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

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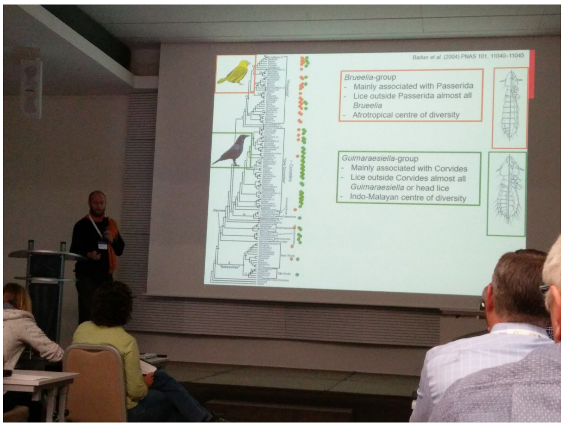
会议报道

第六届国际毛虱目会议（ICP6）在捷克布尔诺召开

2018 年 6 月 23 日—6 月 29 日，“第六届国际毛虱目会议（International Conference on Phthiraptera 6）”在捷克布尔诺召开。来自全世界 30 多个国家的近 100 名代表参加了会议。参加本次会议的中国代表有广东省生物资源应用研究所邹发生研究员，Daniel R. Gustafsson 博士和储杏枝研究实习员。



本次大会的学术交流分为 4 个大会报告（Plenary）、10 组 53 个口头报告（Oral）、31 个墙报（Poster）、2 个圆桌会议（Round Table）。

在本次国际毛虱目会议上，我国学者的研究成果得到了展示。Daniel R. Gustafsson 作了题为“Major distribution patterns in the Brueelia-complex”的口头报告，“The Brueelia-complex chewing lice (Ischnocera) of ‘babblers’ and allies (Passeriformes: Leiothrichidae, Paradoxornithidae, Pellorneidae, Timaliidae)”和“Morphological variation in Guimaraesiella Eichler, 1949 (Phthiraptera: Ischnocera: Philopteridae: Brueelia-complex)”的墙报展示。储杏枝作了“The influence of host body size, migratory status, and diet on prevalence and mean intensity of chewing lice (Phthiraptera) on birds in southern China”的墙报展示。

6 月 28 日，大会召开了学术委员会会议，通过无记名投票，Daniel R. Gustafsson 被增补为委员，并确定 2022 年将在广州举办第 7 届国际毛虱目会议。欢迎中国鸟类学分会的同行到时参会。

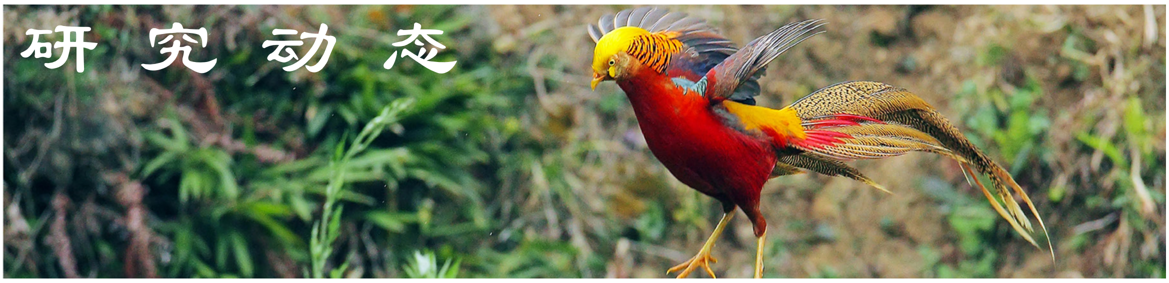
（广东：邹发生）

中国动物学会鸟类学分会常务理事扩大会在辽宁大学召开

2018 年 8 月 10—12 日，中国动物学会鸟类学分会常务理事扩大会在辽宁大学召开，本次会议由鸟类学分会理事、辽宁大学生命科学学院院长万冬梅教授团队承办。鸟类学分会的 21 名常务理事中的 17 人参加了本次会议，鸟类学分会理事、司库贾陈喜副研究员和全国鸟类环志中心钱法文、辽宁大学万冬梅教授参加了本次会议，《*Avian Research*》编辑部程朋军也出席了本次会议，会议由鸟类学分会理事长雷富民研究员主持。张雁云秘书长汇报了学会过去一年的工作，并对下一步要开展的工作进行了介绍；常务理事会讨论确定了第九届理事会专家组的设置；

常务理事王海涛教授介绍15届中国鸟类学大会筹备情况，确定大会主席、秘书长、学术委员会主席人选，并初步确定了大会报告的组成；《*Avian Research*》编辑部程朋军介绍了期刊的现状和面临的一些问题，常务理事们给出了期刊发展的建议和意见；会议还就鸟类学分会网站、简讯的工作进行了讨论。

（分会秘书处）



欧夜鹰繁殖与搬家行为观察

欧夜鹰（*Caprimulgus europaeus*）繁殖期行为极其诡秘，国内研究资料缺乏（马鸣等 2008）。2008年6—8月和2018年6—7月在乌鲁木齐市郊外头屯河流域（43°53′N，87°16′E，海拔715 m）河道中央核心岛及滩地上陆续发现了7个巢，均位于植被稀疏的河滩乱石沙地上，为简陋的浅窝状，没有垫材和遮蔽。每窝产卵2枚。卵呈椭圆形，卵壳白色，具不规则的红褐色斑块，或模糊或清晰，接近钝端较密集。卵长径30.44±0.85 mm，短径21.39±1.00 mm（$n = 5$），重7.3±0.4 g（$n = 3$）。同一窝的2枚卵存在较大差异，不同步孵化。巢之间最近的距离为69 m。

2018年6月17日—7月12日，首次采用红外相机监测3个巢，分别为15 d，23 d，11 d，共拍摄照片8,462张，视频4152个片段，约40 h，有效照片数6,807张。结果显示，欧夜鹰育雏期约18 d。通常4日龄后，开始有搬家行为，一是为了躲避日晒，二是避开干扰（天敌、牧群、洪水及人类活动等）。每次移动1.5~12 m，最远可离开原巢址18~31 m。当7月发生洪水时，幼鸟跟着成鸟向远离河道或更高的位置迁移。

红外相机在10:00—12:00（新疆时间，下同）拍摄的照片数量和视频时长达到峰值，此时段太阳直射，成鸟不断变换位置，以避免幼鸟被太阳光晒伤。白天（6:00—20:00）拍摄的视频时长约31 h，拍摄照片5,735张，占有效照片84.3%。白天成鸟基本不离开巢穴（除了受到强烈的干扰），主要是休息、警戒和护幼。雌鸟看似在闭目养神，其实一直处于紧急状态，随时可以起飞。在20:00—22:00和2:00—4:00，成鸟外出觅食，并饲喂幼鸟。欧夜鹰属半晚成鸟，双腿弱小，不擅行走。但育雏后期喂食期间，幼鸟常跟在成鸟后面跑动，一是索食，因为夏日白昼特长，暴晒一天饥饿难耐；二是成鸟教幼鸟锻炼飞行技巧。

（新疆：王述潮 马鸣）

欢迎合作开展鸟类羽虱研究

2017年通过广东省科学院高层次人才引进计划，广东省生物资源应用研究所引进了瑞典籍Daniel Roland Gustafsson博士。Gustafsson博士于2017年10月到所工作，在鸟类生态与进化研究中心与邹发生研究合作，开展鸟类羽虱的分类及羽虱与鸟类的协同进化研究。Gustafsson博士分别于2007年和2012年毕业于University of Gothenburg，其博士论文研究鸻形目鸟类羽虱分类及鸻形目鸟类的迁徙行为对羽虱分布的影响。2012—2016年，他在University of Utah从事博士后研究，专攻雀形目鸟类羽虱的分类、尤其善长*Brueelia*属（及其复合种）的分类。到了中国之后，主要开展华南森林鸟类的羽虱分类和羽虱与鸟类的协同进化研究，重点关注画眉科及相近种。研究不同海拔、温度等环境条件下，相同宿主鸟类羽虱的分布状况。鉴于目前东亚地区羽虱的研究关注较少，我

们期待与国内有兴趣的专家开展合作，希望在 3~5 年内出版“中国的羽虱物种名录”。

（广东：邹发生）

森林鸟类混种群作为种间关系的保护应用

在保护生物学中，保护单个物种、还是保护有关联的多个物种，目前引起了学术界的广泛关注。而鸟类混种群是一种重要的物种间关系，是研究保护优先次序、保护成本和保护效率的指标性对象。广东省生物资源应用研究所与中山大学、广西大学、美国佛罗里达大学和哥伦比亚亚马逊国立大学（Universidad Nacional de Colombia sede Amazonia）合作，对全球集混种群鸟类开展研究，发现：全世界共有 340 篇（其中 201 篇文章有平均每群鸟种数和个体数的数据）研究论文报道了混种群的研究，包含 2049 种森林鸟类、占全球鸟类的 19.2%；其中 158 个是濒危种、包括 2 个极危种、14 个濒危种、37 个易危种、105 个近危种。在全球不同纬度地区集混群鸟种类和数量不同，热带地区有更多种类参加混种群，并且在不同热带地区间，集混种群的鸟类种类数量有差异，在非洲和亚洲地区，平均每个混种群有更多鸟类种数、美洲热带地区每群鸟的种类数量较少，但参加平均每个混种群的鸟类个体数量在不同纬度间没有明显差异；混种群的鸟类对森林片断化和人为干扰非常敏感，片断化的森林结构简单，平均每群鸟类种数和个体数量明显减少，森林片断化限制了混种群的数量。全球有 190 种鸟是混种群的核心种，其中 22 种鸟既是核心种、又是濒危物种，其保护的价值是双倍的。由于核心种是鸟类维护混种群的基础，核心种引导着多个鸟类种。因此，鸟类保护优先次序，不仅需要看其稀有性、同时还要考虑该种与其它种的关系，以混种群为保护单位可以提高保护效率和节约成本。建议 IUCN 和鸟类国际组织在制定全球鸟类优先保护时，需要考虑混种群、尤其是核心种的重要性。相关成果以“The conservation implications of mixed-species flocking in terrestrial birds, a globally-distributed species interaction network”为题发表在最新一期的《*Biological Conservation*》上。该研究得到了国家自然科学基金（31172076，31200327）、广东省科学院科技发展专项（2017GDASCX-0107）等基金的资助。

