



中国鸟类研究简讯

Newsletter of China Ornithological Society



中国动物学会鸟类学分会
China Ornithological Society



全国鸟类环志中心
National Bird Banding Center

第28卷 第1期 Vol. 28 No. 1 2019年6月

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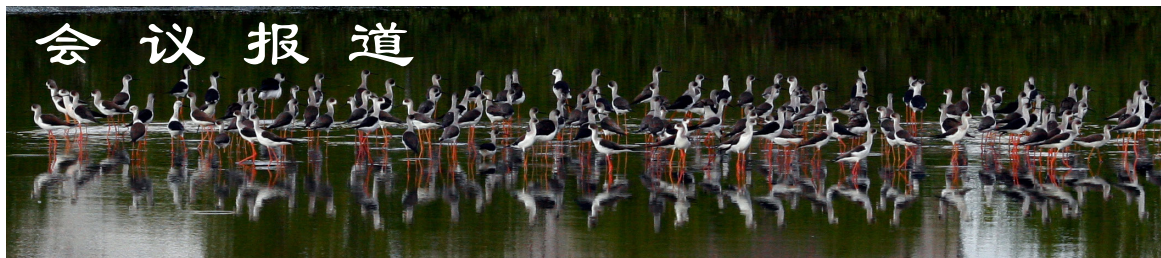
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2019 年全国春季鸟类环志培训班在北戴河举办

2019 年 5 月 6 日—11 日，全国鸟类环志中心在河北省秦皇岛鸟类保护环志站举办了“2019 年全国春季鸟类环志培训班”。参加培训班的学员分别来自全国各鸟类环志站新参加环志工作的人员，共 26 个单位 40 余人。

本期培训主要采取室内授课与野外实践相结合的形式。培训班上，全国鸟类环志中心的相关领导和专家分别介绍了《中华人民共和国野生动物保护法》和鸟类环志管理规定、全国鸟类环志概况、鸟类学基础知识、鸟类环志技术规程、鸟类识别与分类、彩色标记物的制作和佩戴、迁徙鸟类的卫星追踪等相关技术以及鸟类环志野外操作要点等内容。

培训期间，各环志站相互交流了鸟类环志情况、经验以及对出现的问题应采取的解决办法。培训班最后通过试卷考试以及野外实践考核的方式对培训人员进行了考核，参加培训的学员全部通过了考核。本次培训期间，共环志鸟类 24 种 263 只。

通过培训，环志人员进一步熟悉了我国新修订的《野生动物保护法》，掌握了鸟类环志的技术规程，提高了候鸟监测、鸟类环志等专业技术的能力，为规范鸟类环志管理和候鸟迁徙研究等工作的顺利开展提供了技术保障。

本次培训班由秦皇岛市鸟类保护环志站承办，并得到了秦皇岛市海滨林场的大力支

持。

(全国鸟类环志中心：陈丽霞 王毅花)

甘肃机场鸟情监测与鸟击防控系列培训

为积极应对 2019 年鸟类迁徙季，做好机场鸟情预警和防控，受中国人民解放军空军后勤部机场保障局的委托，3 月 12 日，兰州大学张立勋为榆中空军机场做了“机场鸟情观测与鸟击防控”的专题培训，结合多年对榆中盆地鸟类监测与研究成果，对空勤人员和地面保障人员约 75 人进行了培训，同时还与地面驱鸟官兵进行座谈，针对驱鸟官兵日常工作中遇到的问题逐一进行解答，并就榆中机场所处地理位置和鸟情实际，提出了驱鸟工作的方向和防控措施。

3 月 25—27 日，在武威机场进行了鸟击防范培训和现场调查，结合河西走廊东端春季迁徙鸟类的组成、常见鸟种、高危鸟种及迁徙活动规律进行了专题理论培训，重点介绍了鸟类特征、习性，建议机场建立鸟情观测数据库和鸟情预警系统，科学、规范地收集机场及其周边的鸟类多样性数据。期间走访了连队各个部门，与驱鸟队员进行座谈交流，同时与连队领导进行了深入交流，探讨了今后鸟情观测的新思路；还带领业务骨干对武威部分湿地、任务区和基础周边进行了现场鸟情调查方法和技术的指导，提出了“与鸟类迁徙季错峰，调整训练计划，合理安排训练”的建议，得到了连队干部高度认同，

最后签署了“合作协议”。



(兰州：张立勋)

中科院生态环境研究中心曹垒研究员应邀在英国鸟类学年会做阿尔弗雷德·牛顿讲席报告

2019年3月26日，英国鸟类学年会在华威大学召开。中国科学院生态环境研究中心曹垒研究员应邀在年会上做了题为“Using waterbird telemetry data to support freshwater wetland conservation in China”的阿尔弗雷德·牛顿讲席报告。

曹垒研究员介绍了研究团队运用卫星追

踪技术支持中国湿地研究和保护的工作。长期以来，人们关注的焦点主要集中在中国沿海湿地的丧失，但对淡水湿地严重受胁的现状关注较少。研究发现，2000年以来在长江中下游湿地上越冬的关键水鸟物种数量下降，这与远东其他地区相同物种的上升趋势形成了鲜明对比。有证据表明，长江中下游湿地之外的因素可能影响了这些种群的变化趋势。但由于缺乏水鸟迁徙路线结构的趋势数据，即水鸟在繁殖地、换羽地、停歇地和越冬地之间的关联，因此无法分析导致水鸟种群下降的关键区域和因素。最近在欧亚大陆的56种鸟类上部署了大量的遥测设备，为确立这些物种迁徙路线的结构，尤其是年生活周期中关键位点的研究和保护奠定了重要基础。

阿尔弗雷德·牛顿讲席报告(Alfred Newton Lecture)是英国鸟类学会授予在鸟类学领域具有国际影响力科学家的一项荣誉。曹垒研究员是第三位非英籍报告人，也是亚洲首位获此荣誉的学者。

(北京：曹垒)



雷富民研究组在鸟类高海拔适应性进化研究上获重要进展

高海拔环境的选择压力会驱动生物体表和遗传的适应。早期研究表明，不同高海拔物种在形态、生理、生化等表型特征上出现趋同，而这种趋同表型的遗传适应机制是多样的，并可能受到系统发育背景的严重影响。同时，由于野生鸟类采样困难且转录组测序样品质量要求较高，因此早期高海拔适应遗传机制的研究多集中在基因序列水平，而多物种多组织转录调控水平的研究几乎为空白。

中国科学院动物所雷富民研究组在同一个系统发育背景下，选择了 3 种来自青藏高原的高海拔雀形目鸟类 [褐冠山雀 (*Lophophanes dichrous*)、黑冠山雀 (*Periparus rubidiventris*)、棕额长尾山雀 (*Aegithalos iouschistos*)] 以及各自近缘的低海拔物种 [沼泽山雀 (*Poecile palustris*)、黄腹山雀 (*Pardaliparus venustulus*)、红头长尾山雀 (*A. concinnus*)] 进行了比较转录组学分析。该研究应用第二代高通量测序技术完成了 3 对高、低海拔物种 28 只个体 5 个组织 (心脏、肌肉、肝脏、肺脏、肾脏) 共 128 个样品的深度转录组测序，并比较了高、低海拔物种之间在序列水平和表达水平上的差异，从而揭示了鸟类如何响应高海拔的环境压力。序列比较分析发现：3 种高海拔物种在正选择基因上表现出高度的相似性 (218 个共享的正选择基因)，而氨基酸替代上的相似性极低 (3 个

高海拔物种只有 4 个基因中包含相同的氨基酸替代位点)，暗示了高海拔适应性趋同主要表现在正选择基因水平而非氨基酸替代水平。基因表达的比较分析发现：整个基因集的表达谱呈现出组织特异的表达模式 (所有物种样品按照组织聚类)；而差异表达基因集和海拔相关的基因集的表达谱则呈现出海拔相关的聚类模式，暗示了高海拔环境可能驱动了高海拔物种相似的表达改变。此外，还发现 3 种高海拔物种筛选到的正选择基因与差异表达基因存在非常低的共享率 (2.3%，218 个正选择基因中 5 个基因差异表达)，而基因表达、基因连通性及二者和海拔的交互作用与基因的进化速率显著相关。这些结果揭示了 3 种高海拔鸟类可能以序列和表达水平协同改变的方式实现其适应性进化。

不同于其他类群高海拔适应的研究，该研究首次对野生鸟类开展了多物种、多组织、多尺度的比较分析，拓展了人们对物种如何响应高海拔环境的理解。该项工作以 “Comparative transcriptomics of three high-altitude passerine birds and their low-altitude relatives” 为题于 2019 年 5 月 20 日在线发表于国际权威学术期刊《美国科学院院刊》 (*Proc. Nat. Acad. Sci. USA*, <https://www.pnas.org/content/early/2019/05/23/1819657116>)。雷富民研究员和屈延华研究员为论文的联合通讯作者；博士研究生郝艳为论文的第一作者。该项研究得到中国科学院战略先导项目 (XDB13020300) 以及国家自然科学基金重点、面上项目 (31672275、31630069 和

31572249) 的资助。

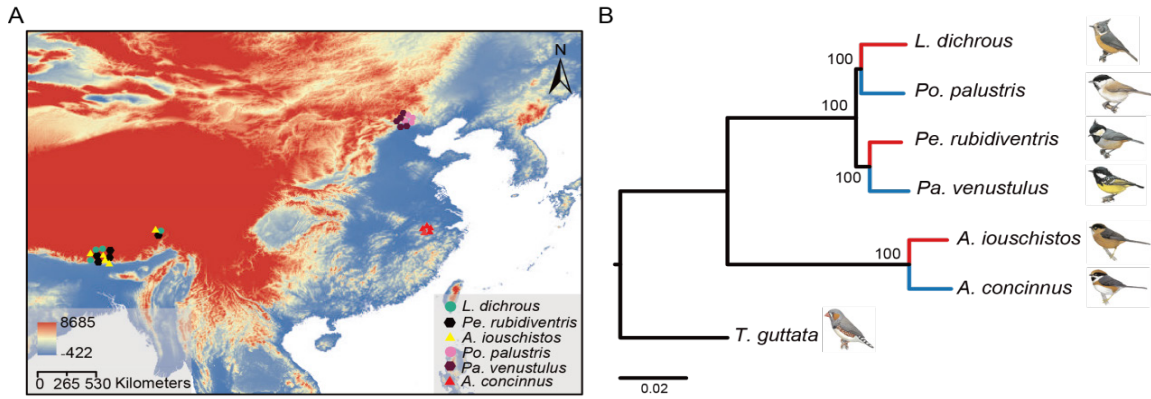


图1. (A) 样品采集地 (B) 物种系统发育关系

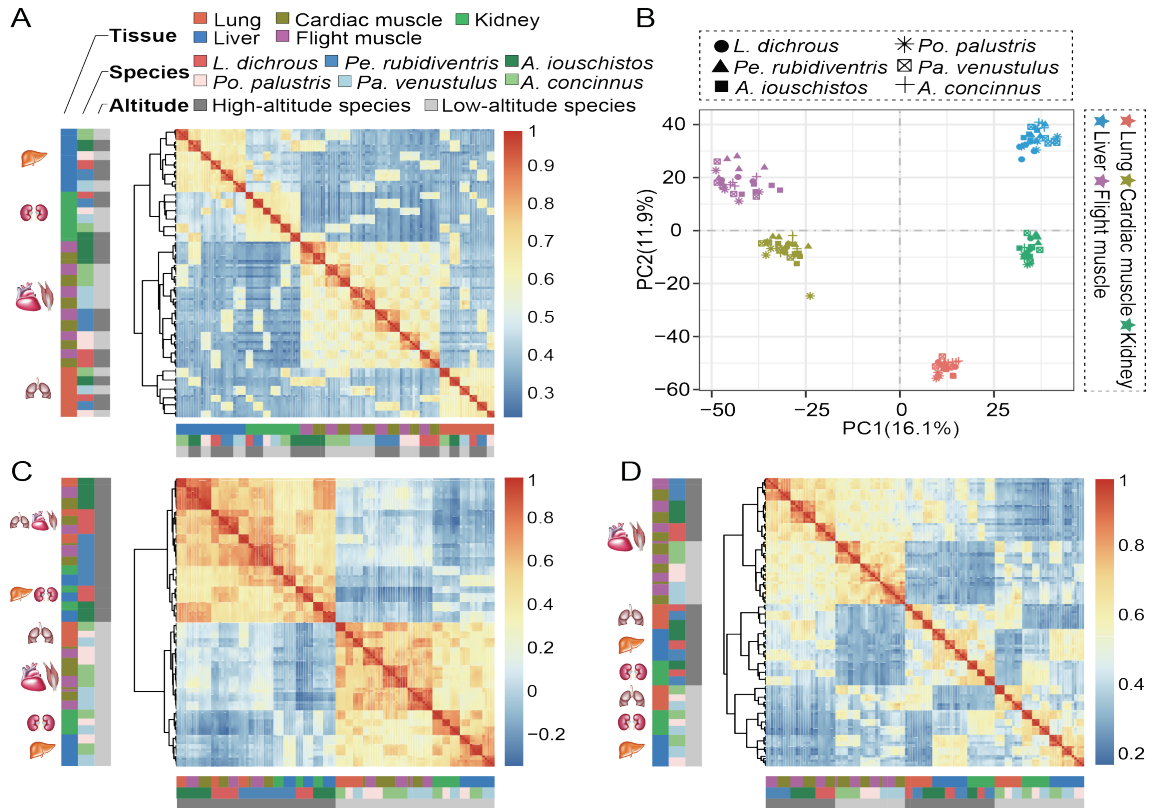


图2. (A) 整个基因集表达谱 (B) 整个基因集PCA (C) 差异表达基因集表达谱 (D) 海拔相关的基因集表达谱

(北京: 郝艳 屈延华 雷富民)

中科院生态环境研究中心曹垒课题组在动物迁徙驱动机制研究方面取得重要进展

动物追随季节性资源迁徙，是自然界最为壮观的生物现象之一。迁徙的动物与途经区域的生物群落发生物质和能量交换，这是全球生态过程的重要组成部分，具有重要的生态系统服务功能。研究动物迁徙的驱动机制，对生态学基础研究以及生态红线和自然保护区规划等国家战略都具有重要意义。中国科学院生态环境研究中心城市与区域生态国家重点实验室曹垒研究员和以色列希伯来大学 Ran Nathan 教授合作，在动物迁徙驱动机制研究方面取得重要进展，相关研究成果发表于综合性学术期刊《*Nature Communications*》上。第一作者为王鑫副研究员，通讯作者为曹垒研究员和以色列希伯来大学 Ran Nathan 教授。

“绿色波浪”假说是关于动物迁徙驱动机制的经典理论，认为食草动物的迁徙是由区域植物叶片生长的高峰驱动。但对该假说的研究和验证，仅涉及单一或少量物种（或种群）、覆盖有限的地理范围、且使用无法排除共线性变量干扰的建模方法，故该假说的普适性一直没有定论。为系统地检验“绿色波浪”假说，该研究创新地引入了随机模拟的方法，研究了欧洲、亚洲和北美洲的迁徙天鹅、雁类和鸭类，共 10 个物种、14 种种群、222 次春季迁徙。结果显示，“绿色波浪”仅能解释个别地区少量草食性鸟类种群的迁徙模式。研究表明，“绿色波浪”不是草食性水鸟春季迁徙的普遍驱动因素，迁徙屏障和人为干扰均对迁徙鸟类追随绿色波浪造成不利影响，这为迁徙鸟类的研究和保护提出了新思路。

该研究得到了国家自然科学基金项目、国家重点研发计划项目、中国生物多样性监测与研究网络的支持。

全文链接 <https://www.nature.com/articles/s41467-019-09971-8>。

（北京：王鑫 曹垒 陈利顶；丹麦：Anthony D. Fox, Jesper Madsen；澳大利亚：Richard Fuller；英国：Larry Griffin, Carl Mitchell；湖南：赵运林 徐正刚；韩国：Oun-Kyong Moon；爱尔兰：David Cabot；蒙古：Nyambayar Batbayar；德国：Andrea Kölzsch；荷兰：Henk P. van der Jeugd；以色列：Ran Nathan）

詹祥江研究员在飞行退化鸟种的趋同基因组特征研究方面取得重要成果

具备飞行能力是鸟类与众不同的生物学特征之一，因此鸟类的飞行进化成为了人们最关注的基本科学问题之一。近几十年来，飞行进化研究主要集中于已灭绝的古代鸟类或恐龙，有关现生鸟类飞行进化的研究鲜有报道。尽管飞行赋予了鸟类极大的生存优势，但现生鸟类中却有百余种（如鸵鸟、家鸡等）的飞行能力发生退化，变得无法飞行或飞行能力降低。

与飞行一样，飞行能力的丢失也是鸟类进化的基本特征。虽然形态和生理上的差异在飞行退化鸟类中得到了人们的认同，但目前它们对现生鸟类进化中反复出现的飞行能力退化的贡献度以及潜在的遗传机制仍不清楚。在对 48 种鸟类基因组的 2.95 亿个核苷酸的分析中，我们发现了两个在飞行退化鸟种中发生趋同进化的位点，这两个位点导致了两个氨基酸的非同义突变 ATGLSer321Gly 和 ACOT7Ala197Val。据我们所知，这两个位点以前没有被报道过与飞行能力退化有关。功能实验表明，Ser321Gly 显著降低了 ATGL 的脂质水解能力，而 Ala197Val 显著提高了 ACOT7 的脂酰辅酶 A 水解活性。数学模拟表

明, 飞行退化鸟种的主要能量来源是从脂类转换为碳水化合物。因此, 我们的研究结果表明, 生理趋同而非结构趋同在飞行能力退化过程中起着重要作用。

该项研究回答了为什么百余种现生鸟类飞行能力发生退化的科学难题, 表明了飞行能力退化是生理趋同的结果, 改变了“鸟类飞行能力退化主要是形态结构变异特别是翅长变短所导致的”这一流行观点。该项工作是中国学者在组学水平上对鸟类宏观进化问题的一次全新思考。该项研究成果于 2019 年 6 月 21 日以“Convergent genomic signatures of flight loss in birds suggest a switch of main fuel”为题在线发表于《*Nature Communications*》上 (<https://doi.org/10.1038/s41467-019-10682-3>)。

(北京: 潘胜凯 林依 刘琼 段金志 林蓁蓁
王昱淞 王雪丽 林茜曼 邹振 税光厚 张昱
张正旺 詹祥江)

城市中的鸟类是如何扩展生态位的?

