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Because the exact evolutionary process of life has disappeared, in species classification, definition and phylogeny reconstruction, we had to use the characters the life are having. However, different character clusters can produce very different results because of homoplasy and different evolving rates of characters. In order to avoid this kind of paradox and weakness, both evolution theory and cladistics argued originally to use homological characters, under and through the natural selection, with different evolved and improved forms. Some cases of Chinese mayfly research show the multi-dimensional characters, especially those ecological and biological characters with some clarified functionary interpretation and explanation, may provide powerful and convincing proposal in systematics.