（广东：邹发生）

基于红外相机监测分析人为干扰对白冠长尾雉种群性比的影响

红外相机适用于野外调查地栖性雉类。尽管红外相机监测的结果可能并不能反映目标种群的实际情况，如雌雄拍摄率可能并不等于实际的性比，但采用统一、标准化的流程使用红外相机监测野生动物，其结果可能很好地反映目标物种相关种群统计特征的变化趋势，并适用于比较其种群特征的空间变化。本研究以地栖森林鸟类白冠长尾雉（*Syrmaticus reevesii*）为研究对象，选取河南连康山国家级自然保护区、湖北省广水市三潭风景名胜区和湖北中华山鸟类保护区三个不同干扰强度的白冠长尾雉栖息地作为研究区域，其中河南连康山国家级自然保护区人为干扰强度最低，湖北广水三潭风景名胜区人为干扰强度最高。我们采用相同的技术流程使用红外相机在三地同时监测区域内白冠长尾雉种群中的雌雄比例，比较不同人为干扰强度下白冠长尾雉种群性别比例的差异。我们在河南连康山国家级自然保护区内安装红外相机 25 台，共收集到 12 个月的数据，

拍摄到的雄性个体和雌性个体分别为 136 次、82 次，雌雄比为 0.60:1；在湖北省广水市三潭风景名胜区安装相机 19 台，共收集到 3 个月的数据，拍摄到的雄性个体和雌性个体分别为 94 次、27 次，雌雄比为 0.29:1；在湖北中华山鸟类自然保护区安装红外相机 23 台，共收集到 3 个月的数据，雄性个体和雌性个体分别为 79 次和 39 次，雌雄比为 0.29:1。我们的结果表明，白冠长尾雉的种群性比在不同人为干扰的区域间变化明显，其种群在人为干扰强度越大的栖息地中雄性个体比例越高，即种群在干扰大的区域是偏雄的。

（北京：华俊钦 徐基良）

在野生动物生态观光效应影响下丹顶鹤警戒行为的生境差异

随着野生动物观光和摄影活动的兴起，这些活动对野生动物的影响越来越受到关注。丹顶鹤是一种备受鸟类摄影爱好者喜爱的珍稀濒危鸟类，每年迁徙季节，成百上千的爱好者如约来到丹顶鹤的重要停歇地，东营黄河口湿地。然而，这些人为活动对丹顶鹤行为的影响缺乏科学评估。在黄河口停歇期，丹顶鹤主要利用翅碱蓬和芦苇交错区两种生境，这两种生境的植被高度存在明显差异，在有芦苇隐蔽物的交错区生境中，丹顶鹤在受到干扰时，如何调整警戒行为是一个非常有意义的科学问题。本研究采用固定个体行为观察法对丹顶鹤警戒行为的生境差异进行研究。研究发现，在有摄影观光活动影响下，丹顶鹤警戒的频率和时间比例均明显上升。然而，在芦苇交错区丹顶鹤的警戒频率升高比例明显高于翅碱蓬滩涂，而警戒的平均时长在两种生境无明显差异。因此，可以看出植被较高的芦苇生境主要起到视野障碍，而不是保护作用，反而影响丹顶鹤对周围的人为干扰的观察，从而需要提高警戒频次；而在翅碱蓬生境中，丹顶鹤在距人群 300 m 以外的区域，可以维持正常的警戒频次，而在 300 m 以内，丹顶鹤的警戒活动明显增加。这说明生态摄影活动作为一种人为干扰类型对丹顶鹤正常的取食活动有较大影响，但是，如果能保持在 300 m 以外的距离，丹顶鹤对摄影等活动则有一定的适应性。该研究对未来湿地管理也具有一定的科学意义，因为在该保护区内，翅碱蓬滩涂生境正不断的退化或向芦苇交错区演替，这些变化对野生鸟类的行为活动具有较大影响。

相关研究详见 Li et al. (2017) *Scientific Reports*, 2017, 7: 16614 | DOI:10.1038/s41598-017-16907-z.

（辽宁：李东来 孙兴海 万冬梅；北京：刘宇 张正旺；英国：Huw Lloyd；山东：朱书玉，张树岩）

广义适合度允许利他和非利他表型共存

利他行为之所以让人们感到困惑，主要是因为它提出一个悖论：在一个竞争的世界里一些个体帮助其他个体而以自己的适合度为代价。显然，建立在个体适合度基础上的达尔文进化理论难以解释这一悖论。进化生物学家汉密尔顿把基因作为进化单位，认为利他基因通过其携带者帮助拥有共同基因的亲属，从而间接地传递自己。一个简单精妙的公式描述了这一思想：$rb > c$，当利他者带给接受者的利益 b 与二者亲缘度 r 的乘积大于利他的代价 c 时，利他行为进化。

卢欣与其博士研究生王长操注意到，被誉为社会进化领域黄金法则的 $rb > c$，只讲出了利他行为进化故事的一部分，即利他基因型在种群中持续扩张的状态。而事实上，在自然界和人类社会，利他与非利他者共存的

现象十分普遍。他们预测，只有 $rb = c$ 才能保持这种稳定共存。利用青藏高原特有物种地山雀长期研究获得的数据，它们为这一预测的有效性提供了有力证据。

这项工作的一个主要意义在于为汉密尔顿的广义适合度理论提供了基本支持。更重要的是，它表明由 $rb = c$ 所介导的等量广义适合度原则，在保持不同社会形态共存中的理论和实际意义。

这项研究发表于《*Proceedings of the National Academy of Sciences of the United States of America*》。

（武汉：卢欣）

濒危物种中华凤头燕鸥和大凤头燕鸥的杂交证据

杂交在自然界中非常常见。杂交可能通过基因渐渗等污染濒危物种的基因库。2018 年 5 月，浙江自然博物馆和中山大学的研究人员合作在《*Ibis*》杂志撰文（doi: 10.1111/ibi.12616），确认了极度濒危物种中华凤头燕鸥（*Thalasseus bernsteini*）与大凤头燕鸥（*T. bergii*）杂交的遗传学证据。本研究首先利用线粒体多个位点的分子数据对其进行了系统发育分析，结果表明两种燕鸥为姊妹种，分化时间不足一个百万年。文章推测，在冰期之后，凤头燕鸥属的异域种群之间产生分化，导致了这些物种的分化与形成。其次，我们基于野外观察发现中华凤头燕鸥和大凤头燕鸥存在混群繁殖现象，进一步通过多个位点（线粒体基因 ND2 和性染色体基因 RP2 和 NHS）的分子数据进行分析，证明了中华凤头燕鸥和大凤头燕鸥之间确实发生了杂交。而杂交导致的后果仍值得评估。本研究得到国家自然科学基金（No. 31572291, No. 31401974）的资助。

（广东：陈国玲；浙江：杨佳）

鸣声特征是否和鸟类混合群中的领导关系有关？

在鸟类混合群（mixed species flocks）中，“核心种（nuclear species）”作为领导者，而另一些物种成为“跟随”者，那么鸟类混合群的这种组织方式是如何形成的呢？广西大学、中山大学、中国科学院西双版纳热带植物园的研究人员合作在《*Journal of Avian Biology*》上撰文（doi: 10.1111/jav.01674），证实了鸟类混合群中的领导关系和鸣声通讯相关。本研究利用鸟类鸣声数据库中鸟类混合群的录音素材，研究鸟类鸣声特征是否和混合群的领导关系相关。首先，研究结果显示领导者比偶尔集群者倾向于有更多的鸣叫；领导者和跟随者的鸣声中的报警鸣叫显著高于偶尔集群者。其次，通过 45 个物种共 169 段鸣声的分析表明领导者比跟随者和偶尔集群者保持沉默的机会更少。然而,和预测相反，领导者的鸣叫声的差异比偶尔集群者更大。本研究的结果支持鸟类混合群的领导关系和声学通讯有关，研究的亮点是通过可公开获得的鸣声数据库来回答行为生态学和群落生态学的重要问题。论文的第一作者为广西大学 Emilio Pagani-Núñez 博士（现为中山大学副研究员）、广西大学和中国科学院西双版纳热带植物园联合培养硕士研究生夏雪，通讯作者为广西大学 Eben Goodale 教授。本研究得到中组部青年千人计划和广西大学引进人才计划的资助。

（广东：Emilio Pagani-Núñez；
广西 & 云南：夏雪）

天然树洞中长尾林鸮的繁殖生态

长尾林鸮（*Strix uralensis*）广布于古北界的针叶林、针叶阔叶混合林中，是当地森

林中的顶级捕食者，对于调节群落有着至关重要的作用。2014—2016 年我们在吉林省吉林市永吉县对长尾林鸮的繁殖生态进行了研究。结果表明，2015 年长尾林鸮在研究样地的密度为 0.15 对 /km^2（18 对 /117 km^2），其中繁殖密度最高的区域达 1.72/km^2 (7 对 /4.08 km^2)。最近的两巢距离为 559 m。通过鸣声回放计算的长尾林鸮积极保卫领域的半径为 358.8 m（$n = 6$）。主要的巢树为白皮柳（69%）及辽东栎（25%），见图 1。巢类型绝大部分为树洞（82%），另有苍鹰旧巢、地面巢以及地面树桩的巢各 1 个。树洞的类型大部分为露天型（64%），其次为侧开口（36%）。长尾林鸮喜好低矮、较大洞口面积及较大洞内面积的树洞。