日前, 来自中山大学刘阳副教授团队的研究人员 Emilio Pagani- Núñez 和梁丹与广西大学 Eben Goodale 教授团队、西南林业大学罗旭副教授一起合作, 在国际生态学著名期刊《*Ecography*》上, 以“Niches in the Anthropocene: Passerine species show niche expansion from natural to urban habitats (人类世下的生态位: 从自然到城市生境中的鸟类生态位扩张)”为题发表了一篇论文, 阐述了由自然到城市生境演替过程中, 鸟类生态位变化的规律。

近年来, 许多研究致力于探讨生境变化对生物多样性格局、个体适合度、物种性状和群落结构的影响。大部分研究强调了生境变化对生物多样性的负面影响。我们的研究从如下两方面获得启发:

第一: 在区域尺度, 生境变化会导致生物多样性的急剧下降;

第二: 随着生物多样性的丧失, 幸存的物种在生态功能上更加相似(即功能同质化), 也因此在同一生态功能上会出现物种过剩现象。

然而, 这些环境改变将如何影响物种和群落的生态位呢? 传统的生态位理论认为, 生态位“填充”和生态位“扩张”是不同环境梯度下生态位变化的两种主要方式。前者是指随着物种多样性的增加, 物种的生态位更狭窄或者物种间生态位有更多重叠, 且群落的生态位空间保持相对稳定; 后者是指随着物种多样性增加, 物种的生态位宽度和生态位重叠度可能都不发生变化, 群落生态位空间则可能因此而增加。

我们对中国南部生境变化梯度(从森林到城市梯度)中的雀形目鸟类的研究检验了生态位填充和生态位扩张假说。因为在自然生境中许多物种都是专化物种, 而在人为改造的生境中许多物种都是生境或食性方面的泛化种, 所以我们预计物种的生态位宽度随着城市化程度的升高(即从自然生境到城市生境)而显著增加。此外, 由于我们的研究位于亚热带区域, 因此即使在人为改造的生境中物种多样性也相对较高。在这种情况下, 如果在人为改造的生境中不同鸟种间有更大的生态位重叠度, 大到足以抵消物种的个体生态位宽度对群落生态位的贡献, 则符合生态位填充假说; 而如果在人为改造的生境中物种间的生态位重叠度保持不变, 群落的总生态位宽度却显著增加, 则更符合生态位扩张假说。为验证以上两种假说, 我们对分属于 28 个种的 608 只鸟类的脚趾甲的碳、氮的稳定同位素进行了测定, 量化了物种的生态位宽度和物种间的生态位重叠度。

我们的结果支持生态位扩张假说。我们发现从自然生境到人为改造生境, 物种的总

生态位宽度显著增加；但物种间的生态位重叠度则相对不变。物种间的生态位重叠度在各生境中保持不变表明在不同的人为干扰情况下各个鸟类群落均包含了一些互补的物种。以往的研究表明，在区域尺度上人为改造生境中许多专化物种消失，但在不同的地方的物种群落仍然保持相对多样化，尤其在热带或亚热带区域。因此，虽然在区域尺度下，生境转化带来了逐步的功能均质化，但在小尺度的群落中物种的觅食生态位仍然较为多样化。

显然，我们需要保护自然生境，因为自然生境中丰富的物种组成了极其复杂的营养网络。然而，在人为改造的生境中，我们仍然可以找到合理地规划、管理这些生态系统的方法从而保持或增加物种多样性和功能多样性。当我们考虑生态变化所导致的生态结果（比如功能均质化）时，我们应该对区域大尺度和当地小尺度区别看待。总之，在多数情况下，在小尺度的群落中的物种的营养生态位可能更倾向于互补而非过剩。

中国南方人口稠密、城市密集，自然生境与人工生境在城市里嵌套分布的。随着中国城市化的加速，城市中生物多样性的变化和生物适应如何适应城市的生态环境越来越受到研究界的重视。这篇研究论文巧妙地使用了稳定同位素的方法测定自然-城市生境梯度中的鸟类营养生态位的变化，具有重要的理论和应用价值。

（广东：Emilio Pagani- Núñez 梁丹 刘阳；

广西：Eben Goodale；云南：罗旭）

异步孵化鸟类产卵顺序的“银勺”效应

在优质环境下生长发育的个体，未来可能获得更高的适合度并且终身受益，被称为“银勺效应”（“silver spoon”effect）。许多影

响生长发育环境的因素，例如繁殖季节、栖息地资源和食物质量，都被证明具有“银勺效应”。然而，作为晚成鸟中普遍存在的异步孵化所造成的卵序差异，虽然有研究报道了其同巢雏鸟生长发育的巨大影响，但却鲜有研究探究卵序对后代长期适合度的影响，即“银勺效应”。

朱鹮是典型的异步孵化鸟类，隔日产卵，窝卵数 2~4 枚。雌鸟产第一枚卵后即开始孵化，同巢雏鸟出壳日期相差 2~7 天，雏鸟日龄差异导致同巢雏鸟间存在严重的等级差。北京林业大学丁长青教授团队利用 15 年的研究数据，探究了卵序对朱鹮个体长期适合度的影响。他们于 2003 和 2004 年测定了 165 只野生朱鹮雏鸟的出生卵序，并用彩色数字环志进行个体标记。从 2004 年开始，在野外通过环志重现追踪这些朱鹮并搜寻、监测其巢址，记录繁殖情况。结果显示，先孵化的个体开始繁殖年龄较早，终身繁殖年份更久，且终身繁殖的后代数量更多。当这些个体性成熟后，于 2008—2017 年监测这些朱鹮的生存率，结果显示成年个体的年生存率随其出生卵序下降。该研究组进一步于 2014 和 2015 年测量了这些朱鹮个体所繁殖的雏鸟体征，发现曾为先孵化出的个体（该亲鸟出生时卵序靠前）所繁殖的后代体型更大且身体状况更好。

以上结果说明，先孵化的朱鹮个体适合度较高，具有明显的“银勺效应”，并且这一影响将会持续到下一代。

（北京：宋紫檀 邹瑀琦 胡灿实 叶元兴

丁长青；陕西：王超 庆保平；荷兰：

Jan Komdeur）

红头美洲鹫的食腐适应性分子机制研究

美洲鹫科是一类大型食腐性鸟类，其中

红头美洲鹫 (*Cathartes aura*) 的分布最为广泛。为了研究红头美洲鹫的化学感受系统、解毒系统和免疫系统,我们将红头美洲鹫基因组和其他 14 种鸟类的基因组进行比较分析,论文发表在《*Molecular Genetics and Genomics*》(Zhou et al., 2019, <https://doi.org/10.1007/s00438-019-01541-3>) 上。

通过比较基因组学研究,我们发现:相对于其他 14 种鸟类来说,红头美洲鹫的化学感受系统相关基因家族发生显著扩张,尤其是嗅觉受体基因家族,而其解毒系统相关基因家族并没有发生明显的扩张。通过正选择分析,我们发现在红头美洲鹫中有 174 个基因受到了正选择作用,部分基因是免疫系统中的重要组成基因,这很可能对红头美洲鹫的免疫防御能力的提高起到重要作用。对得到的正选择基因进行功能富集后,我们发现了许多免疫系统调节相关的通路,这表明这些免疫相关通路及通路中的正选择基因对于红头美洲鹫的免疫系统的调节起到了重要作用,从而使该物种拥有食腐适应性。我们在一个正选择基因 (BCL6) 中发现了 3 个红头美洲鹫特有的氨基酸非同义突变位点,这 3 个氨基酸非同义突变被 PolyPhen-2 预测为可能对 BCL6 编码的蛋白的结构甚至是功能有损害性,因此, BCL6 中的这些非同义突变很可能增强了红头美洲鹫的免疫能力。此外,我们在 3 个 β 防御素 (AvBD8, AvBD10 和 AvBD11) 中发现了 4 个红头美洲鹫特有的氨基酸非同义突变,而 β 防御素是先天免疫中不可或缺的组成部分。本研究为红头美洲鹫的食腐适应性遗传机制的进一步研究打下了基础。

(四川:周闯 岳碧松)

全球鹫类的系统发育分析和分类修订

鹫类是一个分类十分混乱的类群,曾被

称为分类上的“垃圾桶”。为了研究其系统发育关系,本研究基于 12 个基因标记,并用化石和地质历史事件作为时间校正点,构建了包括 89% 的全部鹫类物种的系统发育分歧时间树,并对该类群作了分类修订。结果发现,鹫类大约起源于 22 (26.4—18.6) 百万年前,主要包括 7 个演化支,大部分属都是并系属。根据该系统发育树的结果,我们对鹫类的分类进行了修订,建议将鹫类划分为 7 个科,包括鸢鹫科 Sylviidae, 绣眼鸟科 Zosteropidae, 鸦雀科 Paradoxornithidae, 鹫科 Timaliidae, 幽鹫科 Pellorneidae, 雀鹫科 Alcippeidae 和噪鹫科 Leiothrichidae。此外,我们比较了属级阶元间的形态和生态相似性,参考 10 Ma 的阈值,大致将鹫类划分为 64 属。该分类系统提出了一个新科 (雀鹫科 Alcippeidae) 和一个新属 (领凤鹫属 Parayuhina)。本研究为鹫类的生物地理学、物种多样性格局形成机制和形态演化的研究提供了数据基础。

(北京:蔡天龙 邵施苗 张瑞莹 屈延华 雷富民; 瑞士: Alice Cibois; 瑞典: Per Alström, Martin Irestedt, Per G.P. Ericson, Magnus Gelang; 丹麦: Jonathan D. Kennedy, Jon Fjeldså; 美国: Robert G. Moyle)

杜鹃寄主卵回收和卵识别行为的关系

鸟类的卵回收和卵识别,在行为模型上是截然不同,甚至是相反的。但相对卵识别,鸟类对卵的回收行为是较原始的行为,是对地面巢的一种适应。在鸟类巢寄生中,由于绝大部分被寄生的鸟类,都在灌丛和树上营编织巢,针对其回收行为的研究被严重忽视了。海南师范大学行为生态与进化课题组首次研究了杜鹃寄主的卵回收和卵识别行为的关系,结果表明,寄生卵的模拟程

度决定了寄主对卵的回收、接受或拒绝。然而,对于中等模拟程度的卵,寄主有先回收再拒绝的矛盾行为;而对于高度模拟的卵,寄主出现既不回收又不拒绝的犹豫和妥协行为。本研究表明卵回收和卵识别的行为模式,在寄主认知行为的进化中形成了权衡和特殊适应,揭示了卵回收行为对后生的卵识别行为的重塑与影响。研究结果发表在世界上最古老的学术期刊英国《皇家学会哲学学报》上: Yang et al. (2019) Egg retrieval versus egg rejection in cuckoo hosts. *Philosophical Transaction of the Royal Society B: Biological Sciences*, 374: 20180200.

(海南: 杨灿朝 梁伟)

利用 3D 技术检验杜鹃寄主家燕 (*Hirundo rustica*) 在两个独立维度下的认知能力

研究动物的认知有助于我们了解动物如何适应自然环境。许多鸟类会筑巢、清理巢中异物、甚至对卵有识别能力。以往的研究通过手工制作的模型来研究鸟类对巢中物体的认知能力,然而,手工制作模型的方法有诸多缺点,因为它们难以量化,且在不同几何维度上都存在同时变化而不可控。海南师范大学行为生态与进化课题组通过研究创建了一套方法,利用 3D 建模和 3D 打印技术,实现在控制一个几何维度的同时,量化另一个几何维度的变化,并通过研究实例,在立体容积和表面边缘两个几何维度,检验了杜鹃寄主家燕 (*Hirundo rustica*) 在这两个独立维度下的认知能力,证明了家燕在这两个维度上对物体认知的进化程序。研究结果发表在最新一期的英国《皇家学会开放科学》期刊: Yang et al. (2019) Using 3D modelling and printing to study avian cognition from different

geometric dimensions. *Royal Society Open Science*, 6: 181938.

(海南: 杨灿朝 梁伟)

雄性大杜鹃的鸣声稳定性在繁殖季内逐渐下降

在多种鸟类物种中证明了鸟类的鸣声具有个体性和稳定性。如将鸣声用作监测目标个体的非侵入性标记,这些声音特征必须在较长的时间内能够保持稳定。最近关于大杜鹃鸣声的研究表明,有可能基于声音特征识别出雄性大杜鹃的个体,但这些雄性的鸣声在繁殖季内是否具有稳定性,尚不确定。我们在辽宁盘锦大杜鹃种群录制了来自 30 只雄性的 1,032 个音节。对其中的 6 只个体进行了标记处理,并在繁殖季的 19 天期间内重复录制了它们的鸣叫。通过判别分析 (discriminant function analysis, DFA)、相关分析 (correlation analysis, CA) 和语图交互相分析 (spectrographic cross-correlation, SPCC) 三种方法来识别个体。还通过重复性分析来检测鸣声的稳定性 (每个鸣叫段落中的音节数量) 是否在个体内是可重复的。根据同一天的录音,来自同一个体的音节在特征上比来自不同个体的音节更相似,并且正确识别率为 93.6% (SPCC), 90.8% (DFA) 和 71.5% (CA)。但是,在 19 天的时间跨度下,正确识别率下降到了 40.5% (SPCC), 40.7% (DFA) 和 27% (CA)。两个连续的句子中音节的数量在同一个体内是可重复的,但是经过若干段落 (超过 2 个) 后,或者录自不同天的句子,句子中的音节数量就不存在一致性了。本研究表明,雄性大杜鹃个体识别正确率的下降和音节数量稳定性的下降表明雄性大杜鹃的鸣声比以往的认知更加富有变化。

(北京: 邓竹青 夏灿玮 张雁云;

辽宁：李东来；英国：Huw Llyod.)

雌性大杜鹃鸣声的变异组成

以往对鸟类鸣声的研究主要集中在雄性，雌性鸣声在鸟类中也广泛存在，却很少有研究调查雌性鸣声的特征，特别是在非雀形目的鸟类中。我们收集了来自中国的野外录音和鸣声数据库中的录音，分析了雌性大杜鹃鸣声的节律模式、鸣声稳定性以及地理变异。发现雄鸟和雌鸟的鸣叫高峰都在早晨，这与雌性鸣声的唯一功能是在下午寄生卵后分散寄主注意力的观点不同。雄鸟和雌鸟在状况良好的天气中具有更为频繁的鸣叫活动。研究还发现雌性鸣声的个体内变异较大，推测可能通过增加对寄主物种的刺激而使雌性大杜鹃在巢寄生的过程中获益。雌鸟鸣声的主频随着纬度的增加而降低，而雌鸟鸣声特征的差异与地理距离无关。综上，大杜鹃雌鸟通常在早上发出鸣叫，而不是在产卵高峰期，不过雌鸟的鸣声特征变化很大并且显示出很少的地理变异模式表明雌鸟鸣声的功能，可能比以往认为的更加可变且复杂。由于对雌鸟鸣声的研究还不够充分，因此仍需要进一步的研究。

(北京：邓竹青 夏灿玮 Møller AP 张雁云；
海南：梁伟)

大杜鹃三种主要鸣声类型的功能

声信号在塑造鸟类关系中起着关键作用。大杜鹃会产生几种的鸣声，但这些鸣声的功能近期才开始被学者关注。本研究利用野外获取录音和回放实验来研究大杜鹃鸣声的功能意义。发现雄性双音素“cu-coo”和三音素“cu-cu-coo”鸣声之间的特征存在显著差异，

这两种鸣声类型会在不同的情境下被使用。三音素的“cu-cu-coo”鸣声与雌鸟的鸣声有关。回放实验表明，雄鸟和雌鸟对播放雌鸟鸣声的反应强于雀鹰 (*Accipiter nisus*) 作为对照的鸣声，表明该鸣声类型具有显著的种内通信功能。然而没有发现任何证据支持雄性鸣声的配偶吸引功能，因为与对照组中的雀鹰鸣声相比，雌鸟在回放雄鸟鸣声时并没有表现出强烈的反应。

(北京：夏灿玮 邓竹青 赵晓萌 Anders Pape Møller 张雁云；英国：Huw Llyod)

研究生论文选登

城市化对于鸟类生态位动态和压力反应的影响

生态位可分为基础生态位和实际生态位。在城市的人工生境产生了许多新颖的生态位，生活在该生境中物种的生态位特征可能产生了巨大的变化。但是对于城市化如何影响生态位的动态，以及鸟类物种和个体如何应对不同水平的人类干扰还需要进行深入研究。为回答以上问题，本论文比较了从自然生境到城市生境雀形目鸟类的压力反应、同位素生态位宽度、个体专化和形态差异。本研究在中国西南部进行，该区域正经历着较高的城市化率，同时具有很高的生物多样性。

本论文的主要研究和发现是：1) 生境间压力反应无差异，但压力反应受鸟类食性所介导本研究支持生命节奏假说 (本研究发表在 *Ecology & Evolution* 杂志上)。2) 雀形目鸟类的同位素生态位表明鸟类生态位从自然到人工生境呈现扩张趋势。但是不同生境中的鸟类间的生态位重叠度未表现显著差异 (本研究发表在 *Ecography* 杂志上)。3) 自然和人工生境中雀形目鸟类生态位宽度和个体

专业化关系不一致。首先,人工生境中的物种比在自然生境中的物种有更宽的生态位宽度,但是个体专业化程度在生境之间无显著差异。其次,物种生态位宽度和个体专业化程度的相关性较弱。本结果表明人为干扰引起的生境变化对个体专业化程度起了重要的作用。4)城市物种为生态泛化种但同时也是形态专业化种。为检验以上假说,我们计算了中国南部从自然到城市中的物种的同位素生态位和个体间形态差异。结果表明相比于自然和农村生境,城市生境的物种具有更宽的生态位,但同时其形态差异最小。研究结果表明在城市中的物种为生态泛化种和形态专业化种,且生境转化对于形态变异起着重要的作用。

(中山大学博士生梁丹,导师刘阳)

鹇类和雉类物种多样性格局形成和维持机制研究

随着人口的增长和气候变暖,全球的生态系统遭受了严重的破坏,使得生物多样性正面临日益严重的威胁。研究物种的分布格局,可以确定物种的多样性中心,有助于在制定生物多样性保护计划时划定保护优先区。研究物种多样性格局的形成和维持机制,可以了解物种多样性对环境的响应,从而预测未来的环境变化对物种多样性的影响,从而提前制定合理的保护计划。中国-喜马拉雅山区包含了全球 10% 的脊椎动物和 8% 的植物,是全球最重要的生物多样性热点地区之一。虽然已有一些研究尝试解释该地区物种多样性格局的形成机制,但是该地区作为生物多样性热点的成因,以及维持该地区极高的物种多样性的机制尚不清楚。我们以两个不同演化时间 (evolutionary time, EvolTime) 的鸟类类群:雉类(古老类群,起源于始新世末期-渐新世早期)和鹇类(年轻类

群,起源于中新世早期)为研究对象,从生态、演化和功能多样性的角度出发,探讨了物种多样性格局的形成和维持机制,以揭示中国-喜马拉雅山区成为物种多样性中心的成因。本论文主要包括以下四部分研究内容:(1)鹇类的系统发育分析和分类修订;(2)演化时间、多样化速率 (diversification rate, DivRate) 和扩散对鹇类物种多样性格局的影响;(3)生态过程和演化过程对雉类物种多样性格局的影响;(4)功能特征分化对鹇类物种共存的影响。

鹇类是一个分类十分混乱的类群,曾被称为分类上的“垃圾桶”,目前还没有研究基于广泛的采样去分析它们的系统发育树和修订分类系统。为了解决这一问题,我们基于 12 个基因标记,并用多个时间校正点,构建了包括 89% 的全部鹇类物种的系统发育分歧时间树,并对该类群作了分类修订。结果表明,鹇类大约起源于 22 百万年前 (million years ago, Ma) (95% highest posterior densities, HPD : 26.4~18.6 Ma), 主要包括 7 个演化支,大部分属都是并系属。根据该系统发育树的结果,我们对鹇类的分类进行了修订,建议将鹇类划分为 7 个科,包括莺鹇科 Sylviidae, 绣眼鸟科 Zosteropidae, 鸦雀科 Paradoxornithidae, 鹇科 Timaliidae, 幽鹇科 Pellorneidae, 雀鹇科 Alcippeidae 和噪鹇科 Leiothrichidae; 此外,我们比较了属级阶元间的形态和生态相似性,参考 10 Ma 的阈值,大致将鹇类划分为 64 属。该分类系统提出了一个新科(雀鹇科 Alcippeidae)和一个新属(领凤鹇属 *Parayuhina*)。该部分的研究为后面鹇类的生物地理学、物种多样性格局和物种共存机制的研究提供了数据基础。

鹇类的分布并不均匀,中国-喜马拉雅山区物种多样性最高,而在全球其他地区物种多样性较低。中国-喜马拉雅山区物种多样性较高可能是较高的多样化速率、多次扩散

和较长的演化时间累积更多物种这三个演化过程直接作用的结果。在该部分研究中,我们基于较为完整的鸮类系统发育树,旨在验证多样化速率、扩散和演化时间这三个演化因子对全球鸮类物种多样性格局的影响,以探究中国-喜马拉雅山区作为鸮类物种多样性热点的成因。首先,我们基于 13 个地理区,重建鸮类的祖先分布区,推断鸮类的起源和扩散路径,并估算每个地理区内的扩散事件和最早拓殖时间。然后我们分析了 7 个地理区内物种家系累积随时间的变化;鸮类各支系的分化速率随着时间的变化;以及中国-喜马拉雅山区与其他地区和大陆与岛屿间的多样化速率和扩散速率的差异。最后,我们用一般线性模型检验了 13 个地理区内的物种多样性与多样化速率、首次拓殖时间以及扩散事件的数量之间的相关性。我们的研究结果发现,鸮类在中新世早期起源于中国-喜马拉雅山区,而后扩散到其他地区,表明鸮类在中国-喜马拉雅山区物种累积的时间最长。分化速率分析表明,鸮类的成种速率在 2.5 Ma 时快速增加,这与绣眼鸟属 *Zosterops* 在海洋岛屿的快速成种有关,该时间与第四纪冰期循环导致的海平面升降的时间吻合。一般线性回归分析表明,鸮类物种多样性与首次拓殖时间显著相关,与扩散事件的次数和多样化速率没有显著相关性。根据以上结果,我们可以得到以下结论:(1) 鸮类的物种多样性格局主要受到“时间-成种效应”的影响,即中国-喜马拉雅山区是鸮类的起源中心,鸮类在该地区物种多样性高是长时间演化的结果,而受多次扩散和多样化速率增加的影响较小;(2) 海洋岛屿是鸮类的分化中心,这主要与第四纪冰期导致的海平面下降有关:海平面下降使得浅海地区形成新的陆地,物种从大陆扩散进入这些空白生态位,随后间冰期海平面上升,使得各种群在岛屿上隔离成种。

中国-喜马拉雅山区比临近的低地拥有更高的物种多样性,为了解释这一格局,学者们曾提出多种关于生态和演化过程的假说,主要包括生态约束假说、能量约束假说、多样化速率假说、拓殖频率假说和“时间-成种效应”假说。在该部分研究中,我们以雉类作为研究对象,旨在验证以上 5 种假说对中国-喜马拉雅山区物种多样性格局形成的直接影响和间接影响,以探讨物种多样性格局的形成机制。基于物种分布模型预测的雉类分布区、多基因构建和多个化石校正的雉类系统发育分歧时间树、雉类的功能特征和气候数据,我们使用 Pearson 相关性分析和结构方程模型检验了初级净生产力 (net primary productivity, NPP)、生态位多样性 (niche diversity, NicheDiv)、多样化速率、演化时间和拓殖频率对物种多样性的影响。同时,我们重建了雉类的祖先分布区,分析了系统发育树基部类群和衍生类群的分布格局,以更好的理解物种多样性格局的形成机制。研究结果发现,雉类可能在渐新世早期 (33 Ma, 95% HPD : 28.7~38.2 Ma) 起源于非洲,随后扩散到中国-喜马拉雅山区以及全球其他地区。在中国-喜马拉雅山区,物种多样性与多样化速率、初级净生产力、生态位多样性和拓殖频率高度相关,与演化时间的相关性不显著。结构方程模型表明,多样化速率和生态位多样性对物种多样性的直接影响比初级净生产力和演化时间的直接影响更强。初级净生产力主要通过改变多样性速率间接地影响物种多样性,而生态位多样性通过多样化速率对物种多样性的间接影响力较弱。我们的研究表明,可用生态位空间的增加,快速分化和多次拓殖是造成中国-喜马拉雅山区物种多样性高于临近低地的直接因素;初级生产力对物种多样性格局的形成也有重要的影响,但主要通过改变多样化速率间接地影响物种多样性。因此,中国-喜马拉雅

山区物种多样性高是生态和演化机制共同作用的结果。

鵐类物种丰富,形态和行为差异大,在中国-喜马拉雅山区高度同域分布,是研究物种共存机制的最佳类群。通常认为,同域分布的物种为了避免激烈的种间竞争,需要在生态、食性或觅食层等一个或多个维度上存在差异;而对于同域分布的近缘种,还需要在羽色和鸣声等与性选择相关的特征上发生分化,以避免种间杂交。同域物种间的特征分化可能由两种不同的过程导致:(1)快速成种导致物种间的特征快速分化;(2)长时间演化导致物种间的特征存在巨大差异。然而,目前关于特征分化与物种共存之间的关系的研究较少,其内在机制也尚不清楚。该部分研究旨在分析物种形态、食性、鸣声和羽色等生态和性选择特征的分化对物种共存的影响,同时检验多样化速率和演化时间对特征分化的影响,以揭示物种多样性的维持机制。研究发现,共存物种的数量与鸣声和羽色等相关的社会性特征和性选择特征的功能分散指数(代表特征分化)显著相关,而与形态和食性功能分散指数没有显著相关性。结构方程的结果表明,共存物种的数量主要与性选择特征的分化直接相关,该过程主要受到演化时间的影响,而受到多样性速率的影响较小。因此,在中国-喜马拉雅山区,鵐类高度同域分布是长时间演化导致的性选择特征分化的结果,这种性选择特征的分化可能促进了物种间的生殖隔离,使得同域分布种稳定共存。

基于以上几个研究,我们发现中国-喜马拉雅山区物种多样性热点的形成机制不同:对于年轻类群(鵐类)来说,中国-喜马拉雅山区物种多样性高是长时间演化和积累更多物种的结果;对于古老类群(雉类)来说,中国-喜马拉雅山区物种多样性高是快速分化和多次扩散的结果。也就是说,中国-喜

马拉雅山区是鵐类的起源中心,是雉类的扩散中心和分化中心。中国-喜马拉雅山区不同类群物种多样性格局的形成机制存在差异可能与该地区的地质历史有关:青藏高原大约在渐新世早期达到 4,000 米,因此在雉类分化的早期,中国-喜马拉雅地区尚不能为雉类提供适宜的栖息地,随着后来中国-喜马拉雅山区栖息地的形成,才逐渐为雉类提供了适宜生境,成为雉类的扩散中心和分化中心;但是鵐类形成于中新世早期,在这个时期,中国-喜马拉雅山区大部分地区已形成现有格局(横断山区除外),可以为鵐类的祖先种提供适宜的栖息地,使得鵐类在该地区长时间分化和积累更多的物种。因此,我们在理解一个地区多样性格局的形成机制时,不仅需要综合分析不同类群的生态和演化历史去探究物种多样性格局的形成过程,而且需要考虑该地区的地质和气候历史。最后,我们发现中国-喜马拉雅山区物种多样性的维持机制具有一致性:(1)在雉类中,物种多样性与生态位多样性(即功能特征多样性)显著相关;(2)在鵐类中,共存物种数量与性选择相关的功能特征多样性显著相关。这一结果表明共存物种功能特征的分化可能是维持物种稳定共存的主要途径。

(中科院动物所博士生蔡天龙,
导师雷富民)

马鸡属 (*Crossoptilon*) 物种分化与褐马鸡 (*C. mantchuricum*) 保护遗传学研究

物种分化 (Speciation) 一直是生态学和演化生物学的重要研究内容,其机制往往涉及到生物多样性的形成与维持以及生态系统的演化过程。目前已经形成了物种分化机制的诸多假说,这些假说之间有的互相具有兼容性抑或彼此冲突。随着分子生物学技术的

发展, 目前已经在实验室内以及野外条件下对不同的物种分化假说进行了验证, 但是相关假说仍然存在着争议, 比如物种分化过程中生态位是否保守? 是气候波动还是气候稳定能够促进物种的分化? 为此, 本研究以马鸡属 (*Crossoptilon*) 鸟类为研究对象, 通过对该类群鸟类演化机制的研究来探讨物种分化问题, 并尝试为上述有争议的问题提供答案。

马鸡属鸟类隶属于鸡形目 (*Galliformes*) 雉科 (*Phasianidae*), 其包含 4 个物种, 分别是褐马鸡 (*C. mantchuricum*)、蓝马鸡 (*C. auritum*)、白马鸡 (*C. crossoptilon*) 及藏马鸡 (*C. harmani*), 均为中国鸟类特有物种。以往对马鸡属鸟类的种群现状、栖息地选择、繁殖生态及保护对策等做了一系列深入研究, 但是对该属鸟类物种分化机制的研究相对较少, 而且以往研究也仅使用了少数线粒体基因来探讨马鸡属的演化关系。

本研究使用了核基因、线粒体基因以及基因组的数据, 对马鸡属内物种的演化关系、分化时间、物种间的基因流、物种的有效种群历史动态进行了研究, 结合生态位模型对马鸡属鸟类的生态位进行了构建和比较。同时, 考虑到褐马鸡是一个分布在我国黄土高原及其附近区域的全球受胁物种, 本项目还使用了种群基因组数据对褐马鸡种群所包含的有害突变和种群历史动态等进行了深入分析, 为其保护管理工作提供了有效的科学依据。主要研究结果如下:

1. 邻域分布的白马鸡和藏马鸡在大约 50 万年前开始分化, 两个物种之间存在不对称的单向基因流, 其生态位呈现一定的保守性。异域分布的蓝马鸡和褐马鸡在大约 30 万年前开始分化, 两个物种之间也存在不对称的单向基因流, 其生态位呈现非保守性的特征。

2. 白马鸡和藏马鸡的分化时间位于古乡冰期。白马鸡种群主要分为两个遗传演化单元, 这两个遗传演化单元的分化时间位于白玉冰期。生态位模型显示, 藏马鸡和白马鸡在冰期被澜沧江 - 怒江分水岭隔离, 白马鸡的两个遗传演化单元在冰期被大雪山所隔离。有效种群历史动态分析结果显示, 藏马鸡和白马鸡在冰期经历了瓶颈效应。

3. 种群基因组学数据显示, 在目前已经报道了基因组遗传多样性的鸟类中, 褐马鸡是遗传多样性最低的物种。褐马鸡现有三个明显的地理种群, 并且种群之间没有基因流。对褐马鸡近亲繁殖和有害突变的分析显示, 该物种有严重的近亲繁殖现象, 并且相比于蓝马鸡, 褐马鸡有更多的有害突变。有效种群历史动态分析结果显示, 褐马鸡在末次最大冰期经历了种群的收缩。在末次最大冰期之后, 尽管温度上升, 但是褐马鸡的有效种群数量仍然持续下降。

通过以上结果, 本研究得出如下结论: (1) 生态位不存在严格的保守性; (2) 在物种分化过程中存在基因流的情况下, 导致物种产生局域适应的分化选择可能是促进物种分化的一个重要因素; (3) 冰期的地理隔离导致了青藏高原和横断山脉区域近期的物种分化事件; (4) 褐马鸡是极度濒危的物种, 其遗传负荷较高且适合度较低。

本研究的成果有助于加深人类对物种分化机制、古北区高山生物多样性热点地区的物种形成机制以及物种不均匀分布的演化机制的理解, 同时也为褐马鸡的保护策略的制定提供了种群基因组学的证据, 此外也为其它濒危鸟类的保护遗传学研究提供了案例支持。

(北京师范大学博士生王鹏程, 导师张正旺; Scott V. Edwards)



2018 年我国鸟类环志概况

2018 年全国有 38 个单位开展了鸟类环志工作, 共环志鸟类 395 种 10.4 万只。雀形目鸟类环志数量最多, 共 231 种 9 万余只, 鸛形目 16 种 3,432 只, 猛禽 27 种 2,241 只, 鸽形目 41 种 1,298 只, 雁形目 19 种 1,275 只, 鹤形目 15 种 252 只, 鷺形目 13 种 295 只。

环志数量居前 10 位的种类均为雀形目鸟类, 主要有田鸫 (*Emberiza rustica*)、灰头鸫 (*E. spodocephala*)、红胁蓝尾鸫 (*Tarsiger cyanurus*)、白腰朱顶雀 (*Carduelis flammea*)、黄眉柳莺 (*Phylloscopus inornatus*)、燕雀 (*Fringilla montifringilla*)、黄喉鸫 (*E. elegans*)、小鸫 (*E. pusilla*)、黄腰柳莺 (*P. proregulus*) 以及红胁绣眼鸟 (*Zosterops erythropleurus*)。

2018 年全国开展彩色标记的单位有 14 个, 彩色标记鸟类 101 种 5,722 只。主要种类有雀形目鸟类 49 种 4,903 只、鸽形目 30 种 572 只、雁形目 7 种 120 只、鸛形目 1 种 60 只、鹤形目 5 种 84 只, 鹤形目 2 种 2 只。

(全国鸟类环志中心: 陈丽霞 王毅花)

2019 年春夏季河南董寨鸟类环志网络点环志简报

2019 年 5 月 10 日至 26 日, 河南董寨国家级自然保护区环志站组织环志员在七里冲保护站凉亭环志网络点和鸡笼保护站花门楼环志网络点开展春夏季鸟类环志工作。历时 14 天共环志鸟类 326 只, 隶属于 4 目 18 科 42 种。

5 月 10 日至 5 月 16 日于凉亭环志网络点共环志鸟类 185 只, 隶属于 4 目 14 科 32 种。其中新捕 2 目 14 科 30 种计 172 只; 重捕 2 目 7 科 7 种计 13 只。成功捕获归家鸟 2 只: 发冠卷尾 1 只, 环号为 F10-0063, 于 2015 年 5 月在该点第一次环志; 白眉姬鹀 1 只, 环号为 A167-0671 (♂), 于 2018 年 5 月份在该点第一次环志。捕获蓝喉仙鹀 1 只, 据文献资料显示为董寨鸟类新纪录。

5 月 20 日至 5 月 26 日于花门楼环志网络点共环志鸟类 141 只, 隶属于 4 目 17 科 24 种。其中新捕 4 目 17 科 24 种计 135 只; 重捕 2 目 4 科 4 种计 6 只。捕获归家鸟类红翅凤头鹀 1 只, 环号为 F10-8314。于 2018 年 5 月份在该环志点第一次环志。

(董寨环志站: 溪波 杜志勇 张峻峰)



我分会四位学者参加了第 35 次中国南极科学考察

中国动物学会鸟类学分会的张正旺、邓文洪、夏灿玮和雷维蟠四位学者参加了中国第 35 次南极科学考察，分别对中山站、长城站、罗斯海新站及阿蒙森海区域的鸟类资源与生态习性进行了调查研究和监测。

此次是张正旺教授第三次参加南极科学考察。在中山站实地观测和记录各种鸟类 525 巢，发现该地区为雪鹱、黄蹼洋海燕和南极贼鸥的主要繁殖地；采用红外相机等技术成功监测了南极鸟类的活动规律，发现雪鹱和黄蹼洋海燕在繁殖期的活动高峰均在夜间，且天敌捕食、极端气候和人为干扰是影响鸟类繁殖和种群发展的主要因素。他建议只有进一步减少人为活动、大力加强南极环境和生态系统的保护，方能为南极鸟类资源长期存续和发展提供保障。

邓文洪教授本次的主要任务是调查阿蒙森海区域内的鸟类和哺乳类物种多样性和分布模式，记录沿途和各站位观测到的鸟类和海洋哺乳动物种类、数量、群体大小、地理坐标、行为、距船只的直线距离与冰区距离等。本次考察共记录了包括图像和地理分布数据在内的 29 种鸟类和 5 种哺乳类，记录到的鸟类占南极鸟类物种多样性的 60% 以上。新发现了白头圆尾鹱、克岛燕鸥和白额燕鸥 3 种鸟类，弥补了这 3 种鸟类在阿蒙森海区域记录的空白，并补充了它们在南极陆缘海的新分布区。

夏灿玮副教授参与了罗斯海新站企鵝聚居区的保护区选划项目，在难言岛从事鸟类调查和行为监测的研究。通过 GPS 追踪器和心率监测仪探究了极昼环境下鸟类的活动性和生理状况的日节律，这些研究有望为罗斯海新站的鸟类监测和保护区的建立提供科学依据。

雷维蟠博士对南极长城站地区的鸟类进行了调查和监测。通过实地考察，共记录鸟类 4 目 7 科 15 种，其中 13 种鸟类在长城站地区繁殖；首次采用巢温度记录仪对南极鸟类的活动规律进行了监测，获得了巨鹱、贼鸥和黄蹼洋海燕的孵卵活动的温度曲线。

四位学者在南极考察期间不畏艰苦，勤奋工作，出色地完成了相关的科考任务，为我国南极考察事业做出了贡献。中国南极考察站曾在元旦期间给北京师范大学发来感谢信。中央电视台、新华社等媒体也曾对他们的考察工作进行了多次报道。

(北京：雷维蟠)

卢欣访问美国奥杜邦学会波特兰分会

奥杜邦学会 (Audubon Society) 是美国最负盛名的鸟类保护公益组织和最具影响力的社会团体之一。该学会成立于 1905 年，以著名博物学家、自然画家约翰·詹姆斯·奥杜邦 (1785—1851) 命名，致力于野生动物特别是鸟类及其栖息地的保护，是世界上最早的自然保护公益组织之一，目前有将近 500

个地方分会。

2019年1月12日,美国西北部漫长冬天气雨季中一个难得的风和日丽,我访问了奥杜邦学会波特兰分会。这个分会的历史与奥杜邦总会一样悠久,已有100多年。它的办公地位于俄勒冈州波特兰市郊,是一座藏秀于山林之间的两层别墅,包括办公室、野生动物救助中心和自然商店。奥杜邦学会波特兰分会有多名专职人员和很多志愿者,发行双月会刊(Warbler),组织类型多样的免费或收费的户外观鸟活动、公民科学和公众教育培训项目是学会的主要工作。例如利爪项目(The Talon Program),旨在为有志于从事自然保护、环境教育的年轻人提供素质训练。自然之夜系列讲座(Nature Night Speakers Series)于每月第二个周二晚上邀请专家与公众分享各种自然保护的议题。2019年1月15日的主讲专家是波特兰第一位非洲裔女性市政专员,她在建立“波特兰清洁能源基金”(Portland Clean Energy Fund)过程中发挥了重要作用;2019年2月12日的专题为“哥伦比亚河口双冠鸬鹚与鲑鱼保护的冲突与策略”,由学会保护部主任主讲。

野生动物救助中心每年救助超过3,000只鸟类以及其他野生动物,救助中心还为公众尤其是小学生提供近距离接触动物的机会。特别值得一提的是学会的自然商店,除了销售各种观鸟和自然保护的书籍外,设计精巧的工艺品和纪念品也让人爱不释手。此外,人工巢箱和招引鸟所用的鸟食更适用于普遍拥有独户别墅的美国人的生活情趣。令人惊异的是,这样的自然商店,在波特兰地区就有好几家,由此可见自然保护已经深入美国人的生活。