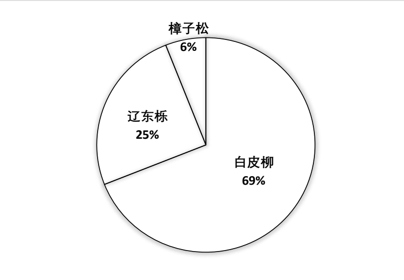


图 1. 长尾林鸮巢树树种所占比例

长尾林鸮产卵期为 3 月 14 日 —4 月 15 日，雌鸟每隔 2~3 天产 1 枚卵，产第 1 枚后雌鸟便开始孵化。平均窝卵数为 2.94（47/16，$n = 16$），最大窝卵数为 4，最小窝卵数为 2。卵为纯白色，无卵斑，表面粗糙并有小颗粒状凸起，近椭球状，尖端、钝端明显。卵重为 39.93 ± 0.72 g（$n = 28$），长径为 48.09 ± 0.30 m（$n = 28$），短径为 40.01 ± 0.15 mm（$n = 28$）。由雌鸟担任全部孵化任务，雄鸟负责保卫领域及为雌鸟递送食物。孵化日期为 4 月 23 日—5 月 22 日，异律孵化，每隔 2-3 天孵化 1 只。出壳率为 61.7%（29/47，$n = 47$），平均每窝出壳 1.81 只（29/16），平均孵化时间为 32 d（$n = 5$）。在孵化期内没有发现被天敌捕食导致繁殖失败的现象，但是由于人为捡蛋、天气原因、操作干扰及未知原因导致其弃巢，繁殖失败率为 38.5%（6/16，$n = 16$）。除掉人为干扰和天气原因导致的巢损失，真实出壳率为 100%（$n = 29$），真实平均每窝出壳为 2.9 只（29/10）。幼鸟死亡率为 10.3%（3/29，$n = 29$），幼鸟离巢率为 89.7%（26/29，$n = 29$），每窝平均出飞数 1.63 只（29/16，$n = 16$），除掉繁殖失败的样本，真实每窝出飞数为 2.6 只（26/10，$n = 10$）。亲鸟育雏时间为 4 月 23 日—6 月 18 日，幼鸟出飞时间为 5 月 22 日 —6 月 19 日，幼鸟离巢时平均日龄为 27.4 d（$n = 17$）。

通过函数拟合我们发现腕部腕掌骨到翅尖的距离、头喙长、翅膀收拢时腕部腕掌骨到羽毛最大长度、飞羽、体重、喙长、跗跖长符合线性生长规律，R^2 均在 0.9 以上，而其中腕部腕掌骨到翅尖的距离的 R^2 到达了 0.9815；飞羽鞘、跗跖粗、尾羽鞘符合对数生长规律，而尾羽则符合幂函数，非线性生长的曲线 R^2 在 0.69~0.85 之间，与线性拟合的 R^2 存在显著性差异（$P < 0.05$），见表 1。对于窝卵数大于等于 3 的巢，出飞时第一只出壳的幼鸟的平均重量为 411.3 ± 29.2 g，最后一只出壳的幼鸟的平均体重为 365.4 ± 12.8 g，两者并没有显著差异（$U = 8.000$，$P = 0.421$）。平均出飞日龄分别为 26.8 ± 0.6 d、23.6 ± 1.5 d，两者差异也不显著（$U = 4.500$，$P = 0.09$）。

食物包括啮齿类的大麝鼩（*Crocidura lasiura*）、棕背䶄（*Myodes rufocanus*）、大林姬鼠（*Apodemus peninsulae*）、黑线姬鼠（*Apodemus agrarius*）等，鸟类的花尾榛鸡（*Tetrastes bonasia*）、大斑啄木鸟（*Dendrocopos major*）、红尾鸫（*Turdus naumanni*）等。

表1. 长尾林鸮雏鸟不同日龄的平均生长参数

日龄	翅长/mm	体重/g	头喙长/mm	喙长/mm	跗跖长/mm	跗跖粗/mm	尾羽鞘/mm	尾长/mm	飞羽鞘/mm	飞羽/mm
1	14.77	29.4	34.38	15.55	14.04	2.76				
2	15.92	28.8	33.97	15.65	14.13	2.35				
3	17.93	41.9	35.93	17.01	15.81	2.99				
4	19.67	63.0	38.93	18.04	18.72	3.83				
5	20.06	60.3	38.50	18.58	16.08	3.34				
6	23.23	83.8	42.36	20.88	19.92	4.40				
7	24.92	101.4	42.92	20.88	22.06	4.62				
8	26.45	112.9	44.33	22.05	21.05	4.48			3.48	
9	31.35	162.5	48.12	23.08	26.08	5.59	2.06		7.86	
10	31.26	141.5	46.11	23.54	23.47	4.93			5.12	
11	34.84	192.0	50.33	23.86	28.85	6.05	1.65		15.94	
12	36.65	215.0	52.66	24.38	28.46	6.07	2.04		14.17	
13	41.31	214.9	52.45	25.99	30.84	6.21			21.55	
14	45.64	273.3	56.10	25.94	33.66	7.20	6.80		27.06	33.49
15	43.61	248.4	55.53	25.94	33.48	6.27	2.72		26.58	35.20
16	48.62	284.0	58.02	27.31	35.54	6.95	3.52		31.65	44.56
17	50.66	299.9	58.41	27.89	34.95	6.40	2.14		34.44	41.81
18	55.06	348.2	61.31	28.30	37.50	7.38	5.11		40.64	58.32
19	53.13	326.4	59.67	28.27	35.13	6.54	2.72	6.30	37.68	48.28
20	57.41	386.8	63.03	29.21	36.36	7.15	7.24	7.95	44.85	68.55
21	58.58	357.2	63.88	29.47	38.07	6.92	9.17	9.93	45.73	66.93
22	62.11	357.9	64.00	30.12	39.22	6.59	10.83	18.57	45.65	73.59
23	67.34	365.9	65.98	30.65	39.88	6.75	11.95	18.33	50.63	83.11
24	66.40	408.3	65.85	30.37	40.25	7.36	13.77	21.68	48.05	88.49
25	69.07	360.4	66.97	30.41	40.41	6.40	18.09	27.22	43.70	95.36
26	70.19	412.9	66.98	31.37	42.38	6.80	19.50	29.49	48.94	99.06
27	70.51	381.3	68.69	30.67	41.07	6.90	19.00	27.67	45.36	100.10
28	74.21	420.3	69.10	31.72	41.40	7.04	24.11	39.64	44.19	108.85
29		395.0		32.63	40.27	5.85	23.41	34.73	47.52	108.32
30	72.30	408.0	71.22	32.94	40.41	7.16	23.37	41.97	41.63	120.01

（北京：邓文洪）

西藏木纠错发现彩鹮

2018年6月26日，在西藏那曲市申扎县木纠错（31°00′19″N，89°4′7.6″E，海拔4,673 m）发现1只喙色浅、体羽色深，闪暗红色光泽的中型水禽在挺水植被中睡觉。次日于该地点数百米外再见此鸟并获得录像，其体型似小白鹭（体长约60 cm），喙角质色，长而下弯，基部有两道白纹。头颈及上背浓栗色，带紫红色光泽，其余体羽近黑色，闪耀金属绿光泽，腿及脚色深（图1）。经鉴定，该鸟为鹈形目（Pelecaniformes）鹮科（Threskiornithidae）的彩鹮（*Plegadis falcinellus*）。发现时，其在浅水区草本植物丛中觅食，机警而惧人，飞行有力，迅捷拍翅间杂猛禽式滑翔。周围还有黑颈鹤（*Grus nigricollis*）、斑头雁（*Anser indicus*）、普通燕鸥（*Sterna hirundo*）等鸟类。

图 1 彩鹮

经查阅相关文献（www.hbw.com，郑光美 2017），其繁殖区离散广布于欧洲南部、非洲至中亚、南亚、东南亚、大洋洲、北美洲太平洋沿岸、西印度群岛至南美洲的委内瑞拉一带，旅鸟可见范围更广。在我国分布于东部、南部沿海各省以及云南、贵州、四川和新疆等地，但未有该物种在西藏分布的确切记录。本次发现证实了彩鹮在藏北高原的分布，推测藏北富有水生植被的湖泊湿地或为彩鹮的繁殖区。

（西藏：杨乐 刘善思 高畅 益西多吉）

自 1990 年以来鸡形目鸟类的研究进展及未来展望

鸡形目（Galliformes）是鸟类中一个重要类群，分布于除南北极以外的世界各地，其中有不少为经济物种，与人类关系密切。作为生态系统的重要成员，其生存状况可在一定程度上监测物种多样性保护和持续利用状况，是应用生态与野生动物保护状况的晴雨表。但由于栖息地的丧失和过度狩猎，许多鸡形目鸟类的种群数量已大幅度减少。因此，对鸡形目鸟类现状进行评估有助于为今后的研究和保护策略提供指导。

我们利用在线数据库（Web of Science）检索了 1990—2016 年间发表的有关鸡形目鸟类的英文文献。首先，我们筛选出与动物学、环境科学、生态学、生物多样性保护、林学、行为学、繁殖生物学、生物化学与分子生物学、细胞生物学、遗传学、进化生物学、生理学和系统发育等研究领域相关的文献。为确保所获取的数据的可靠性，我们根据标题、摘要和全文对文献进行了重复检索。

我们从最初得到的 243,128 份文献中筛选出与鸡形目鸟类研究相关的 1,874 篇文献。研究多以 1~2 个物种（91.4%）为研究对象，且通常历时较短（85.0%）。超过半数的文献集中在宏观生态学（55.5%）研究领域。随着分子生物学的发展，分类学和系统发育学的研究在近二十年中迅速发展。生理学与生物化学的研究不再局限于简单的描述，而是扩展到表型和微进化潜能的机制。另一个越来越受到关注的领域是对鸡形目鸟类的保护，其保护状况及管理效果评估（如物种多样性和遗传多样性）开始成为焦点。

自 1990 年以来，国内外对鸡形目鸟类的研究虽取得了较大成就，但仍需加强对种群动态的长期监测及保护策略研究，将物种保护与宏观生态与分子生态内容相结合。而且，仍有部分鸡形目鸟类的生活史资料存在空缺，有必要加强对生活史的研究，来推进我们对生活史更深的了解。此外，多学科研究和先进技术在鸡形目鸟类研究中并不常见，应予以鼓励。