在办公地周围,一片150英亩的自然林地是学会的野生动物保护区(Wildlife Sanctuary),其土地所有权包括学会购置、私人捐赠和授权使用。保护区免费为自然爱好

者开放,其内大树参天、曲径通幽、溪水潺潺。行走不久,我便遇见黑顶山雀(*Poecile atricapillus*)、歌带鹀(*Melospiza melodia*)这些在研究论文中时常读到的北美鸟类,有一种别样的亲切。

在学会办公室附近,我遇见从华盛顿州来访的母女。妈妈估计已经年近70,但精神甚佳,以前曾12次前往尼泊尔观鸟。受母亲的影响,女儿艾米拉和她10岁的儿子也酷爱自然。当我介绍西藏的鸟类时,她们特别兴奋。为了感谢我们的相遇和交谈,艾米拉特意在自然商店购买了一个纪念品赠送给我。

总结起来,这次访问获得了几点认识:1)美国的鸟类保护组织,即使地方学会,都有自己的专门办公地、保护地和专职人员;2)地方鸟会的活动内容丰富、持久而且质量很高;3)公众的保护意识强。这些经验值得中国鸟类研究和民间保护团体借鉴。

(湖北:卢欣)

阿拉善SEE任鸟飞项目最新进展

阿拉善SEE任鸟飞项目于2016年启动,计划利用十年时间,以超过100个亟待保护的湿地和24种珍稀濒危水鸟为优先保护对象,通过民间机构发起、企业投入、社会公众参与的“社会化参与”模式开展积极的湿地保护工作,搭建与官方自然保护体系互补的民间保护网络,建立保护示范基地,进而撬动政府、社会的相关投入,共同守护中国最濒危水鸟及其栖息地。

2017—2019年,任鸟飞民间保护网络先后资助了49家机构在60个保护空缺湿地上开展湿地巡护、鸟类调查、威胁监测、自然教育等活动。截止到2019年4月,累计开展湿地巡护和鸟调近3,000次,保护了约2,000平方公里的鸟类栖息地;提交鸟类调查记录

约 7 万条，共记录了近 600 种鸟类，提交盗猎、污染和开发建设等威胁记录约 1,000 条；开展自然教育活动 300 余次，累计参与人数超过 10 万人次。

2018—2019 年，任鸟飞的濒危水鸟专项调查启动了“青头潜鸭栖息地保护和监测”、“遗鸥种群数量和繁殖栖息地调查”以及“大鸨回家”项目。在科学研究与政策建议方面，任鸟飞项目与中国科学院地理科学与资源研究所于秀波研究员团队合作开展了“沿海湿地保护绿皮书”项目，“绿皮书”是介绍中国沿海湿地的健康状况、保护进展与热点问题的双年度评估报告，为我国沿海湿地保护提供体检报告。任鸟飞项目还与国家林业和草原局湿地管理司达成了 5 年合作意向，并就湿地公园管理能力提升培训和湿地开发利用监督管理体制研究进行了合作。任鸟飞项目与中国动物学会鸟类学分会张正旺教授、丁长青教授、陈水华研究员、洪剑明教授等专家进行了成功的合作。

2019 年任鸟飞民间保护网络伙伴招募已经开启，计划招募 55 个任鸟飞湿地守护项目。

(北京：张琼)

深圳市质兰公益基金会资助濒危鸟类的研究与保护

深圳市质兰公益基金会（简称质兰基金会）成立于 2018 年 12 月，于 2019 年开始正式运营并在 4 月开始季度征集项目。质兰基金会通过为一线研究与实践者提供小额、灵活、长期的项目资金支持和陪伴成长，来推动包括鸟类在内的中国濒危物种保护，并促进社区的减贫与可持续发展。

质兰基金会征集的项目包括“一般项目”和“紧急项目”两类。其中，已启动的一般项目是指整体实施周期较长，有短期、中期

及长期目标，为应对复杂的根源性问题而采取的一年以上的持续行动。质兰基金会支持个人、团体及机构类等不同类型的申请者，您可以通过访问质兰基金会的官网（www.izhilan.cn）在线上的成长社区申请项目，还可就项目申请和行动中的问题相互交流。

| 申请者 | 一般项目 | | 紧急项目 | |
|------|--------|-------|--------|--------|
| | 资助金额 | 实施周期 | 资助金额 | 实施周期 |
| 个人类型 | ≤ 5 万 | 12 个月 | ≤ 5 万 | ≤ 6 个月 |
| 团体类型 | ≤ 10 万 | 12 个月 | ≤ 10 万 | ≤ 6 个月 |
| 机构类型 | ≤ 20 万 | 12 个月 | ≤ 10 万 | ≤ 6 个月 |

2019 年，质兰基金会计划通过项目公开征集投放的资金总量为 350 多万人民币。从 2019 年第二季度起，每个季度计划投放资金 100 多万元人民币。首期资助项目征集已于 4 月启动，6 月末将公布资助名单。第三季度及第四季度征集将在 7 月、10 月展开，欢迎从事濒危鸟类研究的专家学者及保护团体提交项目申请。

(北京：张颖溢)

新疆大批灰鹤迁徙途中意外死亡

灰鹤 (*Grus grus*) 亦称欧亚鹤，分布相对广泛。2019 年 4 月，一些灰鹤在乌鲁木齐郊区落脚停留时遇到了麻烦，它们集体撞上了 220 千伏输电线路上的避雷线。可能是因为避雷线比较细不容易被看到，约 32 只灰鹤受伤坠落后死亡（之前报道的死亡数更多）。

高压线附近的玉米地是灰鹤喜欢去的地方，但往年的死亡数字没有这么多。我们在野外检查了这 32 只灰鹤，100% 为 2~4 年的幼鹤或者亚成体（体羽较淡，头部无丹顶）。断翅率最高，达到 64%；腿被撞折的比率也很高，达 60%；腹部或背部擦伤占 36%；头

或颈部碰伤约为 20%；几乎有一半的个体是多处受伤（占 52%）。建议有关部门尽快对这个问题采取有效保护措施。



32 只灰鹤集体遇难

（新疆：马鸣）

河北发现夜鹭白化

夜鹭是一种常见、分布广泛的水鸟。2019 年 4 月 30 日，本人在河北省秦皇岛市抚宁县羊河水库（水源地）观察拍摄繁殖季的大白鹭、小白鹭、夜鹭等鸟类时，发现了一只白色、头戴两根白色冠羽、嘴黄色，外形酷似夜鹭的鸟，随拍下照片。经中动协科考委张德志主任、沈阳理工大学周海翔教授、北京林业大学丁长青教授等专家鉴别，确认是白化的夜鹭。



“白化”夜鹭

夜鹭白化，是隐性基因显现，失去了伪装保护色，给生存带来困难。

（河北：范连成）

中国彩鹮的首次繁殖纪录

彩鹮 (*Plegadis falcinellus*) 是世界广泛分布的鹮类，其繁殖地横跨非洲南部、马达加斯加、欧洲南部、中东、东南亚、澳大利亚以及北美和加勒比海的沿岸地区。然而在中国大陆，彩鹮仅作为旅鸟被零星记录，从未有过繁殖的记载。

2019 年 4 月 25 日，作者在陕西省汉中市南郑区大河坝镇汉江支流濂水河 (N33°2'12", E106°59'34", 海拔 493 m) 发现 3 只彩鹮 (图 1)。此处水草丰盛,食物丰富。朱鹮(*Nipponia nippon*) 和多种鹭科鸟类在河道中觅食,附近还有朱鹮的繁殖地。5 月初发现其中的 2 只彩鹮出现了求偶和营巢行为 (图 2)。5 月中旬在附近的鹭类集群繁殖地中观察到彩鹮的孵化行为。6 月初在巢下相继发现了 3 枚破碎的卵壳,蓝绿色,无斑点,直径 3.3~3.6 cm (图 3)。观察发现已经成功孵化雏鸟 3 只。彩鹮营巢地点位于鹭类繁殖地中间,是一片茂密的楠竹 (*Phyllostachys heterocycla*) 林。巢位于竹子顶部,距地面高度约 5 m。估计 6 月底至 7 月初彩鹮雏鸟将成功出飞。这几只彩鹮来自何处我们不得而知,也不知道它们及其后代去往何处。所以后期对其加强跟踪观察很有必要。

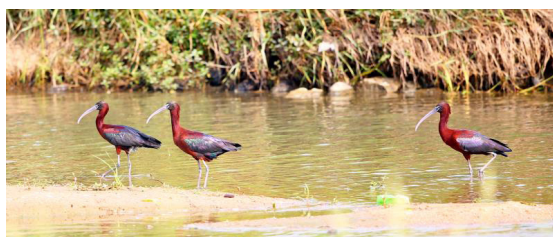


图 1



图 2



图 3

(陕西：于晓平)

我国绿尾虹雉的人工繁育取得重大突破

四川宝兴绿尾虹雉保护研究中心于 2017 年 10 月成立，位于四川蜂桶寨国家级自然保护区内，目前饲养的绿尾虹雉是世界上唯一的人工圈养种群。该中心聘请了北京师范大学张正旺教授任主任，同时还邀请成都大熊猫基地、西华师范大学、四川大学、世界雉类协会、北京动物园、北京林业大学、成都动物园等单位的专家教授组成顾问团队，为中心提供专业技术指导。

2018 年，该中心的饲养管理人员与成都大熊猫基地、北京动物园的科技人员组成了技术攻关小组，首次采用梯度湿度孵化法，提高了绿尾虹雉卵的人工孵化率。种鸟于 4 月 4 日所产下的第一枚卵，经人工孵化于 5 月 5 日成功出壳，成为全球 2018 年人工繁育

成活的第一只绿尾虹雉幼雏。2018 年中心共获得绿尾虹雉受精卵 8 枚，成功孵化出 5 只雏鸟。2019 年，中心的繁育工作继续取得重大突破，共繁育成活绿尾虹雉 7 只个体，繁育数量再创新高，使人工饲养的绿尾虹雉数量翻了一番。

(四川：邓江宇)

全国燕及雨燕调查与保护项目完成第一次同步调查

2019 年 5 月 11—12 日，“中国燕子知多少——全国燕子调查与保护”项目进行了第一次同步调查，共有 16 家机构在各自不同的城市参与了这次调查。据不完全统计，共有 675 人次的志愿者，在东西南北中的 16 座城市的 264 条样点、样线开展了同步调查。调查结果正在统计中。

全国燕子调查与保护项目始于 2017 年，由中国观鸟会、深圳市观鸟协会发起，香港观鸟会、寸草心乡村环境教育促进会给予支持，第一季有 11 家机构参与；第二季(2019 年)扩展为 18 家，得到 SEE 的支持，在任鸟飞 99 公益平台成功申请进行公募。未来 3~5 年，项目预计扩展到 25 家机构参与，争取达到每个省及自治区。

(全国燕及雨燕调查与保护工作组：付建平)

祝贺短信

1. 祝贺我分会常务理事邹发生研究员获得 2019 年国家基金委中美生物多样性重大国际合作项目！

2. 祝贺孙悦华、雷富民、曹垒、詹祥江等研究团队 2019 年上半年分别在 *Science*、*PNAS*、*Nature Communication* 等国际顶级刊

物发表学术论文!

3. 祝贺我分会副理事长邹红菲教授自 2019 年 4 月开始担任东北林业大学野生动物资源学院院长!

4. 祝贺我分会秘书长张雁云教授 2019 年

3 月被任命为北京师范大学生命科学学院党委书记!

5. 祝贺我分会常务理事陈水华研究员荣获第八届阿拉善 SEE 生态奖!



《华北地区常见鸟类野外识别手册》(彩色版)(附数字课程)

由张雁云教授主编的《华北地区常见鸟类野外识别手册》(彩色版)(附数字课程)即将于 2019 年 7 月在高等教育出版社出版。本书是“首都高校生物学野外实习系列”之一。全书分为三大部分。图鉴部分收录华北地区常见鸟类 157 种,除提供精美的鸟类野外生态照片和文字说明外,还给出了鸟类生活史照片和巢、卵的照片(包括科研中长期积累的巢卵标本的照片)。最引人入胜的是,本书提供了每一个鸟种的语图,读者通过扫描二维码,可以聆听每个物种独特的鸣声。部分物种还提供了视频。在鸟类分类的基础知识部分,本书给出了便于野外快速识别的快速检索、中文鸟名生僻字读音、鸟类的特征术语、常用参数测量、鸟类鸣声语图说明、居留型说明等信息。在鸟类野外识别与研究技术部分,本书介绍了鸟类野外识别技术、鸟类环志、鸣声采集与分析、鸟巢温度自动记录、遥测技术等。

本书是一本野外实习和户外观鸟的实用工具书,同时也是读者了解华北地区生物多样性和动物学基础研究的一个窗口。

(北京:董路)

《机场鸟击风险防范原理》出版

2019 年 6 月,我会资深会员赛道建教授

与吕艳博士编著的《机场鸟击风险防范原理》,已经由科学出版社出版。

该书将机场鸟类活动分为两种风险,一是能否侵入航线构成鸟撞风险,二是飞鸟是否存在与飞机相撞的可能形成鸟击风险,并从飞鸟与航线、飞机间静态、动态时空位置关系的不同角度,论述鸟类行为、分布等与飞机飞行之间的关系,探讨鸟击发生的规律性,创新微格风险理念,理论联系实际地介绍鸟类活动风险评估与航线鸟类净空等风险防范相关的专业理论与应用问题,用鸟类微格风险活动与飞行阶段的关系定位评估鸟撞风险、测报鸟击风险,根据人(设备)、机、鸟三者间静态、动态的时空关系,掌握好驱鸟时机,管控鸟撞风险、防范鸟击风险,实现航线鸟类净空保障飞行安全。

(山东:赛道建)

《壶瓶山鸟类图鉴》出版

壶瓶山国家级自然保护区位于湖南省石门县境内,地处武陵山脉东端,总面积 66,568 公顷。由康祖杰、张延祥、杨道德、田书荣主编德《壶瓶山鸟类图鉴》于 2019 年 10 月在云南民族出版社出版。全书 395 页 59 万字,记录了湖南壶瓶山国家级自然保护区鸟类 18 目 63 科 362 种及亚种,描述了各种鸟类的形态特征、生态习性、分布、居留类型,书中附有 960 多张照片。该书对了解壶瓶山保护区以及湖南省的鸟类现状具有重要参考

价值。

(北京：张正旺)

《海口湿地·鸟类图鉴》出版

由冯尔辉、蔡挺、许贺等编著的《海口湿地·鸟类图鉴》2018年12月由南海出版公

司出版。该书15万字，对海口的自然环境、湿地及主要观鸟地点进行了介绍，共记录野生鸟类20目65科300种，对其中的222种进行了详细介绍。该书是一本了解海口的湿地和鸟类资源概况的工具书，具有重要参考价值。

(北京：张正旺)



中国动物学会第十八届全国会员代表大会暨第二十四届学术年会第二轮通知

各省、自治区、直辖市动物学会、学会各分会、专业委员会及学会会员代表：

2019 年是中国动物学会成立 85 周年，经十七届理事会第六次扩大会议及秘书长工作会议暨党建会议研究，决定于 2019 年 8 月 23—25 日在陕西省西安市召开中国动物学会第十八届全国会员代表大会暨第二十四届学术年会。

主办单位：中国动物学会

承办单位：陕西省动物学会、陕西师范大学、陕西省科学技术协会、西北大学、陕西理工大学、陕西省动物研究所、延安大学、西安文理学院、陕西学前师范学院、陕西自然博物馆

大会主题：新时代的动物学：学科交叉，

创新引领

会议主要内容：

一、学会换届选举

1. 召开中国动物学会第十七届理事会第七次会议

2. 召开中国动物学会第十八届全国会员代表大会

(1) 会员代表审议、修改中国动物学会会章

(2) 会员代表审议中国动物学会第十七届理事会工作报告及财务报告

(3) 会员代表选举中国动物学会第十八届理事会理事、选举监事会成员

(4) 召开中国动物学会第十八届理事会第一次理事会会议，选举常务理事，选举正、副理事长，选举理事会党委委员

二、学术交流

1. 大会特邀报告

| 报告人 | 报告题目 |
|--|--|
| 舒德干 院士 (西北大学) | 动物界早期关键创新事件及广义人类由来假说 |
| Hiroyuki Takeda (日本东京大学) | Medaka, Japanese killifish, as a vertebrate model for genome and epigenome |
| Kazufumi MOCHIZUKI (Institute of Human Genetics, Montpellier France) | Small RNA-directed programmed DNA elimination in <i>Tetrahymena</i> |
| 包振民 院士 (中国海洋大学海洋生命学院) | 从扇贝基因组一窥早期动物的发育与进化 |
| 张知彬 (中国科学院动物研究所) | 探索森林鼠类与植物种子之间合作与对抗的奥秘 |
| 高绍荣 (同济大学生命科学学院) | Epigenetic regulation in early embryo development and somatic cell reprogramming |
| 陈启军 (沈阳农业大学) | 疟疾的免疫学问题与防治 |
| 宋尔卫 (中山大学) | 肿瘤微环境对肿瘤发生发展的作用及其机制 |

| | |
|----------------------|---|
| 陈大华 (中国科学院动物研究所) | LC Domain-Mediated Coalescence Is Essential for Otu Enzymatic Activity to Extend <i>Drosophila</i> Lifespan |
| 李保国 (中国科学院西安分院/西北大学) | 人类活动影响下的金丝猴种群维持机制的研究 |

2. 大会青年学者报告

| 报告题目 | 报告人 |
|---|--------------------------|
| 以四膜虫为模式生物: N6-腺嘌呤甲基化酶AMT1的功能研究 | 高珊 (中国海洋大学海洋生物多样性与进化研究所) |
| 两栖爬行动物的多样性与进化研究 | 车静 (中国科学院昆明动物研究所) |
| 基因组数据揭示小熊猫种下分类及演化历史 | 胡义波 (中国科学院动物研究所) |
| 古DNA与人类演化 | 付巧妹 (中国科学院古脊椎动物与古人类研究所) |
| 蜘蛛哺乳与长期亲代抚育 | 陈占起 (中国科学院西双版纳热带植物园) |
| Sex chromosome evolution in birds and bird-like mammals | 周琦 (浙江大学生命科学学院) |