（北京：田姗 徐基良 李建强 张正旺；
美国：王勇）

研究生论文选登

环境重金属通过食物在麻雀体内的富集与暴露风险评价

重金属会通过工农业生产和日常生活进入到土壤、水体和大气等环境中，并对其中生存的动植物造成不同程度的影响。鸟类是生态系统的重要组成部分，对维持生态系统的平衡起着重要作用。然而，环境重金属也可通过土壤、水和食物等途径进入鸟类体内并富集，可能会对鸟类生长、发育和繁殖等产生不利影响，甚至导致鸟类个体的死亡。因此，本研究选择欧亚大陆广泛分布的雀形目鸟类——麻雀（*Passer montanus*）作为研究对象，选取我国重要的矿产资源枯竭城市——甘肃白银地区的梁庄村作为重金属污染样地及相对无污染的旅游胜地——甘肃刘家峡地区的魏川村作为对照样地，探讨Cu、Zn、Pb和Cd四种重金属在麻雀成鸟体内的富集水平及其通过土壤、水和食物途径给麻雀雏鸟、幼鸟和成鸟带来的暴露风险，以期为制定鸟类重金属暴露风险的基准提供参考。

本研究主要取得了以下结果：

1. 两地土壤和水样中的重金属水平。由于土壤和水均是鸟类摄入重金属的途径，因此本研究调查了两地土壤和水样中的重金属浓度。白银地区土壤中除Cd浓度超过土壤环境质量标准（GB 15618-1995）中规定的限值并达到中度污染外，其它三种重金属均未超过相应限值；白银地区水样中Pb和Cd的浓度超过了生活饮用水卫生标准（GB 5749-2006）中规定的限值，Cu和Zn的浓度则低于相应限值。刘家峡地区土壤和水样中四种重金属的浓度均未超过相应限值，且显著低于白银地区土壤和水样中的重金属浓度（$p < 0.01$）。说明选择刘家峡地区作为对照样地是可行的。

2. 两地麻雀幼鸟和成鸟的身体指标。通过测定两地麻雀幼鸟和成鸟体重、体长、尾长、翼长、跗蹠长和喙长等身体指标，结果表明上述指标均无显著差异（$p > 0.05$）。说明重金属污染尚未对白银地区麻雀幼鸟和成鸟的身体指标造成明显影响。

3. 两地麻雀成鸟各部位和粪便中的重金属富集水平。通过对麻雀成鸟各部位和粪便中重金属浓度的检测发现，初级飞羽、尾羽、腹羽和背羽中四种重金属的浓度均较高，Zn和Pb在跗跖骨中有较高的浓度。其它组织中，肝脏、肾脏和粪便中四种重金属的浓度均较高，胸肌和血液中的重金属浓度则较低。此外，白银地区麻雀成鸟的初级飞羽、血液和粪便中四种重金属的浓度均显著高于刘家峡地区（$p < 0.05$），可用于指示环境重金属的污染。

4. 麻雀雏鸟、幼鸟和成鸟的食物组成。本研究利用稳定同位素分析法（Stable Isotope Analysis in R, SIAR）分析了刘家峡和白银地区麻雀的食物组成，结果表明：雏鸟的食物组成中比例最大的是非植食性无脊椎动物，比例最小的是玉米和禾本科C4植物；除个别例外，玉米在幼鸟和成鸟的食物组成中占有最大比例。总之，两地麻雀雏鸟主要以动物性食物为食，幼鸟和成鸟则主要以植物性食物为食。

5. 两地麻雀食物中的重金属水平。在所有的食物源中，非植食性无脊椎动物的重金属浓度最高，玉米的重金属浓度最低。除极少数例外，白银地区所有食物源中的重金属浓度均显著高于刘家峡地区($p < 0.05$)。此外，两地麻雀雏鸟的食物源中重金属的平均浓度（average concentration, AC值）最高，其次是成鸟（夏季）的，白银地区雏鸟、幼鸟和成鸟食物中的AC值均高于刘家峡地区，说明白银地区的麻雀通过食物会摄入更多的重金属。

6. 重金属从食物到麻雀体内的生物放大

效应。除极少数例外，两地麻雀雏鸟、幼鸟和成鸟的生物放大系数（biomagnification factor, BMF 值）均大于 1.0，这说明四种重金属从食物到麻雀体内存在生物放大效应。其中，Pb 的生物放大效应最为显著，从食物到麻雀体内放大了 2.29~7.08 倍。此外，麻雀初级飞羽及其食物源中的重金属浓度与其 $\delta^{15}N$ 值之间存在显著的线性相关（$R^2 \geq 0.3309$, $p < 0.05$），且四种重金属在两地的营养级放大系数（trophic magnification factor, TMF 值）均大于 1.0，表明其随着营养级的升高有生物放大效应。总之，四种重金属从两地食物到麻雀体内存在生物放大效应，且重金属浓度随营养级的升高而升高。

7. 两地麻雀的重金属摄入水平。两地麻雀雏鸟的重金属日摄入量（heavy metal daily intake, MDI 值）和单位体重日摄入量（heavy metal daily intake per unit of body weight, MDIBW 值）最高，其次是成鸟（夏季），幼鸟和成鸟 (冬季) 的水平相当。白银地区雏鸟、幼鸟和成鸟的 MDI 值和 MDIBW 值均显著高于刘家峡地区（$p < 0.05$），说明重金属污染会提高麻雀的重金属暴露水平。此外，不同食物源对麻雀的 MDI 值有不同贡献，无脊椎动物在食物总量中所占的比例与 MDI 值成正比，粮食作物籽粒则与其成反比。总之，白银地区麻雀雏鸟、幼鸟和成鸟的重金属摄入水平均高于刘家峡地区，在麻雀不同生命阶段，雏鸟的重金属摄入水平最高。

8. 麻雀的重金属暴露水平和暴露风险。本研究分析了麻雀通过土壤、水和食物等途径的重金属暴露水平（exposure level, EL 值）、危害商数（hazard quotient, HQ 值）和危害指数（hazard index, HI 值）。结果表明，雏鸟的 EL、HQ 和 HI 值最高，其次是成鸟（夏季）的，幼鸟和成鸟（冬季）的水平相当。其中，两地麻雀雏鸟、幼鸟和成鸟 Zn 和 Pb 的 HQ 值均大于 3.0，说明 Zn 和 Pb 会给麻雀带来高等暴露风险。此外，白银地区的 EL、HQ 和 HI 值均显著高于刘家峡地区（$p < 0.05$）。总之，白银地区麻雀的重金属暴露水平和暴露风险均高于刘家峡地区，两地雏鸟面临较高的暴露风险。

综上所述，白银地区麻雀初级飞羽、血液和粪便中 Cu、Zn、Pb 和 Cd 的浓度均高于刘家峡地区，可用于指示长期环境重金属污染的生物学效应。麻雀雏鸟主要以无脊椎动物为食，幼鸟和成鸟则主要以粮食作物籽粒和草籽为食，由于无脊椎动物体内含有较高的重金属浓度，所以雏鸟的重金属摄入量和暴露风险均高于幼鸟和成鸟。白银地区土壤、水和麻雀食物中 Cu、Zn、Pb 和 Cd 的浓度均高于刘家峡地区，分析结果也表明白银地区麻雀的重金属暴露风险显著高于刘家峡地区。此外，环境重金属从食物到麻雀体内存在明显的生物放大效应，表明即便是长期栖息在低浓度环境重金属污染条件下，麻雀依然面临较高的暴露风险。

（甘肃：艾世伟 张迎梅）

斑鹟种组的线粒体全基因组结构特征及其系统发育研究

近年来，动物线粒体 DNA 全序列的测定和系统发生关系的重建已成为分子系统学研究的热点之一，尤其是线粒体 DMA 全序列已经广泛应用于鸟类的系统学研究上，已成功解决某些鸟类类群的系统发生关系。斑鹟属于雀形目鹟科鹟属。包括两个亚种（指名亚种及北方亚种）和一个中间型。有学者将北方亚种列为独立的种，即红尾鹟。为了进一步澄清斑鹟的分类地位，本文对斑鹟种组的全线粒体基因组进行研究，分析结构和特征，进一步研究鹟科鸟类线粒体基因的排列模式和结构，为鹟科鸟类线粒体谱系基因

组学的研究提供新的数据资料。结果表明三种鹟的全线粒体基因组的长度分别为 16,737, 16,788 和 16,750 bp。全线粒体基因组包括 37 个基因，排列组成方式与其他鹟科鸟类相似。并基于 NCBI 数据库上已有的 21 种鹟科的线粒体基因，利用 Cytb、COI 、ND2 作为联合基因，构建 MP 树和 NJ 树。重建鹟科的系统发育关系，进而对斑鹟种组的分类进一步了解，澄清斑鹟的分类地位。从分子系统学的角度为鹟科鸟类系统发育提供依据，以期为鹟科鸟类系统分类与进化研究提供新的信息。

（安徽：董元秋 李博 周立志）

东亚雀形目鸟类 DNA 条形码研究

生物分类是了解自然界的基础，每个对自然界感兴趣的人首先应该了解的便是生物分类。更好的认识、鉴定物种，才能对其进行充分的研究，随之推行更完善的保护措施。准确快速地鉴定物种，自然成为生物学界关注的热点话题。自 2003 年 DNA 条形码概念被提出以来，便受到生物学领域的广泛关注。DNA 条形码是利用生物体内标准的、有足够变异的、易扩增且相对较短的 DNA 片段对物种进行快速鉴定的技术。在鸟类中，目前普遍的观点是运用线粒体细胞色素 c 氧化酶亚基 1(mtDNA CO1) 基因的一段 648 bp 的序列作为 DNA 条形码，这在北美 260 种鸟种鉴定中获得较好的支持。然而，东亚鸟类和北美洲鸟类有着十分不同的进化背景，条形码技术在东亚鸟类中是否同样适用，尚有较大疑问。

雀形目鸟类物种丰富，占鸟纲物种数目的一半以上，作为世界野生动物资源的重要组成部分，加强雀形目鸟类的保护对维护全球生物多样性、生物资源的可持续利用具有重要意义。关于雀形目鸟类的繁殖、鸣声、生态、行为等已开展过许多研究，但由于雀形目鸟类数目众多，一些物种在形态上的差异十分微小，不易被鉴别，而有些物种种下形态学变异较大，导致雀形目中许多鸟类的物种鉴定、分类关系等一直争论较多。因此，探讨 DNA 条形码能否用于雀形目鸟类的物种鉴定显得十分有意义，不仅能为我们提供物种分类和定种的证据，也能在鸟撞、刑侦、海关缉私等多个领域有应用价值。本研究选择东亚雀形目鸟类作为研究对象，旨在解决 2 个科学问题：1）条形码间断（barcoding gap）在东亚雀形目鸟类中是否存在？ 2）在东亚雀形目鸟类物种鉴定中运用 DNA 条形码，在多大程度上可信？

本研究收集整理了东亚 5 国（俄罗斯、中国、日本、韩国、蒙古）雀形目鸟类 4525 条 DNA 条形码原始序列，计 49 科 156 属 427 种；新扩增 275 条序列，计 19 科 52 属 72 种。发现东亚雀形目鸟类种内平均遗传距离为 1.355％，变异范围为 0~17.5％，遗传距离在 0~2％的占 77.8％。属内近缘种间平均遗传距离值为 10.557%，变异范围为 0％ ~18.8％，遗传距离在 5~15％的占 92.2％。东亚雀形目鸟类的种间平均遗传距离是种内平均遗传距离的 7.79 倍。

以上结果表明，在目前的鸟类分类系统下，东亚雀形目鸟类中不存在明显的条形码间断，种间和种内遗传距离呈现较大的重叠。这有以下提示：一、以往的研究表明，取样不足更容易出现条形码间断，本研究没有出现明显的间断，排除了取样不足的情况；二、目前东亚鸟种在通行的鸟类分类系统下，可能存在待完善的地方，尤其是隐存种、复合种的存在会导致种下遗传距离偏高。更有意义的发现是：由于东亚鸟类进化历史较长，导致不论种间或是种内的遗传距离均高于北美鸟类，因而适用于北美鸟类的阈值并不适用于东亚雀形目鸟类的鉴定。通过分析，我

们建议将 DNA 条形码遗传距离 4.9% 作为东亚雀形目鸟类物种鉴定的阈值。在这个阈值下，东亚鸟类的鉴定成功率最高，达到 94.2%，大多数东亚雀形目鸟类物种可以使用这个阈值进行物种鉴定，但是对于近期分化的物种或者是隐存种、复合种，DNA 条形码技术在运用上尚有局限。此外，东亚鸟类的种下遗传距离远远高于北美鸟类的种下遗传距离，这表明在东亚进行鸟类保护不仅需要从物种水平开展保护，也应该关注种群水平的遗传多样性保护。

（云南：陈熙 罗旭）

黄河三角洲繁殖东方白鹳巢址选择的研究

巢址选择在亲鸟繁殖成功和幼鸟孵育方面具有重要意义，同时巢址选择也受到食物资源，植被盖度和人为干扰等其他众多因素的影响。因此研究鸟类巢址选择可以更好地了解和保护鸟类种群数量和现状，特别对于濒危鸟类来说更为重要。在本研究中，收集了 2003 年 —2017 年间，黄河三角洲东方白鹳巢址数量及空间分布，实地测量 2017 年大汶流范围内的 62 个东方白鹳巢址样方与 32 个潜在可能营巢点的 20 种生境因子，通过回归模型建立和多元统计分析，研究黄河三角洲东方白鹳巢址数量和分布的时空变化，以及影响东方白鹳巢址选择的关键限制因子。结果表明，由于黄河三角洲地区没有高大乔木，东方白鹳的主要营巢点位于分布在核心区芦苇生境中的电线杆巢和人工招引巢，少数分布在泥滩生境，随着东方白鹳繁殖数量的逐年增多，核心区范围内能够提供的营巢位点逐渐饱和，东方白鹳开始选择位于试验区农田生境中的高压输电线塔进行营巢，且数量逐年增多。此外，在巢址选择方面，对于电线杆巢，人为干扰和输电线密度是影响巢址选择的重要因素，对于人工招引巢，距公路和适宜生境距离是影响程度最大的两个生境因子，对于高压输电线巢，巢间距和距人为干扰的距离是巢址选择最重要的两个影响因素。

（安徽：程磊 周立志）

人为干扰对越冬后期稻田中小天鹅 *Cygnus columbianus* 昼间能量消耗的影响

能量的消耗模式是动物适合度的重要体现，动物的日常行为和栖息地特征共同影响日能量消耗。稻田生境是越冬水鸟重要的觅食场所之一，同时又容易受到人为干扰，越冬水鸟应对日间不同的人为干扰因素而合理进行能量消耗配置，对于在越冬后期为迁徙而贮备能量的水鸟来说尤为迫切和重要。本文采用焦点动物取样法，观测越冬后期稻田中小天鹅（*Cygnus columbianus*）在干扰和非干扰环境中昼间行为的时间分配，推算其能量消耗。结果表明，小天鹅在干扰环境中警戒行为的时间分配和能量消耗($P_{\text{警戒时间}} = 0.00$，$P_{\text{警戒能耗}} = 0.00$)、单次警戒时间和警戒频次（$P_{\text{回合时间}} = 0.03$，$P_{\text{警戒频次}} = 0.00$）显著大于非干扰环境，游泳频次也是如此（$P_{\text{游泳频次}} = 0.04$）；在稻田中的昼间警戒能耗随干扰时间增加而增加，随干扰距离增加而降低。干扰造成小天鹅减少高能耗的取食行为，增加低能耗的警戒，降低昼间总能量的消耗（$t = -2.22$，$P = 0.04$）。

（安徽：于超 周立志 宋昀微）

亚洲大陆雉鸡（*Phasianus colchicus*）的谱系地理学研究

雉鸡是广泛分布于古北界地区的典型物种，在羽色等形态方面具有明显的种内分化。基于生物地理学和形态学特征，雉鸡种下的30个亚种根据其形态共性被分为5个亚种组，占据了多种多样的栖息地，并被引入西欧、北美和澳大利亚作为一种常见的猎鸟。为了全面地研究不同雉鸡地理种群的遗传多样性和分化程度，我们首次从西亚 - 中亚 - 东亚这一广阔的地理尺度上进行采样，对在雉鸡分布区内的102个地点的278个个体（涉及22个亚种）进行单个基因测序（2个线粒体及7个内含子位点，共5,609 bp序列长度）并对13个常染色体微卫星位点进行分型。同时，基于下一代测序技术，我们对中国9个亚种 / 种群的110个个体进行基于酶切的简化基因组测序（RAD-seq），得到了基因组水平的单核苷酸多态性（SNPs）

研究结果表明雉鸡的种群存在显著的遗传结构，形成了七个主要的进化分支：分布在青藏高原东南部的横断山雉鸡（对应的是elegans亚种）是基部类群，在约1.36百万年前开始分化；东亚地区的雉鸡形成了最大的分支，并在约0.7百万年前基于亚洲季风性气候与大陆性气候分界线呈东西部分化，即东亚东部雉鸡和东亚中部雉鸡。分布在塔里木盆地的塔里木雉鸡和分布在哈萨克斯坦、新疆的准噶尔雉鸡是两个单系进化的分支（约1百万年前形成），与中亚地区的雉鸡形成姐妹类群（从0.7百万年前开始分化）。扩展贝叶斯天际线图表明在扩散过程中，除了塔里木雉鸡和准噶尔雉鸡保持稳定的种群大小外，其他5个进化支的雉鸡都存在近期的种群扩张。对东亚地区雉鸡构建的种群结构显示除了在东亚中部地区斑块分布的独立小种群(如青海柴达木种群,甘肃玉门种群,蒙古国种群,横断山种群)，东亚东部连续分布的雉鸡种群间存在基因渗透。基于迁移 - 隔离模型的分析结果显示存在从东亚东部到东亚中部的基因流。根据雉鸡种群的分化时间及重构的扩散路线，我们推测雉鸡起源于中国西南部的云南和四川的亚热带森林，从早更新世开始扩散。青藏高原的隆起导致了亚洲内陆的干旱区及东亚南亚季风区的形成，气候隔离减弱了东亚地区雉鸡的基因流。中亚地区的雉鸡由于高加索山脉以及沙漠的扩张形成斑块分布，地理隔离促进了种群分化。本研究表明亚洲大陆的历史上的地理事件和气候变化强烈地影响了雉鸡的地理分布格局、遗传多样性和进化历史。

（广东：刘思敏 刘阳）

四川盆地的陆地岛屿效应——基于麻雀的形态变异与遗传结构

以麻雀（*Passer montanus*）为研究对象，通过研究四川盆地内、外种群形态特征差异与遗传结构，探讨四川盆地的陆地岛屿效应。

采集四川盆地及周边地区558个麻雀样本的7项形态指标,根据海拔将麻雀分为3组:四川盆地（219~725 m）、华中平原（46~784 m）、盆地周边山地（807~4,472 m）。单因素方差分析表明:3个麻雀种群的体质量、翅长、尾长、跗跖长之间的差异有高度统计学意义($P < 0.01$)，盆地周边山地种群的体质量显著或极显著大于四川盆地及华中平原（$P < 0.05$或$P < 0.01$）。同时，四川盆地与华中平原种群的体质量、体长、尾长、翅长、跗跖长、嘴峰、嘴裂差异均无统计学意义（$P > 0.05$），麻雀体型随海拔升高而显著增大，说明麻雀的形态变异与海拔变化密切相关，符合贝格曼定律。

将172个麻雀分为29个地理种群，采用

4 个线粒体基因（12srRNA、Cytb、Dloop、Co1）和 1 个核基因（Myo）作为分子标记，通过计算核苷酸多样性、遗传距离等，构建系统发育树与单倍型网格图，探讨盆地内、外麻雀的种群动态与遗传结构，主要结果如下：