3. 专题学术交流

| 专题名称 | 组织者 |
|--------------------|---|
| 灵长类行为生态与适应进化 | 灵长类学分会李保国教授、灵长类学分会李明研究员 |
| 动物行为学 | 西北大学齐晓光教授、陕西省动物学会邵发道教授、动物行为学分会张健旭研究员 |
| 全球变化下的海洋动物学研究 | 甲壳动物学分会李新正研究员、鱼类学分会何舜平研究员 |
| 青藏高原动物学多样性与保护 | 鸟类学分会雷富民研究员、两栖爬行学分会江建平研究员、北京大学高克勤教授、广东省动物学会胡慧建研究员 |
| 系统进化 | 蛛形学专业委员会李枢强研究员、天津动物学会卜文俊教授 |
| 圆口类学学术研讨会 | 辽宁师范大学李庆伟教授、中山大学黄盛丰教授 |
| 两栖爬行动物多样性与保护 | 两栖爬行动物学分会屈彦福副教授、李成副研究员 |
| 模式动物和发育生物学 | 发育生物学专业委员会刘峰研究员、黄勋研究员 |
| 原生动物的多样性与进化 | 原生动物学分会宋微波院士、缪炜研究员 |
| 生殖细胞及胚胎发育的分子调控 | 细胞与分子显微技术学分会高绍荣教授、生殖生物学会分会孙青原研究员 |
| 脊椎动物基因组进化与适应 | 兽类学分会胡义波研究员、刘志瑾副研究员 |
| 动植物关系与协同进化 | 华中师范大学张洪茂教授、江西师范大学易现峰教授、陕西省动物学会常罡教授 |
| 动物肠道微生物的多样性与生态行为适应 | 合肥师范学院李进华教授、吉林农业大学冯江教授 |
| 迁徙鸟类的研究与保护 | 鸟类学分会马志军教授、曹垒研究员 |
| 同一个健康: 人兽共患寄生虫病 | 空军军医大学赵亚教授、西安交通大学程彦斌教授 |
| 协同创新发展的比较内分泌学 | 比较内分泌学专业委员会李赞东教授、张勇教授 |
| 绿色一带一路建设与生态保障 | 甲壳动物学分会李富花研究员、贝类学分会阙华勇研究员 |
| 野生动物基因编辑 | 中国科学院昆明动物研究所赖彻研究员、昆明理工大学牛昱宇教授 |

4. 动物学博士生论坛

由陕西师范大学、中国动物学会主办。拟资助 100 人, 经审查符合条件的免去参加博士论坛期间 (8 月 22—23 日) 的食宿费、博士生论坛注册费; 若参加 24—25 日大会, 需交大会注册费。博士生论坛的参会人员请按照中国动物学会本届学术讨论会的正式代表注册并注明同时参加博士生论坛, 详情和具体要求见陕西师范大学研究生院 <http://newyjs.snnu.edu.cn/>; 生命科学学院 <http://lifesci.snnu.edu.cn/> 网页。

三、会议论文摘要征集及壁报

学会在会前刊印《中国动物学会第十八届全国会员代表大会暨学术讨论会论文摘要》汇编, 为内部发行。现向广大会员、动物学科技工作者征集论文摘要, 同时向参加动物学博士生论坛者征集论文摘要, 论文摘要均不收取审稿费及版面费。

1. 论文摘要格式要求

1200 字以内, 使用 Word 系统排版录入, 页边距为 (上下各 3 cm、左右各 2.3 cm)。文中尽量不用图表, 不附参考文献。文责自负。

题目: (三号黑体居中)

作者: (四号仿宋居中)

作者单位: (五号宋体居中, 含城市名称,

邮政编码并用逗号分开, 外面括号; 如有两个以上作者, 作者间用分号分开)

正文: (五号宋体字, 单倍行距)、可分段落。文中所用计量单位, 一律按国际通用标准或国家标准, 并用英文书写, 如 km², kg 等。面积请勿用“亩”表示, 而要换算为公顷, 用 hm² 表示。文中年代、年月日、数字一律用阿拉伯数字表示。

关键词: 摘要后附关键词, 关键词之间用分号间隔。

2. 论文摘要提交及截止日期

(1) 论文摘要请通过中国动物学会主页 (<http://czs.ioz.cas.cn/>) 左侧菜单栏“学术会议系统”提交 (详见附件), 截止时间为 2019 年 7 月 15 日。(2) 参加“动物学博士生论坛” (由陕西师范大学、中国动物学会主办) 并提供论文摘要, 通过中国动物学会主页 (<http://czs.ioz.cas.cn/>) 左侧菜单栏“学术会议系统”提交 (详见附件), 截止时间为 2019 年 7 月 15 日。

3. 申请做壁报的参会人员, 壁报通过评审后, 会务组会邮件通知本人自行打印海报携带到报到现场, 壁报统一尺寸为 90 cm (宽) * 120 cm (高)。

四、会议费用

注册费

| 6月15日前注册 | 6月16日-7月31日注册 | 8月1日 - 现场注册 |
|------------|---------------|-------------|
| 会员 ¥ 1300 | 会员 ¥ 1500 | 会员 ¥ 1700 |
| 非会员 ¥ 1500 | 非会员 ¥ 1700 | 非会员 ¥ 1900 |
| 学生 ¥ 900 | 学生 ¥ 1100 | 学生 ¥ 1300 |

(注: 可带家属, 费用自理)

住宿宾馆及费用

(注: 曲江华美达广场酒店、曲江银座酒店、百事特威酒店住宿预订请登陆 <https://jinshuju.net/f/msLKUt?code=081UqR9d1GJhDy0meGcd1qRQ9d1UqR9t> 链接, 内附预订须知, 住宿预订需要交纳 1 晚预定金, 预定金会议结束后两日内退回。)

| 宾馆名称 | 房间类型 | 价格 (元/天/间) | 间数 | 到会场的距离 |
|-------------------|------|---------------|------------|-----------------------------------|
| 曲江华美达广场酒店 | 标单 | 580 | 标间200、大床30 | 汇新路, 离大会地点约200米, 离分会地点约1.5公里 |
| 西安曲江银座酒店 | 标单 | 490 | 标间100、大床50 | 翠华路, 离大会地点约400米, 离分会地点约1.2公里 |
| 百事特威酒店 (西安曲江店) | 标单 | 350 | 标间45、大床15 | 翠华路, 离大会地点约1.4公里, 离分会地点约800米 |
| 陕西师范大学 学术活动中心 | 标间 | 220 | 合计210间 | 陕西师范大学校内, 离大会地点约1.5公里, 离分会地点约500米 |
| 陕西师范大学 启夏苑 | 标间 | 240 | | 陕西师范大学校内, 离大会地点约1.5公里, 离分会地点约500米 |

注: 1、价格可能稍有浮动; 2、由于部分酒店价格超标, 建议参会人员尽量考虑2人合住。

五、注册费付款方式(请通过电汇或邮政汇款)

1. 银行汇款帐号:(请注明“西安会+参会人姓名”)

开户名称: 中国动物学会

银行帐号: 0200004509089152663

开户银行: 中国工商银行海淀西区支行

2. 缴纳注册费联系人:

张欢 电话: 010 - 64807051 邮箱: iszs001@aliyun.com

张永文 电话: 010 - 64807051 邮箱: czs@ioz.ac.cn

注: 本届大会将按照国际惯例, 严格执行不同时期注册, 缴纳注册费不同的原则, 请各位代表及时注册付款, 享受早期注册的优惠。如果您不是中国动物学会会员, 可前往中国动物学会网站 (<http://czs.ioz.cas.cn/>) 首页页面左侧“申请入会”处网上填写入会申请, 以享受会员待遇。

注册完成后, 请您及时付款, 注册费的缴纳以在学术会议系统网站注册 <http://czs.bitcast.org.cn/czsweb/> (详见附件), 同时在规定时间内缴纳注册费为界限; 只在会议系统

注册, 缴纳注册费延迟的, 以延迟日的会议注册费标准缴纳。如注册付款后, 因意外原因不能参加会议的, 请发信和电话联系“缴纳注册费联系人”, 会议主办方将根据情况返还注册费。

具体返还说明:

在2019年7月1日前申请取消的, 将100%返还注册费, 仅收取开发票费用。

在2019年8月9日前申请取消的, 将返还50%注册费。

2019年8月10日以后, 注册费将不再返还。

3. 会务组联系人:

常 罡, 电话: 18792606171 E-mail: snow1178@snnu.edu.cn

贾蕊, 电话: 15991626796

E-mail: jiarui@snnu.edu.cn

4. 摘要咨询联系人: 王程亮 电话: 13891847670

5. 预订酒店联系人: 王芝尹 电话: 15398046759

六、大会不组织会后考察

若参加会后考察, 在旅行社自行报名,

费用自理。

(中国动物学会)

2019年全国博士生学术论坛(动物学)会议通知

1、论坛简介

“2019年全国博士生学术论坛(动物学)”将于8月22—23日在陕西师范大学隆重举办。届时,配合中国动物学会第十八届会员代表大会暨第二十四届学术年会的召开,将邀请全国动物学领域博士生及知名学者和专家700余人共聚一堂进行学术交流与研讨。

博士生论坛由陕西师范大学和中国动物学会主办,欢迎广大在读动物学博士生踊跃提交论文摘要申请参加。拟资助100人,经审查符合条件的免去参加博士生论坛期间(8月22—23日)的食宿费、博士生论坛注册费;若参加24—25日中国动物学会第十八届会员代表大会暨第二十四届学术年会,需交大会注册费。博士生论坛的参会人员请按照中国动物学会第十八届会员代表大会暨第二十四届学术年会的正式代表注册并注明参加博士生论坛,详情和具体要求见中国动物学会和陕西师范大学研究生院<http://newyjs.snnu.edu.cn/>;陕西师范大学生命科学学院<http://lifesci.snnu.edu.cn/>网页。

2、论坛宗旨

荟萃精英、思想创新、交汇融合、团结协作

3、论坛主题

“一带一路”下的动物学新发展

4、论坛议题

- (1) 动物分类与动物系统演化;
- (2) 动物生态学和动物行为学;
- (3) 生物多样性与野生动物保护;
- (4) 动物细胞、分子、生理与生化;

(5) 生物技术在动物学研究中的应用。

5、论坛活动内容

- (1) 国内外知名专家专题学术报告;
- (2) 博士生代表学术报告及专家点评;
- (3) 优秀学术报告评选。

6、论坛举办时间、地点

时间:2019年8月22—23日

地点:中国西安陕西师范大学雁塔校区

第十五届全国野生动物生态与资源保护学术研讨会(第一轮通知)

为了促进和探讨我国兽类学、动物生态学的发展战略和学术交流,经研究和讨论,“第十五届全国野生动物生态与资源保护学术研讨会”将于2019年11月17—20日在海南省海口市召开。此次会议由中国生态学会动物生态专业委员会、中国动物学会兽类学分会、中国野生动物保护协会科技委员会、国际动物学会和海南省动物学会联合主办;热带岛屿生态学教育部重点实验室(海南师范大学)和海南师范大学生命科学学院承办;中国科学院动物研究所动物生态与保护生物学院重点实验室等单位协办。

1. 会议内容

我国兽类学、动物生态学相关领域所取得的最新研究成果交流和研讨。

2. 会议时间和日程安排

2019年11月17—20日(17日报到,18—19日会议,20日离会)。

3. 会议地点

海南省海口市(澄迈县西海岸大酒店)。

4. 会议主办单位

中国生态学会动物生态专业委员会、中国动物学会兽类学分会、中国野生动物保护协会科技委员会、国际动物学会和海南省动物学会。

5. 会议承办单位

热带岛屿生态学教育部重点实验室 (海南师范大学)、海南师范大学生命科学学院

6. 会议协办单位

中国科学院动物研究所动物生态与保护生物学院重点实验室、海南科海商务会议有限公司

7. 会议注册费

会员代表 ¥1200 元、学生代表 ¥800 元。食宿自理。

8. 会议相关事宜

第一轮会议通知不需要填写会议回执, 详见第二轮通知发布。

9. 会议论文摘要

本次会议将采用专题征集形式开展相应的学术交流, 并编印内部印刷的会议论文摘要集。目前专题正在征集中, 并将在会议第二轮通知中确定本次会议的专题名称、内容、专题召集人及联系方式, 各专题的主题报告和一般口头报告均有专题召集人组织和确定。凡有兴趣者均可与相应专题的召集人联系。

10. 优秀青年动物生态学工作者评选

为奖励参会的优秀青年动物生态学工作者, 本次会议将评选出 3~5 名优秀青年动物生态学工作者 (2019 年度), 并给予每位 2,000 元奖金及证书。男性申请者 35 周岁及以下, 女性申请者 40 周岁及以下。申请者请于 2019 年 10 月 15 日前将发表论文 PDF 文件 (限于 2017—2019 年间发表, 申请者为第一作者或通讯作者发表的国内外核心期刊论文), 以及身份证复印件一并报送到中国科学院动物研究所黄乘明研究员 (cmhuang@ioz.ac.cn), 过期不再受理。由大会秘书处组织有关专家根据申请材料进行评选, 并于会议期间公布评选结果。已经获得过历届同等奖励的青年学者不再参加评选。

11. 青年学生参会资助

为鼓励学生参加学术研讨会, 由兽类学

分会发起并资助 10 名学生每人 1,000 元, 用于参加本次会议。有意申请的学生, 请于 2019 年 10 月 15 日前将申请发至兽类学分会秘书长胡义波研究员 (ybhu@ioz.ac.cn)。

12. 会议墙报

为鼓励学术交流多样化, 本届会议继续开展墙报 (Poster) 交流形式, 设立专门的墙报展示区, 会议期间安排时间进行墙报交流。墙报的尺寸为: 120 cm (高) × 90 cm (宽)。

13. 会后考察

详见第二轮通知。

14. 会议联系人

会议代表可随时发送邮件到 animalecology2019@126.com, 索取每年最新的会议通知。

联系人 (北京):

胡义波 (010-64807603, 13501310275)、
宛新荣 (010-64807106, 18910252305)

地址: 北京市朝阳区北辰西路 1 号院 5 号,
中国科学院动物研究所

邮编: 100101

联系人 (海口):

梁伟 (0898-65818360, 13976699091)、
汪继超 (0898-65888302, 13976081340)

地址: 海南省海口市龙昆南路 99 号, 海南师范大学生命科学学院

邮编: 571158

(信息来自中国动物学会网站)

第 15 届全国鸟类学研究生“翠鸟论坛” 报名通知

各位老师、同学:

第十五届“翠鸟论坛”将于 2019 年 8 月 7 日—8 日在东北师范大学举办。本次会议由中国动物学会鸟类学分会主办, 东北师范大学生命科学学院承办。

1、论坛内容：

本次论坛包括专家报告、学生报告、墙报展示和师生交流午餐会等内容。学生报告的报告人和主持人均为在读研究生。墙报展示环节中，展示者需做 3 分钟口头介绍。

最后由各参会单位投票选出金翠鸟奖、银翠鸟奖、优秀报告奖和优秀墙报奖。

本次论坛不收注册费，往返旅费及研究生的住宿费用自理。

2、注册要求：

注册者必须为在读研究生，每位导师参加论坛的研究生不超过 4 人，总名额限于 80 人。已通过中国动物学会会议系统注册翠鸟论坛的同学不需要重复提交注册信息（名单见后）。已注册大会专题报告的研究生，可以同时注册翠鸟论坛。注册时需提交摘要，未提交摘要的注册者将视为无效注册。组委会将根据提交的摘要遴选 20~25 名同学做口头报告，未入选口头报告的同学可再次提交墙报申请。

3、注册方式

报名以提交的报名回执内容为准（电子版和含导师签字的扫描版），报名文件以“单位+姓名”命名，发给予江萍（yujp539@nenu.edu.cn）。

注册及提交摘要截止日期：6 月 20 日。

注册信息及摘要经审核筛选后，于 6 月 25 日在会议系统公布参会名单和口头报告名单。

4、组委会及联系人

组委会：张雁云 屈延华 于江萍 刘阳 董路

联系人：于江萍 yujp539@nenu.edu.cn；董路 donglu@bnu.edu.cn

（中国动物学会鸟类学分会）

2019 年中国鹤类及其栖息地保护学术研讨会暨中国野生动物保护协会鹤类联合保护委员会年度工作会议（第一轮通知）

为促进我国鹤类的科学研究和保护管理工作，加强各单位之间在鹤类栖息地管理、栖息地恢复、疫源疫病防控、自然保护地建设、人工繁育与迁地保护、种群调查监测、迁徙保护网络大数据建设等方面的学术研讨和经验交流，进一步推动中国野生动物保护协会鹤类联合保护委员会的组织建设，经中国野生动物保护协会批准，定于 2019 年 11 月 28 日—12 月 1 日在安徽省池州市召开“2019 年中国鹤类及其栖息地保护学术研讨会暨中国野生动物保护协会鹤类联合保护委员会年度工作会议”。本次会议由中国野生动物保护协会鹤类联合保护委员会和安徽省池州市人民政府联合主办，湿地生态保护与修复安徽省重点实验室（安徽大学）、池州市林业局承办，安徽升金湖国家级自然保护区管理局、安徽省动物学会、安徽省野生动植物保护协会和安徽大学资源与环境工程学院等单位协办。

一、会议内容：

中国鹤类及其栖息地保护的学术研讨；中动协鹤联会年度工作会议

二、会议时间：

2019 年 11 月 28 日—12 月 1 日

三、会议地点：

安徽省池州市

四、会议议程：

2019.11.28（周四）下午：报到，地点在东裕度假酒店（池州九华山店）

2019.11.29（周五）上午：中国野生动物保护协会鹤类联合保护委员会工作会议；下午：中国鹤类及其栖息地保护学术研讨会。

2019.11.30（周六）上午：学术交流和工作总结研讨。

2019.11.30（周六）下午：考察升金湖国

际重要湿地

2019.12.1 (周日): 代表自由考察、观鸟或离会

五、学术交流形式:

会议形式包括学术报告、墙报、圆桌讨论会、摄影展。学术报告 20 个, 其中主旨报告 3~5 个, 专题报告 15~17 个。会议将评优秀学术论文奖, 限在读研究生或本科生, 参与评奖者需要提交 2018 年 1 月—至今已发表或接收的论文, 须参会并做学术报告。

请参加代表于 2019 年 8 月 25 日前提交参会回执。

六、费用和住宿安排:

本次会议不收会议注册费, 代表的食宿和交通费自理。住宿统一安排在安徽池州市东榕度假酒店(池州九华山店)。

七、会议联系人及联系方式:

徐文彬: 13856668157

赵放武: 13665665850

蔡天龙: caitianl@qq.com

于超: 15155124771, yc-107@163.com

鹤联会秘书处: 王毅花(电话 13552059980, 邮箱: wangyihua2113@163.com)

(北京: 钱法文)

第七届黑颈鹤网络年会暨国际重要湿地监测管理研讨会会议通知

由国际鹤类基金会、中国科学院昆明动物研究所、全国鸟类环志中心、甘肃省林业和草原局主办, 碌曲县人民政府和甘肃尕海-则岔国家级自然保护区管理局承办, 中国野生动物保护协会鹤类联合委员会和兰州大学生命科学学院协办的“第七届黑颈鹤网络年会暨国际重要湿地监测管理研讨会”, 将于

2019 年 7 月 30 日—8 月 3 日在黑颈鹤重要的繁殖地——甘肃尕海湖国际重要湿地召开, 诚邀黑颈鹤繁殖地及越冬地各省林业主管部门、自然保护区、科研院所及国内外专家参加交流。

研讨会将围绕黑颈鹤的科学研究、保护管理、宣传交流和国际重要湿地建设与保护等多方面展开信息交流和科学分享, 商讨未来黑颈鹤保护与研究方向。黑颈鹤 (*Grus nigricollis*) 作为国际保护联盟 (IUCN) 的易危物种, 中国 I 级重点保护野生动物, 是全世界 15 种鹤类中唯一的高原鹤, 青藏高原和云贵高原湿地的旗舰物种。中国政府和学者通过三十多年的研究与保护方面取得了卓越的成效, 但仍然存在很大的保护与研究空间, 也是我们义不容辞的责任。

会议日程:

会议时间: 2019 年 7 月 30 日—8 月 3 日; 7 月 30 日全天报到; 7 月 31 日—8 月 1 日学术研讨会; 8 月 2 日野外考察黑颈鹤繁殖地; 8 月 3 日离会。

会议地点: 碌曲县洮河源大酒店(甘南州碌曲县玛艾镇)

联系人: 常云艳 13577027159 (昆明动物所)、范龙 18794002901 (尕海)

联系方式: 0941-6625586; 邮箱: 821815839@qq.com

本次会议不收会务费, 参会代表交通、住宿费用自理。为保证会议质量, 每个参会单位限报 1~2 人, 通过扫描微信码进行网络报名。



(云南: 杨晓君; 甘肃: 张立勋)

中国动物学会动物行为学分会第三届(2019)学术年会暨全国动物行为学第七次研讨会(第一轮通知)

为促进我国动物行为学的科学研究与学术交流,提高我国动物行为学的研究水平,拟于2019年11月15—18日在海南省海口市召开“中国动物学会动物行为学分会第三届学术年会暨全国动物行为学第七次研讨会”。

1. 会议主题

快速发展的中国动物行为学。

2. 会议内容、时间和日程安排

本届会议除开展学术研讨和交流,还将进行中国动物学会动物行为学分会的理事会换届选举。2019年11月15—18日(15日报到,16—17日会议,18日离会)。会议详细日程安排请关注中国动物学会学术会议网站(<http://czs.bitcast.org.cn>)。

3. 会议地点

海南省海口市(澄迈县西海岸大酒店)。

4. 会议主办单位

中国动物学会动物行为学分会。

5. 会议承办单位

热带岛屿生态学教育部重点实验室(海南师范大学)、海南省动物学会和海南师范大学生命科学学院。相关会务活动由海南科海商务会议有限公司协助安排。

6. 会议注册和缴费

会议期间各位代表的住宿和会后考察费用自理,非正式会议期间(15日和18日)的餐费自理。会议注册费分网上和现场注册,以缴纳日期为准,缴费注明“行为学会议”。注册费缴纳方式请见中国动物学会学术会议系统网站(<http://czs.bitcast.org.cn/czswweb/>),详细方法请阅读《中国动物学会“学术会议注册系统”操作流程》(<http://czs.bitcast.org.cn/czswweb/showNewsDetail.asp?nsId=70>)。

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|----------------------------------|------------------------|
| 网上注册和缴费 2019年5月15日—10月 31日 | 现场注册和缴费 2019年11月15日 |
| 会员代表 ¥1,200 | 会员代表 ¥1,500 |
| 学生代表 ¥800 | 学生代表 ¥1,000 |

中国动物学会开户行及帐号:

开户行名称:中国工商银行海淀西区支行

开户名称:中国动物学会

帐号:0200004509089152663

欢迎您申请加入中国动物学会动物行为学分会,请在中国动物学会个人会员管理系统网站(<http://app01.cast.org.cn:7001/cast/reg.jsp?sid=S18>)在线进行会员申请,相关事宜可联系刘伟博士(liuwei@ioz.ac.cn)。

7. 会议报告和墙报

为鼓励学术交流多样化,本次会议设有大会特邀报告、专题报告和墙报(Poster)等交流形式,会务组鼓励和倡议大家多通过墙报交流。大会特邀报告由大会学术委员会邀请,专题报告由专题组推荐和与会代表自由申请两种方式,请关注第二轮通知。

大会官方语言为中文。论文摘要提交须为中文。会议报告ppt可为中文或英文,如为英文,须给出关键词的中文注释。大会墙报可为中文和英文,如为中文,欢迎给出英文摘要。如为英文,必须给出中文摘要。为提高研究生的学术交流能力,会议设立专门的墙报展示区进行墙报交流。在参会博士后和研究生中将评选出最佳口头报告奖,最佳壁报奖予以奖励。墙报的尺寸为:120 cm(高)×90 cm(宽)。

论文摘要通过学术会议网站提交,截止日期为2019年10月30日。摘要字数要控制在500字以内,包括题目(中英文)、作者、单位(含地址及邮编)、摘要正文、关键词项目资助等。提交论文摘要时,需注明申请口

头报告还是墙报，对口头报告要经大会组委会（见第二轮通知）筛选，鼓励墙报交流。

8. 住宿安排和会后考察

会议地点位于海南省海口市（澄迈县西海岸大酒店）。会后安排有海南吊罗山国家级自然保护区考察等（费用自理）。欢迎全国各研究单位、大专院校、博物馆、动物园、自然保护区和野生动物管理部门等单位的动物科技工作者报名参会。

9. 会务联系

刘 伟（中国科学院动物研究所，13661347297，liuwei@ioz.ac.cn）

梁 伟（海南师范大学，13976699091，13976699091@139.com）

汪继超（海南师范大学，13976081340，190610244@qq.com）

（海南：梁伟）

封面：酒红朱雀 (*Carpodacus vinaceus*)，摄影 顾云芳。

English Abstract



Notes of Meetings

Spring Bird Banding Training Class of 2019 was held in Beidaihe, Hebei

“Spring Bird Banding Training Class of 2019” was held in Beidaihe, Hebei province. The main topics of the training class included the knowledge of ornithology knowledge, bird classification and identification, wildlife rescue, birds banding database management, the application of satellite-tracking in migration researches and color mark made and so on. 30 Trainee were took part in the banding examination. 40 banders from Heilongjiang, Inner Mongolia, Hebei, Shandong, Henan, Yunnan and Great Khingan attended the training class.

(Chen Lixia and Wang Yihua, National Bird Banding Center of China)

Training Course on Bird Monitoring and Bird-Strike Control was held in the Airports in Gansu Province

For the purpose of controlling the bird-strike accidents in the airports, Prof. Zhang Lixun from Lanzhou University attended several training courses in Gansu Province in March 2019. On March 12th he gave a lecture to aircrew and ground support personnel in the Yuzhong Airport, with an topic of “Bird observation and bird-strike prevention and control at the airport”. In combination with years of monitoring and research on birds in the Yuzhong Basin, he trained about 75 aircrew and ground support personnel. In March 25-27th, He was invited to organize another training course in Wuwei Airport.

(Zhang Lixun, Lanzhou University)

Professor Cao Lei made a presentation on the British Ornithology Annual Conference

On March 26th of 2019, Prof. Cao Lei from Chinese Academy of Sciences was invited to attend the British Ornithology Annual Conference. As a speaker of Alfred Newton Lectures, she made a presentation entitled “On using waterbird telemetry data to support freshwater wetland conservation in China”.

(Cao Lei, Beijing)

Research Reports

New insights in molecular mechanism of high-altitude adaptation in birds

The harsh environment of the Qinghai-Tibet Plateau, the highest and largest plateau in the world, exerts severe selective pressure that has resulted in the evolution of similar phenotypic adaptations in humans, mammals, and birds (e.g. hypoxic resistance, cold tolerance, enhanced metabolic capacity and increased body masses). However, genomic studies have shown that different organisms adapt to high altitudes via multiple genetic routes, which may be largely subject to phylogenetic context. Comparisons of phylogenetically distinct species in previous studies may have underestimated the actual degree of similarity in genomic evolution. In addition, although high-altitude adaptation has been well investigated at the gene sequence level, studies of gene expression across multiple tissues across multiple species are rarely concerned.

Recently, a study entitled “Comparative transcriptomics of 3 high-altitude passerine birds and their low-altitude relatives” was published in PNAS on May 20, 2019. The research team led by Prof. LEI Fumin from Institute of Zoology of the Chinese Academy of Sciences, compared transcriptomic data of three high-altitude passerine birds with those of their low-altitude relatives by integrating protein-coding sequence comparison and gene expression analysis across multiple tissues to explore high-altitude adaptation within a phylogenetic framework.

Sequence comparison revealed that the three high-altitude birds were genetically convergent on positively selected genes, but their amino acid substitutions mostly occurred at divergent sites, suggesting that adaptive convergence seldom occurred at the amino acid substitution level. Gene expression analysis found that the high-altitude environment might have promoted substantial expression shifts in the three high-altitude birds since expression profiles of differentially expressed genes and altitude-associated genes (altitude-clustered pattern) largely differed from those of all genes (tissue-clustered pattern). Few genes under positive selection for all three high-altitude species overlapped with differentially expressed genes, but the interaction between gene expression and altitude and the interaction between gene connectivity and altitude were correlated with evolutionary rates of genes.

Taken together, these new findings suggested that the high-altitude birds might evolve in a concerted way through both sequence changes and expression shifts.

This study was funded by grants from the Strategic Priority Research Program, Chinese Academy of Sciences and the National Science Foundation of China.

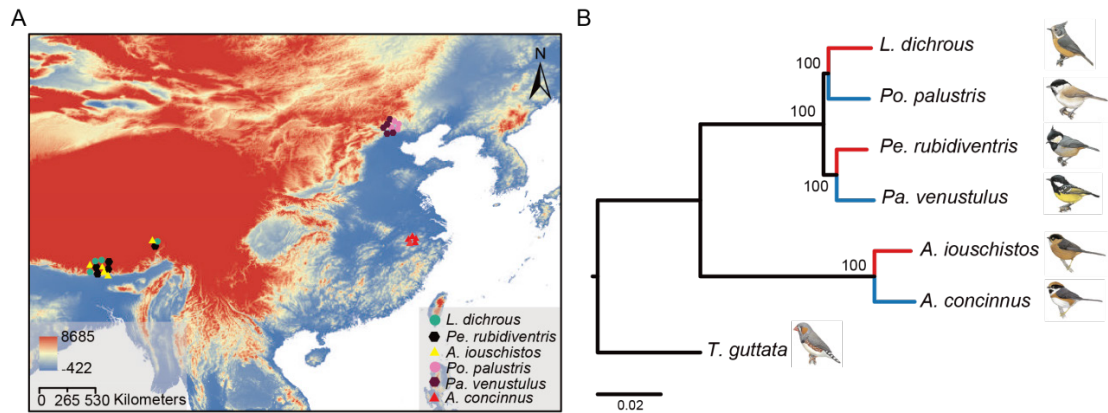


Figure 1. (A) Sampling locations. (B) Maximum likelihood phylogeny of the six studied species with the zebra finch (*Taeniopygia guttata*) as an out-group. Red branches indicate the high-altitude species; blue branches indicate the low-altitude species. (Image by IOZ)

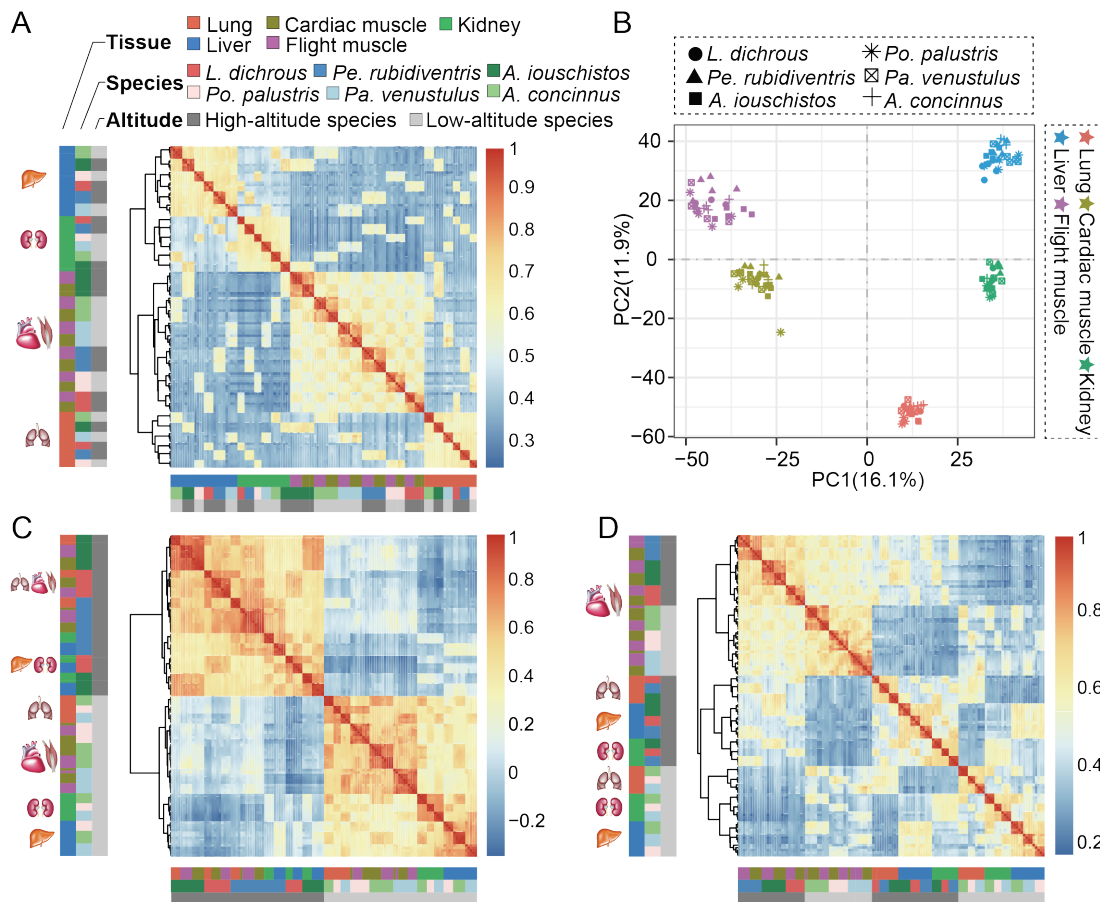


Figure 2. Gene expression patterns across the six species. (A) Symmetrical heat map of Spearman's correlation coefficients between all pairs of samples across all genes. (B) PCA of the log-transformed normalized expression levels of all orthologs across all species and tissues. (C) Symmetrical heat map of Spearman's correlation coefficients between all pairs of samples across differentially expressed genes. (D) Symmetrical heat map of Spearman's correlation coefficients between all pairs of samples across altitude-associated genes. (Image by IOZ)

(Hao Yan, Qu Yanhua and Lei Fumin, Beijing)

Stochastic simulations reveal few green wave surfing populations among spring migrating herbivorous waterfowl

Tracking seasonally changing resources is regarded as a widespread proximate mechanism underpinning animal migration. Migrating herbivores, for example, are hypothesized to track seasonal foliage dynamics over large spatial scales. Previous investigations of this green wave hypothesis involved few species and limited geographical extent, and used conventional correlation that cannot disentangle alternative correlated effects. Here, we introduce stochastic simulations to test this hypothesis using 222 individual spring migration episodes of 14 populations of ten species of geese, swans and dabbling ducks throughout Europe, East Asia, and North America. We find that the green wave cannot be considered a ubiquitous driver of herbivorous waterfowl spring migration, as it explains observed migration patterns of only a few grazing populations in specific regions. We suggest that ecological barriers and particularly human disturbance likely constrain the capacity of herbivorous waterfowl to track the green wave in some regions, highlighting key challenges in conserving migratory birds.

(Wang Xin, Cao Lei and Chen Liding, Beijing; Zhao Yunlin and Xu Zhenggang, Hunan; Anthony D. Fox and Jesper Madsen, Denmark; Richard Fuller, Australia; Larry Griffin and Carl Mitchell, UK; Oun-Kyong Moon, Korea; David Cabot, Ireland; Nyambayar Batbayar, Mongolia; Andrea Kölzsch, Germany; Henk P. van der Jeugd, The Netherlands; Ran Nathan, Israel)

Convergent genomic signatures of flight loss in birds suggest a switch of main fuel

Flight loss in birds is as characteristic of the class Aves as flight itself. Although morphological and physiological differences are recognized in flight-degenerate bird species, their contributions to recurrent flight degeneration events across modern birds and underlying genetic mechanisms remain unclear. Here, in an analysis of 295 million nucleotides of 48 bird genomes, we identify two convergent sites causing amino acid changes in ATGLSer321Gly and ACOT7Ala197Val in flight-degenerate birds, which to our knowledge have not previously been implicated in loss of flight. Functional assays suggest that Ser321Gly reduces lipid hydrolytic ability of ATGL, and Ala197Val enhances acyl-CoA hydrolytic activity of ACOT7. Modeling simulations suggest a switch of main energy sources from lipids to carbohydrates in flight-degenerate birds. Our results thus suggest that physiological convergence plays an important role in flight degeneration, and anatomical convergence often invoked may not.

This paper has been published on Nature Communication, more detail please see Pan, S., Lin, Y., Liu Q., Duan, J., Lin, Z., Wang, Y., Wang, X., Lam, SM., Zou, Z., Shui, G., Zhang, Y., Zhang, Z., Zhan, X.

(2019). Convergent genomic signatures of flight loss in birds suggest a switch of main fuel (*Nature Communications*. 10: 2756).

(Pan Shengkai, Lin Yi, Liu Qiong, Duan Jinzhi, Lin Zhenzhen, Wang Yusong, Wang Xueli, Sin Man Lam, Zou Zhen, Shui Guanghou, Zhang Yu, Zhang Zhengwang and Zhan Xiangjiang *, Beijing)

Niches in the Anthropocene:

Recently, a myriad of studies is investigating the impact that habitat transformation has on biodiversity patterns, individual fitness, species' traits and community structure. Overall, most of these studies stress the evident of negative consequences that habitat transformation has on biodiversity. Two main effects are of special interest for our research. First, at a regional scale there is a sharp decrease in biodiversity paralleling habitat transformation. Second, as a result of this process of biodiversity loss, persisting species are more similar to each other and, thus, redundant, i.e. there is functional homogenization.

A key question is how these environmental changes affect species' and assemblages' niches. Traditionally, niche packing and expansion are the main ways in which niches changes across environmental gradients are interpreted. Niche packing means that, with increasing diversity, species should have narrower or more overlapped niches at a relatively constant assemblage niche space. Niche expansion means that, with increasing diversity, species' niche width and overlap should be rather constant and, thus, assemblage niche space might increase.

In our study, we tested whether niche packing or expansion was the main mechanism explaining niche changes across a habitat transformation gradient, from natural forests to urban areas. However, we had to reformulate this paradigm. This is because two elements of this formula were fixed in our system. We expected that species' niche width would steeply increase from natural to urban areas because species in natural habitats are specialists, while species in transformed habitats are habitat and diet generalists. Moreover, because our study was conducted in a subtropical region, we also expected that diversity would be rather similar among locations, either natural or transformed.

In summary, we found support to the idea that there is niche expansion, rather than packing, from natural to urban areas. We found that species' niche width strongly increased from natural to urban habitats, while niche overlap among species at each assemblage remained rather unchanged across this gradient. The fact that niche overlap among species was nearly constant, in spite that it showed no phylogenetic signal, suggests that passerine at each assemblage -natural, rural or urban- were composed of complementary species.

While at regional scales the loss of specialized species typical of natural habitats is evident, at each location species assemblages can be relatively diverse. While at a regional scale there may be progressive functional homogenization with habitat transformation, at a local scale assemblages are usually composed of complementary species. Since transformed habitats are human constructs, there is room to improve the way in which we manage these ecosystems to increase and maintain taxonomic and functional diversity.

We obviously have to protect natural habitats because they comprise many wonderful species structured in extremely complex trophic webs. Yet, our study is important in stressing that when considering the ecological consequences of habitat transformation, such as functional homogenization, it is very important to discriminate between regional and local processes. We may conclude suggesting that in most cases, in any assemblage, species will tend to be complementary rather than redundant.