（1）大多数种群均表现为较低的遗传多样性（$Pi < 0.01$），遗传多样性表现为以四川盆地向周边山区（川西高原和云贵高原）递增的趋势；

（2）遗传变异主要来自于盆地周边山地种群之间，盆地内种群与盆地外种群存在一定的基因交流；

（3）在四川盆地西北一线，盆地内种群存在向盆地外扩张的现象。

综合以上分析，四川盆地周边的山系对四川盆地内、外的麻雀种群产生了一定的隔离作用，表现出四川盆地的陆地岛屿效应。

（四川：赵文海 刘方庆 文陇英）

长江中下游湖泊水鸟群落及其种群下降的驱动力

长江流域季节性洪水对东亚地区的越冬水鸟具有重要意义。在过去的 60 年中，水鸟数量显著下降，因此理解影响水鸟种群丰度和分布的因子对于水鸟保护至关重要。本文利用混合线性模型探索 2005—2016 年间中国 72 个湖的气候、冬季水域面积、涨落区面积（最大洪水面积与冬季干旱面积的差值）对于水鸟丰富度和多样性的影响。结果表明冬季水位面积和气候因素都不是最适模型，而涨落区面积才是影响水鸟种群丰度和多样性的关键因子，因此推断，未来的水土利用和开垦对水鸟丰度和多样性的影响将大于气候变化影响。从 2005 年到 2016 年，水鸟数量和多样性的显著下降不能用模型变量来解释，也不能用湿地淹没面积的减少来解释这些下降，这证实了其他因素的作用。这些潜在因素包括湿地质量的下降会影响其承载能力 (例如 : 洪水物候学、扰动、栖息地丧失和退化、富营养化和污染导致的水质下降) 和 / 或其他生命周期其他阶段限制迁徙水鸟数量的因素。长江湖泊最适合水鸟越冬，许多湖泊因水鸟生物多样性而受到保护，这也表明，当受到其他目前未知因素的威胁时，这种保护不能充分保护这些全球性运动的种群。因此迫切地需要进行更多的研究，以保护这些具有全球生物多样性的意义短暂的湖泊系统。

（北京：贾强 王鑫 曹垒；江苏：张永；
Denmark: Anthony David Fox)

四种共域鸟类对大杜鹃巢寄生的反寄生策略比较

对利用同一芦苇生境中的东方大苇莺（*Acrocephalus orientalis*）、钝翅苇莺（*Acrocephalus concinens*）、震旦鸦雀(*Paradoxornis heudei*)和棕头鸦雀(*Sinosuthora webbiana*）4 种共域分布的杜鹃宿主的的巢址选择、繁殖成效以及 4 种宿主对大杜鹃（*Cuculus canorus*）寄生的反寄生适应策略进行了比较。4 种繁殖鸟类的巢址选择具有行为可塑性，同时存在空间分化。4 种鸟类繁殖成效的主要因素是巢捕食，其次为恶劣天气（洪水），而巢寄生则为影响东方大苇莺繁殖成效的重要因素。4 种宿主均具有卵识别能力，其中东方大苇莺与棕头鸦雀能 100% 拒绝实验卵，而钝翅苇莺和震旦鸦雀仅有中等的卵识别能力。东方大苇莺具有强烈的巢防御行为，同时种内帮手协助防御较常见，“邻里互助”的防御行为能有效降低寄生风险。

（海南：杩来坤 梁伟）

杜鹃多样性与鸟类多样性的相关性

近年来，大杜鹃（*Cuculus canorus*）作为鸟类多样性的可靠指示物种已成为一项研究热点。但以往的工作主要在杜鹃种类极少的欧洲开展，其研究结果尚需要在更多的地区，特别是杜鹃种类丰富的地区如亚洲和非洲进一步验证。中国有寄生性杜鹃 17 种，为检验杜鹃是否可以作为鸟类多样性，甚至生物多样性的指示种提供了难得的机遇。本文对多杜鹃寄生系统下杜鹃多样性与鸟类多样性的相关性进行了调查。杜鹃种类有由南到北逐渐减少的趋势。在小尺度上，森林鸟类种类的同质化高于城市鸟类种类的同质化，而大尺度上城市鸟类种类同质化高于森林鸟类种类的同质化。而城市鸟类的物种数及其离散程度、香农威纳指数和均一性指数均低于森林鸟类，表明城市鸟类的物种丰富度相较于森林鸟类更低。有杜鹃存在的样点的平均鸟类多样性均比没有杜鹃存在的样点的鸟类多样性高。在某种杜鹃出现的地区，该种杜鹃出现的样点的平均鸟类多样性均高于没有杜鹃出现的样点的平均鸟类多样性。杜鹃种类数、数量均与鸟类多样性呈显著正相关。

（海南：周博 梁伟）

鸟类的鸣声演化与物种分化研究：以树莺科（Cettiidae）和大杜鹃（*Cuculus canorus*）为例

鸣声是鸟类用于通讯的重要手段，其丰富的鸣声多样性也是鸟类的多样性的重要体现。鸣声的演化可以发生在多个尺度，如个体水平、种群水平、物种水平等。同时，自然选择、性选择、文化漂变、演化历史、种间作用等多种因素都能影响鸣声的演化。结合多个鸟类类群，从多个尺度、多种不同因素对鸣声进行研究，能够帮助我们更加全面的理解鸣声演化的机制。同时，鸣声分化也是鸟类中不同物种之间维持生殖隔离的重要手段，结合鸣声分化以及遗传学、形态学等数据，我们可以进行整合分类学的研究，进行物种边界的厘定，从而增加对于物种分化以及物种多样性的认识。在本研究中，我们从物种间水平以及地理尺度的种群间水平讨论了树莺科鸟类的鸣声演化。同时，结合鸣声以及遗传和形态等数据对强脚树莺复合种（*Horornis foritpes* complex）内部类群的分化程度进行了研究，对这些类群的分类地位进行了探讨。除了树莺等鸣禽，我们还研究了非鸣禽中的大杜鹃（*Cuculus canorus*）的鸣声地理分化。本论文的主要发现和结论如下：

1. 我们对树莺科（Cettiidae）鸟类的种间鸣唱频率和鸣唱长度的演化格局以及影响两者演化的因素进行了研究。我们利用树莺属的系统发育树，讨论了树莺科鸟类的鸣声特征与体型大小、繁殖纬度分布、居留型等生态因素的相关关系，并试图了解这种相关关系在演化上是如何起源的。我们发现树莺科鸟类中鸣声频率与体型大小呈负相关关系，而鸣唱长度与繁殖纬度呈正相关，这样的结论与其他研究的发现是较为一致的。同时，我们发现繁殖纬度和鸣唱长度的相关性只在非迁徙物种中存在但在迁徙物种中则关系不显著。通过模型比较我们也发现纬度是预测鸣唱长度的最主要因素，而不是居留型。我们发现体型大小与体重在进化上较为保守，他们之间的相关性出现在演化的较早时期。鸣唱长度与纬度之间的相关性则出现在演化的较晚时期，两者在演化上都较为易变。我们推测鸣唱长度与纬度的相关性的产生可能是由于繁殖纬度的改变导致物种面对的性选择压力的变化，从而引起了鸣唱长度的改变。

2. 对于鸟类鸣唱的曲目大小以及句子复杂性的影响因素已经有许多研究对其进行

了探究，但是很少有研究工作对于两者之间的关系进行过讨论。我们假设由于学习能力的限制，曲目大小与句子复杂性之间应该存在权衡关系，从而在地理尺度上种群之间这两个变量之间会表现出负相关的关系。我们对强脚树莺（*Horornis fortipes*）的大部分分布区的鸣声录音进行了采样，并利用鸣声数据对这一假设进行了检验。我们发现强脚树莺的曲目大小存在自东向西沿经度增加的趋势，而句子复杂性则存在相反的地理变异趋势，并且两者之间在地理种群尺度上确实存在负相关的关系。通过 Mantel test 和 Partial Mantel test, 我们排除了这种相关性是由空间自相关或是气候因素的影响。我们的结果表明对于强脚树莺而言，可能存在曲目大小和句子复杂性之间的权衡关系，从而导致了地理上的变异格局。这项工作为理解鸟类的鸣声演化机制提供了一些新的见解。

3. 物种是多个生物学领域的基本研究单位，对于物种的界限的研究是相关研究的基础。然而由于缺乏足够的分类学校订，亚洲的鸟类多样性尤其是中国 - 喜马拉雅地区的鸟类多样性有可能存在被较大程度低估的情况。已有研究暗示强脚树莺内部可能存在实际独立的多个物种，但已有研究使用的数据量都相对较小。在本研究中，我们进行了较为全面的采样，通过多方面的遗传学分析方法特别是基于多物种溯祖分析的方法对于强脚树莺这个在亚洲东南部广泛分布的种组进行了物种界定研究。我们还同时分析了鸣声与形态学的差异以了解是不同类群之间具有可识别的性状差异以获得关于分化的多方面线索。遗传学分析的结果支持该种组中至少存在 3 个独立的演化支系，但我们同时发现分类单元间的鸣声与形态差异较小。我们认为强脚树莺内部的独立的演化支系代表了处于物种形成的早期阶段的新成种。我们认为中国 - 喜马拉雅地区的鸟类多样性可能存在低估并需要进一步的深入研究。

4. 关于大杜鹃的大尺度上的鸣声分化及格局的形成原因缺乏研究。我们对欧亚大陆的大杜鹃（*Cuculus canorus*）的鸣声地理变异格局进行了分析，并探讨了可能的影响因素如距离隔离、亚种分化、气候、海拔等因素。我们发现不同亚种的大杜鹃鸣声存在显著差异，其中 *subtelphonus* 亚种的鸣声频率显著高于其他亚种，且在判别分析中具有很高的正判率。我们发现鸣声差异与地理距离显著相关，而鸣声差异与气候差异及海拔差异等因素则没有显著关系。对华中地区不同生境中大杜鹃的鸣声比较表明，两者间存在显著差异。我们的结果表明，在大尺度上，亚种分化与地理距离是影响鸣声分化的主要因素，而在小尺度上，生境分化与鸣声分化相关。

（北京：魏晨韬 张雁云 Trevor Price）

灰头鸫的个性在性选择、亲代投入和巢址选择中的作用

近些年来，随着动物适应性进化的研究尺度转向同一种群的不同个体间的差异性，动物个性正在成为国际上行为生态学研究的热点。动物个性指不同动物个体的各种行为类型在不同时间和背景下所表现出来的一致性差异。动物个性与生活史特征相关，并且会影响个体的适合度。因此，动物个性可能受到自然选择和性选择的影响。

在 2015—2016 年间，将甘肃莲花山自然保护区内的灰头鸫（*Turdus rubrocanus*）野外种群作为研究物种，以简易笼子实验和手握实验对灰头鸫成鸟的活动性、新奇性和勇敢性这三个个性特征进行了评估。研究发现灰头鸫个体在活动性和勇敢程度上都表现出显著的重复性，而新奇性却没有重复性。此外，勇敢性和活动性之间存在相关性，即勇

敢的个体活动性强。说明甘肃莲花山地区灰头鸫种群的个性特征是活动性和勇敢性。此外，灰头鸫存在基于个体的活动性和勇敢性的选型配对。

研究发现灰头鸫雌、雄亲鸟的勇敢性与其自身的递食频次不相关。配对亲鸟之间勇敢性的相似程度不仅可以影响亲鸟在育雏过程中递食任务的分配模式，还可影响亲鸟的总递食频次，从而影响雏鸟的体重。自然状态下，相似的配对个体具有相似的递食频次，这样可以缓解亲代投入过程中的两性冲突。在配偶移除实验中，雄性亲鸟会减少亲代投入，而雌性则会根据自身和配偶的勇敢性相似程度做出不同的行为反应。与相似个体配对，雌性会补偿雄性缺失后的递食频次。与不相似的个体配对，雌性则会降低其递食频次。

水平遮蔽度、乔木和灌木的盖度、距居民区距离和距农田距离是影响灰头鸫巢址选择的主要因素。勇敢的雌性灰头鸫会选择水平方向遮蔽度更好的巢址筑巢，并倾向于选择巢密度低的区域。同时，在研究期间还发现基于个性的巢分布模式变化，这种变化可能是由于食物资源的丰富度引起的。在 2015 年，相似个性的雌性灰头鸫倾向于在一起筑巢繁殖。勇敢的雌性筑巢在巢密度低的区域时成功率高，同时胆小的雌性筑巢在巢密度高的区域时成功率高。在 2016 年，不相似个性的雌性灰头鸫倾向于在一起筑巢。勇敢的雌性筑巢在巢密度高的区域时成功率高，胆小的雌性筑巢在巢密度低的区域时成功率高。

（北京：楼瑛强 孙悦华）

第 14 届全国鸟类学研究生“翠鸟论坛”报名通知

各位老师、同学：

第十四届“翠鸟论坛”将于 2018 年 8 月 30—31 日在北京师范大学举办。本次会议由中国动物学会鸟类学分会主办，北京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、学生报告和墙报展示等内容。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，展示者要在自己的墙报前做 3 分钟口头介绍。

本次论坛将在 8 月 31 日下午安排两个研究方法工作坊（鸟类鸣声与鸟类血孢子虫），每个工作坊限 20 人。

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、报名要求：

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。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。

若申请参加工作坊（每人限申报 1 个主题），请与提交的摘要内容做成一个文档在系统中进行提交，文档中需写明申请工作坊的主题（鸟类鸣声或鸟类血孢子虫），并附申请理由（不超过 300 字），组委会将根据申请书遴选参加者。

3、注册方式

请登录中国动物学会的学术会议系统网站注册并提交摘要：http://czs.bitcast.org.cn/czsweb/。

注册及提交摘要截止日期：7 月 20 日。

注册信息经审核后，于 7 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 董路 刘阳 张剑

联系人：

张 剑 zhangjian@mail.bnu.edu.cn

董 路 donglu@bnu.edu.cn

（中国动物学会鸟类学分会）

第七届国际黑鹳会议将在西班牙召开

中国是黑鹳分布范围最大、种群数量最多的国家，但研究者却比较少。第七届国际黑鹳会议将在西班牙南部地区的安达卢西亚召开（2018 年 11 月 28—30 日），注册费为 40 欧元。因开会地点比较偏僻，这次主办方限制性邀请参会人数（25~30 人）。但对中国代表特别开放，非常希望中方有代表参加。

联系方式：Dr. Luis Santiago Cano (Co-chair): catuche.gallego@gmail.com

（新疆：马鸣）

第四届野生动物疟原虫及血孢子虫国际学术研讨会将在北京召开

第四届野生动物疟原虫及血孢子虫国际学术研讨会将于 2018 年 11 月 1—5 日在北京师范大学召开。本届会议由北京师范大学生物多样性与生态工程教育部重点实验室、北京动物园圈养野生动物技术北京市重点实验室和中国动物学会鸟类学分会联合主办，北京师范大学生命科学学院承办。

一、会议主题：野生动物疟原虫和血孢子虫的多样性、进化与动物健康

二、时间：2018 年 11 月 1—5 日

三、地点：北京师范大学京师学堂、北京动物园科普馆

四、日程安排：2018 年 11 月 1 日报到，2—4 日为学术报告，5 日为会后培训

会议详细日程安排请关注会议网站：www.malariaconference2018.com

五、特邀报告专家：

- Carter Atkinson (Pacific Island Ecosystems Research Center, Hawaii, USA)
- Farah Ishtiaq (Indian Institute of Science, Bangalore, India)
- Dina Fonseca (Rutgers, State University of New Jersey, USA)
- Ravinder Sehgal (San Francisco State University, USA)
- Robert Ricklefs (University of Missouri at St. Louis, USA)
- Ana Rivero (Centre National de la Recherche Scientifique, Montpellier, France)
- Gediminas Valkiūnas (Nature Research Centre, Vilnius, Lithuania)

六、注册费用：

请登录中国动物学会的学术会议系统网站注册并交纳注册费 http://czs.bitcast.org.cn/czsweb/。以在注册截止日期（2018 年 7 月 15 日）之前缴纳注册费为准（以邮局汇款、银行转账凭证等为据）。会议期间各位代表的住宿费用和会后考察费用自理。

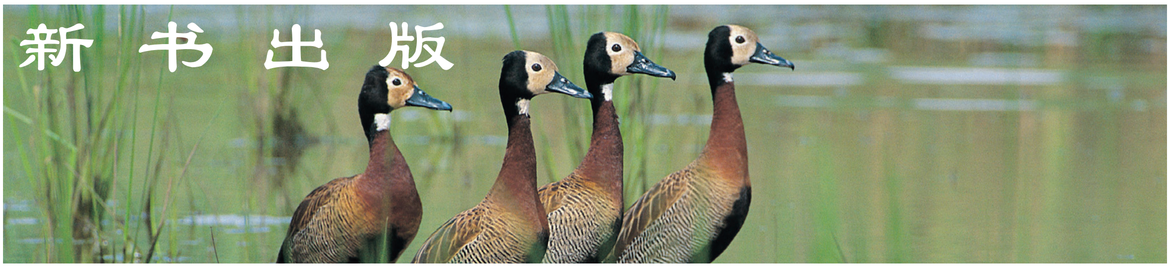
七、论文摘要提交

向大会提交论文摘要的截止日期为 2018 年 7 月 15 日。摘要以英文撰写，字数不超过 350 单词，包括题目、作者、单位（含地址及邮编）、摘要正文和关键词。请在提交前确保以上 5 项内容全部撰写清楚。具体要求详见学术会议系统的会议动态栏目中提交摘要样例及要求，所有论文摘要通过网上递交。提交论文摘要时，请务必注明该论文申请报告的类型 (口头报告或墙报)，最后大会学术委员会依据本人申请报告类型和日程安排确定报告类型。

八、住宿安排

本届大会的会议地点位于北京师范大学京师学堂，会议酒店包括校园内的“京师大厦”及周边的“汉庭酒店（积水潭店）”等。由于可预订宾馆房间有限，需要大会会务组协助提前预定宾馆的代表，请在 7 月 15 日之前登陆中国动物学会网站 (http://czs.ioz.cas.cn/) 的学术会议系统并预订宾馆。

正常注册 6 月 25—7 月 15 日	延期及现场注册 7 月 15—11 月 1 日
普通代表 ￥ 1500	普通代表 ￥ 1800
学生代表 ￥ 800	学生代表 ￥ 1000



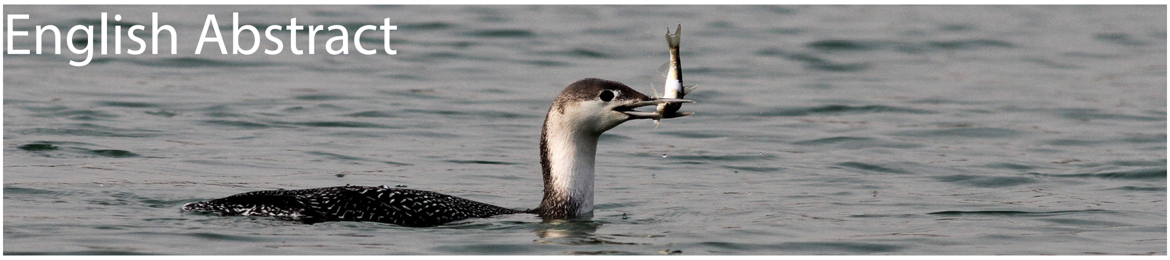
介绍林业出版社珍稀鸟类新书——黑鹳的故事

最近，中国林业出版社出版了绿野寻踪系列丛书之《黑鹳的故事》出版了，作为审稿人，特别向大家推荐这本科普新书。黑鹳是国家I级重点保护野生动物，在中国有一定的分布和种群数量，但缺少研究资料。该书是由山西省灵丘黑鹳自然保护区管理局主编，以黑鹳保护区为背景，讲述黑鹳生活的故事，并且从多年的野外观察中总结出黑鹳的栖息地、形态、分布、繁育、迁徙、行为、觅食、越冬、保护与管理等方面知识。其内容丰富，故事生动，文图并茂，雅俗共赏。书中的彩色照片有200多幅，24开，72页，定价：20元。林业出版社的绿野寻踪系列已经出版十余种图册，这些精美的图书不仅具有科普作用，对于科研工作者也具有一定的参考价值。

（新疆：马鸣）

封面照片 蓝喉蜂虎（*Merops viridis*）由李全民2010年7月18日摄于湖北。

English Abstract



Notes of Meetings

ICP6 was held in Brno, Czech Republic

International Conference on Phthiraptera 6（ICP6） was held in Brno, Czech Republic during June 23-29, 2018. Nearly 100 representatives from more than 30 countries attended the meeting. The Chinese representatives attending this conference included Fasheng Zou, Daniel R. Gustafsson and Xingzhi Chu from Guangdong Institute of Applied Biological Resources (GIABR).

The scientific program of this conference included 5 plenary lectures, 10 groups comprising a total of 53 oral reports, 31 posters and 2 round table discussions.