(Emilio Pagani-Núñez, Liang Dan and Liu Yang, Guangdong; Eben Goodale, Guangxi; Luo Xu, Yunnan)

Silver spoon effects of hatching order in an asynchronous hatching bird

The silver spoon hypothesis proposes that individuals that develop under favorable conditions will gain fitness benefits throughout their lifetime. Hatching order may create a considerable size hierarchy within a brood and lead to earlier-hatched nestlings having a competitive advantage over their siblings, which has been illustrated in some studies. However, there have been few explorations into the effect on subsequent generations. Here, using a 15-year-long study, we investigated the long-term fitness consequences of hatching order in the endangered crested ibis, *Nipponia nippon*, a species with complete hatching asynchrony. In this study, we found strong support for silver spoon effects acting on hatching order. Compared with later-hatched nestlings, first-hatched nestlings begin reproduction at an earlier age, have higher adult survival rates, possess a longer breeding life span, and achieve higher lifetime reproductive success. Interestingly, we found carry-over effects of hatching order into the next generation. Nestlings which hatched earlier and became breeders in turn also produced nestlings with larger tarsus and better body condition. Additionally, we found a positive correlation among life-history traits in crested ibis. Individuals that started reproduction at a younger age were shown to possess a longer breeding life span, and the annual brood size increased with an individual's breeding life span. This suggests that the earlier hatched nestlings are of better quality and the "silver spoon" effects of hatching order cover all life-history stages and next generation effects.

(Song Zitan, Zou Yuqi, Hu Canshi, Ye Yuanxing, Wang Chao, Qing Baoping, Jan Komdeur and Ding Changqing)

Genome-wide analysis reveals the genomic features of the turkey vulture (*Cathartes aura*) as a scavenger

Cathartidae is a small family of large-bodied carrion-feeding birds, of which the turkey vulture (*Cathartes aura*) is the most widespread distributed. For investigation of the chemoreception system, detoxification system, and immune system of the turkey vulture, we conducted comparative genomics analysis based on the genomes of the turkey vulture and other 14 birds. Our analysis revealed the expansion in the chemoreception system, especially the olfactory receptors, while the genes in the detoxification system of the turkey vulture did not show obvious expansion. Five positively selected genes related to the immune system were identified in the turkey vulture, possibly strengthening the immune defense against pathogenic invasion. Functional enrichment analysis demonstrated that many positively selected genes were involved in the regulation of immune system processes, implying important reorganization of the immune system in the turkey vulture. The turkey vulture-specific missense mutations were found in one positively selected gene (BCL6), and all the missense mutations were classified as deleterious by PolyPhen-2, possibly contributing to immune adaptation to the carrion feeding. Moreover, we identified four turkey vulture-specific missense mutations in three β -defensin genes of the turkey vulture, which was an indispensable part in the innate immunity (a natural barrier against invasive microbes including bacteria, fungi, and viruses). Our genomic analyses in the turkey vulture laid solid foundation to the investigation of the genetic signatures of the adaptation to the carrion feeding.

(Zhou Chuang and Yue Bisong, Sichuan)

Near-complete phylogeny and taxonomic revision of the world's babblers

The babblers have a chequered taxonomic history, and the group was long regarded as a “scrap basket” for genera that did not fit well into other families. In this study, we used a multi-locus dataset combining published and newly generated sequences to reconstruct a time-calibrated phylogeny and taxonomic revision for 89% of the world's babblers species. By calibration using a fossil and a biogeographic event, our phylogeny implies that babblers originated in the late Oligocene–early Miocene, at approximately 22 Ma (26.4–18.6 Ma). The phylogeny supports seven primary clades with non-monophyly for some genera. It suggests that babblers could be recognized as seven families including Sylviidae, Zosteropidae, Paradoxornithidae, Timaliidae, Pellorneidae, Alcippeidae and Leiothrichidae. We used a cut-off limit of 10 Ma for recognizing genera, while also taking morphological and ecological similarity into account, which supports 64 genera of babblers. The taxonomic revision proposed a new family (Alcippeidae) and a new genus (Parayuhina). This near-complete phylogeny provides a backbone for further studies on biogeography, species richness patterns and traits evolution of babblers.

(Cai Tianlong, Shao Shimiao, Zhang Ruiying, Qu Yanhua and Lei Fumin, Beijing; Alice Cibois, Switzerland; Per Alström, Martin Irestedt, Per G.P. Ericson and Magnus Gelang, Sweden; Jonathan D. Kennedy and Jon Fjeldså, Denmark; Robert G. Moyle, USA)

Within-season decline in the call consistency of individual male Common Cuckoo (*Cuculus canorus*)

Numerous studies have identified individually distinctive vocal characteristics and call consistency in different bird species. If these are to be utilised as non-invasive markers for monitoring purposes, then these vocal characteristics must remain stable over time. Three recent studies have shown that it is possible to identify individual male Common Cuckoo (*Cuculus canorus*) based on vocal characteristics but whether these are stable over the duration of a breeding season, remains unknown. We recorded 1032 syllables from 30 male Common Cuckoos in a Northeast Asian population. We colour-banded six of these males and made repeated recordings of their cu-coo advertisement call across a 19-day period of the breeding season in China. We used three methods to identify individuals: discriminant function analysis (DFA), correlation analysis (CA) and spectrographic cross-correlation (SPCC). We also used repeatability analysis to test whether call consistency (the number of syllables in each calling bout) was repeatable within individuals. Based on the same day recordings, calls from the same male were more similar in their characteristics than those of different males, and yielded correct rates of classifying individuals of 93.6% (SPCC), 90.8% (DFA), and 71.5% (CA). However, these rates declined to 40.5% (SPCC), 40.7% (DFA) and 27% (CA) when using recordings over the 19-day period. Call consistency was repeatable within individuals across two successive calling bouts, but this individual repeatability disappeared when several (more than two) calling bouts from the same day or bouts from the different days were included in the analyses. Declines in the correct rate of identifying individual male cuckoos and call consistency in this study raise concerns that individual male cuckoo calls may be more variable than previously thought.

(Deng Zhuqing, Xia Canwei and Zhang Yanyun, Beijing; Li Donglai, Liaoning)

Components of variation in female common cuckoo calls

Investigations on bird vocalizations have largely focused on males. Female vocalizations are widespread in birds but few studies have investigated female vocal characteristics, particularly in non-Passeriformes. In this study, we use new field recordings from China, and calls available from an online sound library to examine temporal patterns, call consistency and geographical variation in vocalizations of female common cuckoos *Cuculus canorus*. The peak in vocal activity (both

male and female) was in the morning, which contrasts to what would be predicted if the sole function of the female call was to distract the attention of hosts after parasitizing a host's nest in the afternoon. Both male and female common cuckoos were more vocally active in sunny weather, than rainy weather. We also found larger intra-individual variation in female rather than in male calls, which may benefit female cuckoos by increasing stimulation to host species. Peak frequency of female calls decreased with increased latitude, while differences in female call features were not associated with geographic distance. In summary, our findings that female calls are used in the morning, rather than at peak egg laying, yet are highly variable and show little geographic patterns suggest that the function of these female calls may be more variable and intricate than previously thought. However, because research on female vocalizations is underrepresented, future studies are still needed.

(Deng ZQ, Lloyd H, Xia CW, Møller AP, Liang W, Zhang YY)

The function of three main call types in common cuckoo

Acoustic signals play a key role in shaping the relationships in birds. Common cuckoos *Cuculus canorus* are known to produce various call types, but the function of these calls has only been studied recently. Here, we used a combination of field recordings (conducted in 2017) and playback experiments (conducted in 2018) to investigate the functional significance of common cuckoo calls. We found significant differences in the characteristics between male two-element 'cu-coo' and three-element 'cu-cu-coo' calls, with these two call types being used in different contexts. The three-element male 'cu-cu-coo' calls were associated with females emitting their 'bubbling' call. Playback experiments revealed that both males and females exhibit stronger responses to playing female "bubbling" calls than with the calls of Eurasian sparrowhawk (*Accipiter nisus*) serving as a control suggesting a significant intraspecific communication function for this call type. However, we did not find any evidence to support mate attraction in male calls, as females were not stimulated by playback of male calls compared to sparrowhawk calls in the control group.

(Xia CW, Deng ZQ, Lloyd H, Møller AP, Zhao XM, Zhang YY)

The effects of Urbanization on Stress Responses and Niche Dynamics in Birds

In the Anthropocene, human-made habitat transformation is increasingly evident around the world. Such environmental change is usually associated with a considerable reduction in species richness and in functional diversity across several taxa, from which the case of avian species is particularly well-known. Niche was commonly defined as n-dimensional hypervolumes of environmental factors and resources, and it can be divided into the fundamental and the realized

niche. In human-made habitats completely novel niches are available, so that species' low niche specificity may drive drastic changes in niche characteristics. Still, it is unclear how this process influences niche dynamics, and how individuals and species cope with the different habitats with considerable anthropogenic disturbances. To answer these questions, in this thesis, we compare stress response, isotope niche, individual specialization, morphological variation of songbirds from natural to urban habitats. We did this in Southwest China, an area which is experiencing one of the highest urbanization rates in the world and has very high biodiversity.

Our results show 1) BR showed no differences among habitats, but it can be diet-mediated; 2) Isotope niches of passerines showed niche expansion from natural to human-made habitats; 3) Divergent relationships between niche width and individual specialization in natural and human-made habitats; 4) Urban species are ecological generalists but morphological specialists. Overall, the results of this thesis demonstrate that species seems well adapted to the habitats where they are found and habitat transformation dramatically altered niche dimensions. This thesis has begun to disentangle the complex differences in niche width, niche overlap, individual specialization, and morphological variation among habitats. The results of this thesis suggested niche expansion of species in novel habitats seems mostly driven by the differences in intra- and interspecific competition among habitats.

Dr. Dan Liang studied as a PhD student at School of Life Sciences, Sun Yat-sen University. He was supervised by Dr. Yang Liu and successfully defended his PhD thesis in November 2018. Now Dan is a postdoctoral research fellow at the Department of Ecology and Evolution, Princeton University, USA.

(Liu Yang, Guangdong)

The factors determining and maintaining the diversity patterns of babblers and pheasants

With the increase of population and the global warming, the ecosystem has suffered serious damages, leading to the growing threats for the global biodiversity. Studying the spatial distributions of organisms is critical to identify biodiversity hotspots, which contributes to the designation of priority areas for conservation when making a biodiversity conservation plan. By revealing the mechanisms underlying the build-up and maintenance of the diversity patterns, we can understand how the diversity patterns interact with climate, and predict the impact of climate change on biodiversity in the future. The Sino-Himalayan Mountains (SHM) region, which harbors 10% of vertebrates and 8% of plants on earth, is one of the most important diversity hotspots. Previous studies made attempts to reveal the mechanisms underlying the diversity patterns in this region.

However, the ecological factors and evolutionary processes that drive and maintain the high biodiversity remain unclear. In this study, two groups of birds with different ages were chosen as subjects: (1) pheasants as an old group which originated at the late Eocene–early Oligocene, and (2) babblers as a young group which originated at the late Oligocene–early Miocene. We integrated ecological factors, evolutionary processes and functional diversity to fully understand their roles in the build-up and maintaining of the extraordinary diversity in the SHM. This thesis contains four topics as follows. (1) Phylogeny and taxonomic revision of the world’s babblers. (2) The role of evolutionary time, diversification rates and dispersals in determining the global diversity of babblers. (3) The role of ecological and evolutionary processes in build-up diversity hotspots of pheasants in the SHM. (4) The role of functional traits divergence in co-existence of babblers.

The babblers have a chequered taxonomic history, and the group was long regarded as a “scrap basket” for genera that did not fit well into other families. In this study, we use a multi-locus dataset combining published and newly generated sequences to reconstruct a time-calibrated phylogeny and taxonomic revision for 89% of the world’s babblers species. By calibration using a fossil and a biogeographic event, our phylogeny implies that babblers originated in the late Oligocene–early Miocene, at approximately 22 Ma (26.4–18.6 Ma). Our phylogeny supports seven primary clades with non-monophyly for some genera. Our phylogeny suggests that babblers could be recognized as seven families including Sylviidae, Zosteropidae, Paradoxornithidae, Timaliidae, Pellorneidae, Alcippeidae and Leiothrichidae. We used a cut-off limit of 10 Ma for recognizing genera, while also taking morphological and ecological similarity into account, which supports 64 genera of babblers. The taxonomic revision proposed a new family (Alcippeidae) and a new genus (Parayuhina). The near-complete phylogeny provides a backbone for further studies on biogeography, species richness patterns and co-existence of babblers.

The species richness of babblers varies widely across the earth’s surface with the highest diversity in the SHM. The megadiversity of babblers in the SHM could be the direct result of accelerated diversification rate, multiple dispersals and longer evolutionary time to accumulate species. In this section, we evaluate the role of diversification rate, dispersals and evolutionary time on shaping global species richness patterns of babblers based on a near-complete phylogeny. Firstly, we reconstructed the ancestral ranges of babblers and inferred their origin and dispersal routes based on 13 geographic regions. We estimated the first colonization time and the number of immigration events in each region. Secondly, we estimated diversification dynamics through time and among seven geographic regions. In addition, pairwise comparisons of speciation, extinction and dispersal rates between SHM and non-SHM (or continental vs. insular regions) were conducted using GeoSSE models. Lastly, we used the ordinary linear model to compare the relative predictive power of evolutionary time, speciation rate and the number of immigration events upon the species diversity of babblers. We found that babblers originated in the SHM in the early

Miocene and from here they colonized other regions, suggesting a longer time for diversification and accumulation of species in the SHM. The diversification rate analysis marked a rate increase at 2.5 Ma associated with the radiation of Zosterops in oceanic islands, which coincides with the period of repeated sea level fluctuations in the late Pliocene–Pleistocene. Multiple regression analyses showed the global diversity of babblers can be well explained by the timing of the first colonization within major regions, while the effects of speciation rate and repeated colonizations have been relatively weak. Our results suggest that the global diversity patterns in these birds have mainly been caused by the “time-for-speciation effect”. Our findings also support tropical and subtropical mountains (e.g., SHM) as an origin centre and oceanic islands as the evolutionary cradle for babblers, which provide new insights into the generation of global diversity hotspots.

The SHM have higher species richness than adjacent lowland regions, making them a global biodiversity hotspot. Various mechanisms, including ecological constraints, energetic constraints, diversification rate variation, “time-for-speciation effect” and multiple colonizations, have been posited to explain this pattern. We used pheasants (Aves: Phasianidae) as a model group to test these hypotheses and to understand the ecological and evolutionary processes that have contributed to the extraordinary diversity in these mountains. Using distribution maps predicted by species distribution models (SDMs) and a multi-locus time-calibrated phylogeny for pheasants, we examined the relationships between species richness and predictors including net primary productivity (NPP), niche diversity, diversification rate, evolutionary time and colonization frequency using Pearson’s correlations and structural equation modelling (SEM). We reconstructed ancestral ranges at nodes and examined basal/derived species patterns to reveal the mechanisms underlying species richness gradients in the Sino-Himalayas. We found that ancestral pheasants originated in Africa in the early Oligocene (33 Ma, 95% HPD: 28.7–38.2 Ma), and then colonized the SHM and other regions. In the Sino-Himalayas, species richness was strongly related to diversification rate, NPP, niche diversity and colonization frequency, but weakly correlated with evolutionary time. The SEMs indicate that the direct effects of niche diversity and diversification rate on species richness were stronger than NPP and evolutionary time. NPP indirectly influenced species richness via diversification rate, but its effect on richness via niche diversity was relatively weak. An increase in available niches, rapid diversifications and multiple colonizations was found to be key direct processes for the build-up of the diversity hotspots of pheasants in the Sino-Himalayan Mountains. Productivity had an important but indirect effect on species richness, which worked through increased diversification rate. Our study suggests that higher species diversity in the Sino-Himalayas was generated by both ecological and evolutionary mechanisms.

The species-rich group of babblers exhibits great disparity of ecomorphological traits, as well as high levels of sympatry in the SHM, making this group an ideal model for studying the mechanism of species coexistence. It is generally believed that coexistence species would be divergence in

morphology, diet or foraging strata to avoid interspecific competition and divergence in traits in terms of sexual selection such as plumage and song to avoid interspecific hybridization. The comorphological traits divergence among coexistence species may be caused by rapid speciation or long time for diversifying. However, only few studies have tested the relationship between divergence in comorphological traits and species coexistence, and the underlying mechanism is still unclear. In order to understand the underlying mechanisms maintaining the diversity in the assemblages, we used morphology, diet, vocalization and plumage as proxy to the ecomorphological traits that correlated with foraging and sexual selection and estimated their roles on species coexistence. The results show that the number of coexisting species is strongly correlated to functional dispersion indices of traits including vocalization and plumage which are related to sociality and sexual selection, while the correlation between the number of coexisting species and functional dispersion indices of morphology and diet is weak. The results of SEM show that the number of coexisting species is directly linked to the divergence of sexual selective traits which is closely related to evolutionary time rather than diversification rate. Therefore, the high levels sympatry of babblers in SHMs is caused by long evolutionary time for divergence in sexual selection traits which can promote reproductive isolation within coexistence species.

In this study, analyses based on different groups reveal various mechanisms underlying species richness gradients in the SHMs. For young group babblers, the megadiversity in the SHMs is the result of accumulation of species along an extensive evolutionary time, while for older group pheasants, higher diversity in the SHM was caused by the higher diversification rate and multiple dispersals into this region. The SHM plays roles of evolutionary museum for babblers and cradle for pheasants. The discrepancies of mechanisms that contribute to the build-up of megadiversity between two groups are related to the geological history of SHMs. The Qinghai-Tibetan Plateau, which reached 4,000 m above sea level at early Oligocene, failed to provide suitable habitat for pheasants during their initial diversification. It is not until the formation of Sino-Himalayan Mountain habitats did this region become the center of colonization and diversification for pheasants. On the other hand, during the early diversification of babblers in the early Miocene, the most regions of SHM (except for Hengduan Mountains) have already undergone extensive uplift and remained elevations till present day. The SHM was able to provide suitable habitats for ancestors of babblers and subsequently become a museum that accumulated a large amount of species. Therefore, in order to understand the mechanism underlying the pattern of species diversity, it is crucial to integrate ecological and evolutionary history of groups, as well as the geological and climatic history of a given region. However, how the mechanisms to maintain metadiversity in SHMs are consistent between two groups. For the pheasants, the species richness is highly related to niche diversity (= functional diversity). For babblers, the number of coexisting species is related to divergence of sexual selection-related traits. Thus, our results show that the divergence in eco-

morphological traits plays an important role in promoting species coexistence.

(Cai Tianlong, Beijing)

Studies on speciation mechanism of the eared pheasants and conservation genetics of the brown eared pheasant

The speciation mechanism is one of the most fascinating fields in ecology and evolutionary study, because it acts on the pattern of biodiversity and the stable of ecosystem. There have several hypotheses about speciation, but some of these hypotheses are compatible with each other, some of them have conflicts with each other. Although with the development of molecular biology technology, almost all the speciation hypotheses have been tested in both the laboratory and field, there still has controversy. For instance, whether the ecological niche is conservatism during the speciation process? Whether climate fluctuation or climate stability promotes speciation? Here, aims to deep understanding the speciation process and resolving the controversy, the current study explored the speciation process of the Eared Pheasants (*Crossoptilon*) and reconstructed the demographic history of species within this genus.

The genus of the Eared Pheasants belongs to the Phasianidae of Galliformes, which contains four species, i.e., Brown Eared Pheasant (*C. mantchuricum*), Blue Eared Pheasant (*C. auritum*), White Eared Pheasant (*C. crossoptilon*) and Tibetan Eared Pheasant (*C. harmani*). Previous researchers have reported the breeding strategies and habitat preferences of the four species, however, the information of the speciation mechanism among the Eared Pheasants is scarce. The current project combined the mitochondrial genes, nuclear genes and genomic data to analyze the evolutionary relationship, divergence time, gene flow among the four species within the genus, and analyzed the historical dynamics of the effective population of the organisms. The current project also constructed the ecological niche and compared the ecological niche between closely related species. Given the Brown Pheasant is an endangered species endemic to the Loess Plateau and the adjacent region, the current project also measured the relative genetic burden of each species and the history of effective population size, which could serve the conservation of the Brown Eared Pheasant. The main findings are available as follows:

1. The parapatric sister species (*C. crossoptilon* and *C. harmani*) diverged with each other at about 500,000 years ago, and an asymmetric gene flow was found between these two species. The background similarity test showed the two species had significantly similar ecological niche. The allopatric sister species (*C. auritum* and *C. mantchuricum*) diverged with each other at about 300,000 years ago, and the asymmetric gene flow was also detected between these two species. The background similarity test showed the ecological niche of them had significantly divergent pattern.

2. The divergence time between *C. crossoptilon* and *C. harmani* was in the Guxiang glacial epoch. The current project found there were two genetic groups within *C. crossoptilon* and the divergence time between them was in Baiyu glacial epoch. The historical potential distribution showed the Mekong–Salween Divide was geographical barrier between *C. crossoptilon* and *C. harmani* in glacial epoch. The two genetic groups within *C. crossoptilon* were isolated by the DaXue Mountains in glacial epoch. The curves of historical effective population size of *C. crossoptilon* and *C. harmani* showed they experienced extreme bottlenecks in glacial epoch.

3. The population genomic data of *C. mantchuricum* suggested this threatened species has the lowest genetic diversity among the birds that have been reported the genomic data. The *C. mantchuricum* has three genetic groups, who are corresponding with the isolated geographical groups. The results suggested there was no gene flow between the three genetic groups and they had seriously inbreeding. The analysis of deleterious mutations found *C. mantchuricum* accumulated much more deleterious mutations than *C. auritum*, who is not threatened and has larger population size than *C. mantchuricum*. The current project also found the effective population size of *C. mantchuricum* began to continuously shrink from the Last maximum ice age.

The current project got the conclusions as follows: (1) The ecological niche does not conservatism in all organisms; (2) In the presence of gene flow during speciation process, the divergent selection may be one important power promoting speciation; (3) Geographical barrier promoted speciation in the Qinghai-Tibetan Plateau and Hengduan Mountains in the recent time; (4) *C. mantchuricum* is an extremely endangered species with high genetic load and low fitness.

The current project would promote the development of speciation theory, make us have a deep understanding of the formation mechanism of the Palearctic alpine biodiversity hotspot and the evolution mechanism of the uneven distribution of the organisms. The current project also provides detailed population genomics evidence for planning protection strategies for *C. mantchuricum* and provides a case for performing conservation genetics studies of other threatened birds.

(Wang Pengcheng, PhD student; Prof. Scott V. Edwards, Supervisor, Harvard University; Prof. Zhang Zhengwang, Supervisor, Beijing Normal University)

Bird Banding Report

Bird Banding of China in 2018

In China, a total of 398 species one hundred and four thousand were banded at 38 stations in 2018. Passeriformes account for the largest proportion: 231 species and ninety thousand birds. Others included 3,432 birds of 16 Herons and Egrets, 2,241 birds of 27 raptors, 1,298 birds of 41 shorebird species, 1,275 birds of 19 duck and geese species, 252 birds of 15 cranes and coots, and 395 birds of 13 woodpeckers.

The top ten banded species were Rustic Bunting (*Emberiza rustica*), Black-faced Bunting (*E. spodocephala*), Red-flanked Bush Robin (*Tarsiger cyanurus*), Common Redpoll (*Carduelis flammea*), Yellow-browed Warbler (*Phylloscopus inornatus*), Brambling (*Fringilla montifringilla*), Yellow-throated Bunting (*E. elegans*), Little Bunting (*E. pusilla*), Pallas's Leaf Warbler (*P. proregulus*) and Chestnut-flanked White-eye (*Zosterops erythropleurus*).

There were 101 species 5,722 birds color marked at 14 bird banding stations, of which 49 species of 4,903 songbirds, 30 species of 572 shorebirds, 7 species of 120 ducks and geese, 6 species of 144 herons and storks, 2 species of 2 cranes.

(Chen Lixia and Wang Yihua, National Bird Banding Center of China)

A report of spring-summer bird banding in Dongzhai National Nature Reserve in 2019

Bird banding was conducted in the Qilichong and Jilong protection stations of the Dongzhai National Nature Reserve from 10th to 26th May, 2019. During the 14 days, a total of 326 individuals, which belong to 42 species, 18 families and 4 orders, were banded.

In Qilichong protection station, 185 birds of 32 species, 14 families and 14 families were captured from 10th to 16th May. Among these birds, 13 were recaptured individuals that were banded in previous years. A Hair-crested Drongo (ring number F10-0063) which was first banded in 2015 and a Yellow-rumped Flycatcher (ring number A167-0671) which was first banded in 2018, were recaptured, suggesting these migratory birds are philopatry. In addition, a new distribution record of birds of Dongzhai National Nature Reservewas found for Blue-throated Flycatcher.

In Jilong protection station, a total of 141 individuals belonging to 24 species, 17 families and 4 orders were captured from 20th to 26th May. These included 6 individuals of 4 species that were

banded in previous years. A notable recapture record is the Chestnut-winged Cuckoo (banding number F10-8314). This bird was first banded at the same site in May, 2018.

(Bo XI, Du Zhiyong and Zhang Junfeng, Banding Station of Dongzhai National Nature Reserve)

News from China and Abroad

Four scholars from our society participated in the China's 35th Antarctic Expedition

The four scholars of Zhang Zhengwang, Deng Wenhong, Xia Canwei and Lei Weipan from the China Ornithology Society participated in the China's 35th Antarctic Expedition, and investigated and monitored the bird diversity and ecological habits at Zhongshan Station, Great Wall Station, Ross Sea New Station and Amundsen Sea area respectively.

This is the third time that Professor Zhang Zhengwang participated in the Antarctic scientific expedition. He observed and recorded 525 nests of different species of birds at the Zhongshan Station, which was the main breeding ground for Snow Petrel *Pagodroma nivea*, Wilson's Storm Petrel *Oceanites oceanicus* and South Polar Skua *Stercorarius maccormicki*. The activities of Antarctic birds were successfully monitored by infrared camera and other techniques. The activities of Snow Petrel and Wilson's Storm Petrel peaked at night during the breeding season, and predation by predators, extreme weather and human disturbance were the main factors affecting bird reproduction and population growth. He suggested that only by further reducing human activities and strengthening the protection of the Antarctic environment and ecosystems would guarantee for the long-term survival and development of Antarctic bird resources.

Professor Deng Wenhong's main task is to investigate the diversity and distribution patterns of birds and mammals in the Amundsen Sea region, and to record their species, quantity, population size, geographical coordinates, behavior, linear distance from the ship, and distance from the ice. A total of 29 species of birds and 5 species of mammals, including images and geographical distribution data, were recorded. The recorded birds accounted for more than 60% of the diversity of Antarctic birds. Newly discovered three species of White-headed Petrel *Pterodroma lessonii*, Kerguelen Tern *Sterna virgata* and Little tern *Sternula albifrons*, filled the record gaps of these three species in the Amundsen Sea region and complemented their new distribution in the Antarctic continental margin.

Associate Professor Xia Canwei participated in the location planning of penguin colony protected

areas in the Ross Sea New Station, and conducted research on bird survey and behavior monitoring in the Inexpressible Island. The GPS tracker and heart rate monitor were used to explore the daily rhythm of bird activity and physiological conditions in extreme environments. These studies are expected to provide a scientific basis for the establishment of bird monitoring and protected areas in the Ross Sea New Station.

Dr. Lei Weipan investigated and monitored birds in the Great Wall Station area of Antarctica. Through the survey, a total of 15 species belong to 7 families and 4 orders of birds were recorded, 13 of which were breeding in the Great Wall Station area. For the first time, the activity of Antarctic birds was monitored by nest temperature logger, and the temperature curve of the hatching activities of Southern Giant Petrel *Macronectes giganteus*, skuas and Wilson's Storm Petrel were obtained. During the Antarctic expedition, the four scholars worked hard and worked diligently to complete the relevant scientific research tasks and contributed to the Antarctic investigation. The China Antarctic Research Station sent a thank-you letter to Beijing Normal University during New Year's Day. CCTV, Xinhua News Agency and other media have also reported on their investigations.

(Lei Weipan, Beijing)

Xin Lu's visit to the Audubon Society of Portland

Although I have known Audubon Society for many years, I have not any perceptual knowledge about it. With a great interest, I visited the Audubon Society of Portland, one of the nearly 500 local charters of the National Audubon Society, on 12 January 2019.

Located in mountain forests nearby by Portland city, the headquarter of the Audubon Society of Portland includes the offices, Wildlife Care Center and Nature Store. With a history of more than 100 years, the branch of Audubon Society is a non-profit organization dedicated to conservation of birds and their habitats in northwest America. Every year, over 3,000 injured and orphaned native wild animals are treated and released to the wild. I was impressed by a variety of nature books and field guides presented in the Nature Store, as well as lovely ornaments, bird feeders and houses. Around the headquarter is the Wildlife Sanctuaries consisting of forests, streams and trails, which are home to many birds of northwest America, such as the Black-capped chickadee *Poecile atricapillus* and Song sparrow *Melospiza melodia*.

At the headquarters, I met two visitors from Washington State, a mother and daughter. I had a nice talk with them and was impressed by their enthusiasm to birds and nature conservation.

Taken together, my visit to the Audubon Society of Portland allowed me to recognize 1) conservation organizations in America, including local chapters, have their own full-time administrators, offices and natural sanctuaries, 2) local conservation organizations provide various, regular activities with the public, and 3) American people have a high awareness of conservation. These are inspiring to the organizations committed to natural conservation in China.

(Lu Xin, Hubei)



The Progress of the “Free Flying Wings” Program

Free Flying Wings is a comprehensive conservation program that aims to safeguard the most endangered water birds and their habitats. The program plans to spend 10 years (2016-2026) on building a public conservation network that complements with the government’s official system and establishing conservation pilot sites through joint actions initiated by NGOs, enterprises, and the public. As of April 2019, Free Flying Wings has supported accumulatively 60 wetland conservation projects of 49 organizations, conducted 3,000 wetland patrols and bird surveys with 70,000 entries recording 600 bird species, and organized 300 times of nature education activities reaching out to a total of 100,000 people. It has launched 3 special survey projects on endangered waterbirds species. The strategic cooperation was initiated with the Wetland Management Department of State Forestry and Grassland Administration in 2019.

(Zhang Qiong, Beijing)

Zhilan Foundation Call for Project Proposals of Threatened Species

Zhilan Foundation is a private foundation established in December 2018. The foundation is to promote the conservation of endangered species in China including threatened species of birds and the sustainable development of local communities by providing flexible and long-term small-grants for frontline researchers and practitioners. Call for proposal in 2019 has been initiated,

and more than 1 million RMB is planned for each quarter.

(Zhang Yingyi, Beijing)

Accidental death of a large number of common cranes during their migration in Xinjiang

Common cranes *Grus grus*, also known as Eurasian cranes, are relatively widespread in China. In April 2019, some common cranes had trouble landing and stopping in the suburbs of Urumqi. They hit a 220 kV transmission line. Perhaps because the lightning lines above them are relatively thin and difficult to see, about 32 cranes were injured and fell (more deaths were reported previously).

Corn fields near high-voltage lines are the favorite places for the cranes, but the number of deaths in the past year has not been so high. We examined these 32 cranes in the field. Almost 100% of them were young cranes or sub-adults (with light feathers and no red-crowned head) for only 2 to 4 years. The highest rate of broken wings was 64%. The rate of broken legs was 60%. Abdominal or back abrasions accounted for 36%. Head or neck injuries accounted for 20%. Almost half of cranes suffered multiple injuries (52%).

(Ma Ming, Urumqi)

First breeding record of the Glossy Ibis in China

The Glossy Ibis (*Plegadis falcinellus*) has a cosmopolitan distribution, which breeds across south east of Africa, Madagascar, the south of Europe, the Middle East, South East Asia, Australia, as well as the coasts of North America and the Caribbean. However, in mainland China, the bird has been found sporadically as passengers, but there has never been a record of reproduction.

On April 25, 2019, three Glossy Ibises (Figure 1) were found in Lianshui River (N33°2'12", E106°59'34", altitude at 493 m), one of the tributaries of Hanjiang River, in Daheba Town, Nanzheng District, Hanzhong City, Shaanxi Province. Shrubs and aquatic plants are overgrown, and aquatic invertebrates are luxuriant in river course. The Crested Ibis (*Nipponia nippon*) and several herons and egrets foraged in the river, in which the Crested Ibis nested in the immediate vicinity. Two of them display courtship and nesting behaviors in early May (Figure 2). In mid-May, the hatching behavior of the Glossy Ibis was observed in a heronry. Three broken pure blue-green eggshells with 3.3-3.6 cm in diameter, were found under the nest in early June (Figure 3). It was found that three chicks have been hatched successfully. The nesting site is located in a dense

bamboo forest (*Phyllostachys heterocykla*) in the heronry, where the nest is built at the upper parts of the bamboo, approximately 5 meters above the ground. It is estimated that the chicks will fledge successfully from the end of June to the beginning of July. We don't know where they come from, let alone where they are going. Thus, follow-up monitoring is urgently needed.

(Yu Xiao-ping, Shaanxi Normal University)

Publication

Field Identification Manual of Common Birds in North China (Color Edition) (with digital course)

The "Field Identification Manual for Common Birds in North China"(with digital courses) edited by Professor Zhangyanyun will be published in the Higher Education Press in July 2019. The book is divided into three parts. The illustrated section contains 157 species of common birds in North China. In addition to providing exquisite wild ecological photographs and text descriptions of birds, photographs of bird life history and photographs of nests and eggs (including photographs of nest egg specimens accumulated over the long term) are also provided. Most fascinating of all, this book provides a diagram of each bird species. By scanning the two-dimensional code, readers can listen to the unique sounds of each species. Some species also provide video. In the basic knowledge part of bird classification, this book gives information such as rapid retrieval for rapid identification in the wild, pronunciation of Chinese bird names, special terms for birds, measurement of common parameters, description of bird vocal language, and description of residence type. In the field identification and research technology of birds, this book introduces bird field identification technology, bird ring records, sound collection and analysis, bird nest temperature automatic record, telemetry technology and so on.

This book is a practical tool for field practice and outdoor bird watching.

(Dong Lu, Beijing)

"Birds Guide of Hupingshan" published

The new book was published in Yunnan Ethnic Publishing House in October 2019. The book with 395 pages and 590,000 words, records 362 species and subspecies belong to 63 families and 18 orders of birds in the Hupingshan National Nature Reserve, Hunan Province. Containing more than 960 photos, it describes the morphological characteristics, ecological habits, distribution and

residence types of various birds. The book has important reference value for understanding the Hupingshan Nature Reserve and the status of birds in Hunan Province.

(Zhang Zhengwang, Beijing)

“Haikou Wetland • Birds Guide” published

The “Haikou Wetland • Birds Guide”, edited by Feng Erhui, Cai Ting and Xu He, was published by Nanh Hi Publishing Corporation in December 2018. The book covers 150,000 words and introduces the natural environment, wetlands and main bird-watching sites in Haikou. A total of 300 species belong to 65 families and 20 orders of wild birds were recorded, and 222 of them were described in detail. The book is a reference book for an overview of the wetlands and bird resources in Haikou and has important reference value.

(Zhang Zhengwang, Beijing)

“Principle of Bird Strike Risk Prevention at Airport” Published

In June 2019, the book “Principles of Airport Bird Strike Risk Prevention”, compiled by Dr. Lu Yan and Professor Sai Daojian, has been published by the Science Press of China.

The book divides airport bird activities into two kinds of risks: one is whether the invasion of airlines constitutes the risk of bird collision; the other is whether there is the risk of bird collision with aircraft. It also discusses the relationship between bird behavior, distribution and aircraft flight from different angles of the static and dynamic space-time position relationship between birds and airlines.

(Sai Daojian, Shandong)

Announcement

Second Notice of the 18th National Congress of the Chinese Zoological Society and the 24th Annual Academic Conference

2019 is the 85th anniversary of the establishment of the Chinese Zoological Society. After the sixth enlarged meeting of the 17th session of the Governing Council and the Secretary-General's working meeting, it was decided to hold the 18th National Congress and the 24th Annual Academic Conference of Chinese Zoological Society in Xi'an, Shaanxi Province, from August 23-25, 2019.

Sponsor: Chinese Zoological Society

Hosted by: Shaanxi Zoological Society, Shaanxi Normal University, Shaanxi Science and Technology Association, Northwest University, Shaanxi Science and Technology University, Shaanxi Provincial Institute of Zoology, Yan 'an University, Shaanxi Natural Museum.

Theme: Zoology in the New Age: Interdisciplinary, Innovation Leadership

(China Zoological Society)

2019 National PhD Student Academic Forum on Zoology

The National PhD Student Academic Forum (Zoology) will be held in Shaanxi Normal University from August 22 to 23, 2019. At that time, in conjunction with the 18th Congress of the Chinese Zoological Society and the 24th Annual Academic Conference, more than 700 doctoral students and scholars and experts in zoology will be invited to gather for academic exchanges and discussions.

(China Zoological Society)

Fifteenth National Symposium on Wildlife Ecology and Resources Protection (First Announcement)

In order to promote and discuss the development strategies and academic exchanges of veterinary and animal ecology in China, the Fifteenth National Symposium on Wildlife Ecology and Resources Protection will be held in Haikou City, Hainan Province, from November 17 to 20, 2019. The meeting will be co-sponsored by the Animal Ecology Committee of the Chinese Ecology Society, the Mammalogy Society of the Chinese Zoological Society, the Science and Technology

Committee of the Chinese Wildlife Conservation Association, the International Zoological Society and the Hainan Zoological Society, the Key Laboratory of the Ministry of Tropical Island Ecology Education (Hainan Normal University) and Hainan Normal University.

(China Zoological Society)

Notice of the 15th National “Kingfisher Forum”

The 15th Kingfisher Forum will be held in Northeast Normal University from August 7 to 8, 2019 in Changchun City, Jilin Province. The Forum will be sponsored by the China Ornithology Society and hosted by the College of Life Sciences of Northeast Normal University.

(China Ornithological Society)

The 2019 Symposium on Crane and Habitat Conservation in China and Annual Working Meeting of Joint Crane Conservation Committee of China Wildlife Conservation Association (First Announcement)

The conference will be held in Chizhou City, Anhui Province, from November 28 to December 1, 2019. The meeting will be co-sponsored by the Crane Joint Protection Committee of China Wildlife Conservation Association and the People’s Government of Chizhou City, Anhui Province. It will be hosted by the Key Laboratory of wetland ecological protection and restoration (Anhui University), Chizhou Forestry Bureau, Shengjin Lake National Nature Reserve, and Anhui Zoological Society.

(China Ornithological Society)