The topics and speakers of the plenary lectures were：

1）“Mitochondrial genomes of parasitic lice: high-throughput sequencing, gene shuffling, genome fragmentation, and insights into high-level phylogeny & classification” by Renfu Shao (Faculty of Science and Education, University of the Sunshine Coast, Australia)

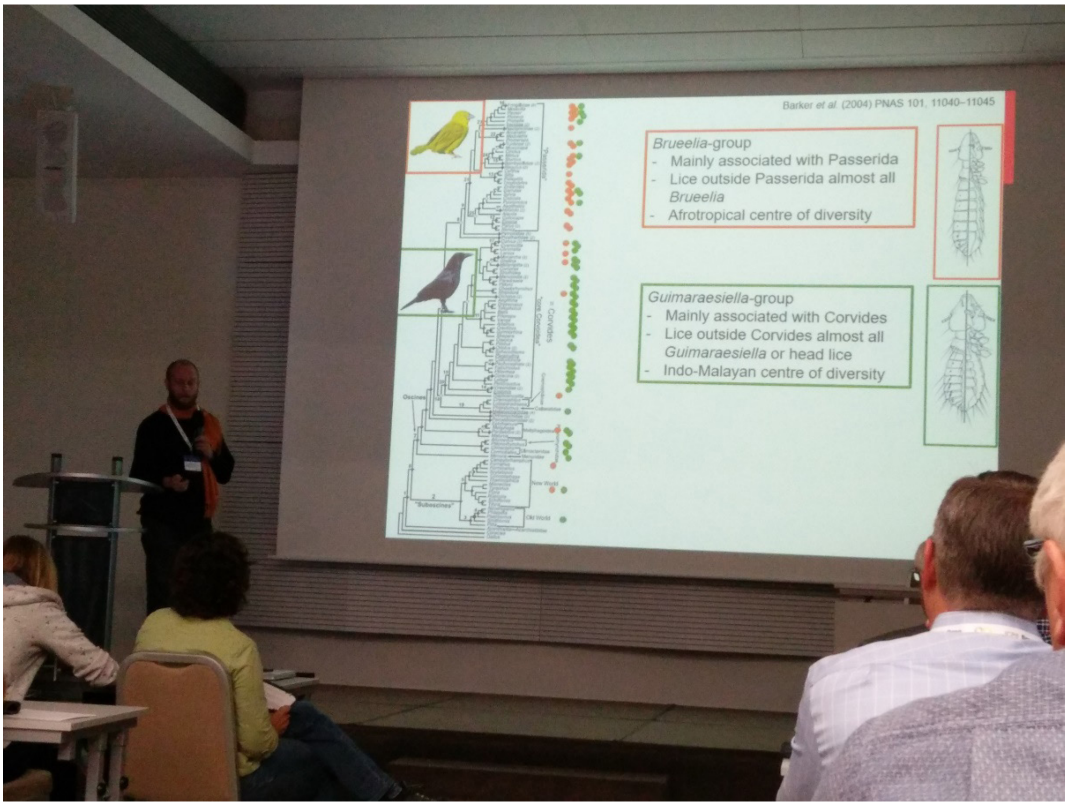
2) “The lice that splice: the search for the genomic underpinnings of two morphs” by Araxi Urrutia (Department of Biology & Biochemistry, University of Bath, UK)

3) “Finding relations in multi-species communities of birds and ectoparasites” by Oleg Tolstenkov (Severtsov Institute of Ecology and Evolution Russian Academy of Sciences, Center of Parasitology, Moscow, Russia)

4) “New Zealand Lice and their hosts: a pictorial review” by Ricardo Palma (Museum of New Zealand Te Papa Tongarewa, Wellington, New Zealand)

5) “Head lice systematic review” by Robert Vander Stichele (Department of Pharmacology, Ghent University, Belgium)

At this conference, Daniel R. Gustafsson gave an oral presentation “Major distribution patterns in the Brueelia-complex”. In addition, two posters were presented by Daniel R. Gustafsson, and one by Xingzhi Chu. Daniel R. Gustafsson presented “The Brueelia-complex chewing lice (Ischnocera) of ‘babblers’ and allies (Passeriformes: Leiothrichidae, Paradoxornithidae, Pellorneidae, Timaliidae)” and “Morphological variation in Guimaraesiella Eichler, 1949 (Phthiraptera: Ischnocera: Philopteridae: Brueelia-complex)”. Xingzhi Chu presented “The influence of host body size, migratory status, and diet on prevalence and mean intensity of chewing lice (Phthiraptera) on birds in southern China”.



Barker *et al.* (2004) PNAS 101, 11040–11045

Brueelia-group
- Mainly associated with Passerida
- Lice outside Passerida almost all *Brueelia*
- Afrotropical centre of diversity

Guimaraesiella-group
- Mainly associated with Corvides
- Lice outside Corvides almost all *Guimaraesiella* or head lice
- Indo-Malayan centre of diversity

Daniel R. Gustafsson during his oral presentation

The academic committee meeting for the International Society of Phthirapterists (ISOP) was held on June 28, 2018. Daniel R. Gustafsson was added as a councilor of the ISOP for the period 2018–2022. It was also decided that the next conference, the 7th International Conference on Phthiraptera, will be held in Guangzhou in 2022, hosted by the GIABR. Preliminary plans were also made for a workshop on chewing louse biology, morphology, and classification in Salt Lake City during 2019 or 2020; students interested in this workshop should contact Daniel R. Gustafsson. Plans were made for collaborations between our lab in Guangdong and 12 other research labs in Australia, USA, Czech Republic, Romania, South Africa, and Russia.

(Zou Fasheng, Guangdong)

Research Reports

Observation on breeding and moving behavior of Eurasian Nightjar (*Caprimulgus europaeus*)

The breeding behavior of the Eurasian Nightjar (*Caprimulgus europaeus*) is mysterious, and the data are scarce in China. In June-August 2008 and June-July 2018, seven nests were found in the central islands of the Toutun River in Urumqi (87°16'E, 43°53'N, at an altitude of 715 m). The nests were located on the sloping sands of the riverbanks with sparse vegetation, and they were simple and shallow, without mats and shadows. There were two eggs per nest, the eggs were oval, white, with irregular reddish-brown markings, brown spots were blurred or clear, with length diameter 30.44 ± 0.85mm, short diameter 21.39 ± 1.00mm (n = 5), weighing 7.3 ± 0.4 g (n = 3). There was great variation in size between the eggs of the same nest, and the hatching was not synchronized. The average nearest distance between the two nests was 69m.

We used infrared cameras from June 17 to July 12, 2018 for the first time to monitor 3 nests for 15 days, 23 days and 11 days, respectively, a total of 8462 photos, 4152 video clips, about 39.9 hours, and 6807 valid photos. The results showed that the Eurasian Nightjar brooding period was about 18d. After 4 days of age, they began to move, either to avoid the sun or interference (natural enemies, herds, floods, human activities, etc.). The birds moved 1.5-12m each time and could be as far as 18~31m away from the original nest site. When a flood occured in July, the young birds followed the adults to a higher grand further away from the river.

The photos and videos peaked between 10:00 to 12:00 (Xinjiang time, same below) when the sun was shining, and the birds were constantly changing positions to prevent the young birds from being sunburned. 31.3h video and 5,753 pictures were taken during the day (6:00-20:00), accounting for 84.3% of the valid photos. Adults rarely left their nests during the day (except when disturbed), mainly were resting, alert or caring for young birds. During 20:00-22:00 and 2:00-4:00), the adults went to forage and feed their youngs. The European Nighthawk is a half-altricial species, young birds had weak legs for walking. In the later brooding period, young birds often followed the adults for food, and learned the flight skills from adults.

(Wang Shuchao and Ma Ming, Xinjiang)

Please join us for study of bird feather louse

Dr. Daniel Roland Gustafsson started his work in Guangdong Institute of Applied Biological Resourses, Guangdong Academy of Sciences in October 2017 as one full-time high-level talent.

Dr. Gustafsson is collaborating with Professor Fasheng Zou in this institute and will focus on classification of avian feather louse and coevolution between birds and lice, especially babblers in forest of South China. Dr. Gustafsson received his Master and PhD degrees at University of Gothenburg, Sweden, in 2007 and 2012 (supervisor: Dr. Urban Olsson), respectively. Dr. Gustafsson's PhD dissertation was the study of chewing lice (Phthiraptera) of shorebirds (Charadriiformes), and the effect of host migration on the distribution and phylogeny of chewing lice. Dr. Gustafsson moved to the Clayton/Bush Lab at the University of Utah, USA, for a post-doc position after 2012. There he studied the *Brueelia*-complex of chewing lice, which parasitize songbirds and some other groups. This resulted in a complete revision of one of the largest and most complicated groups of chewing lice and an updated checklist and identification key to chewing lice known from Sweden.

Since October 2017, Dr. Gustafsson has been working in the Avian Ecology and Evolution Study Group at the Guangdong Institute for Applied Biological Research, Guangzhou. The primary focus of his research there is the chewing lice of "babblers" and allies (Leiothrichidae, Paradoxornithidae, Pellorneidae, Timaliidae, Zosteropidae). This includes discovering and describing new species of lice, construction phylogenies of both hosts and lice, and examining the ecological and biological factors that limit host and geographical distributions of chewing lice in South China. For these projects, Dr. Gustafsson wants to catch and examine as many species of babblers as possible, including examining the same host species in different parts of its range under different environmental conditions (e.g. humidity, altitude, and temperature). As the chewing louse fauna of all of East Asia is poorly known, all groups of birds and their chewing lice are of interest. Eventually he aims to publish an updated checklist and identification key to all chewing lice known from Chinese birds.

(Zou Fasheng, Guangdong)

The conservation implications of mixed-species flocking in terrestrial birds, a globally-distributed species interaction network

Conservation biologists now view species interaction networks as systems that should be targets of conservation, but there are few actual cases in which networks have formed the basis for management strategies. Terrestrial mixed-species bird flocks (hereafter, TMSF) represent one such potential system: they form throughout the world, and in most cases have an asymmetric organization in which one or a few species play ‘nuclear’ roles, being particularly important for flock formation or maintenance. A quantitative study on the distribution of TMSF and how they respond to anthropogenic disturbance (AD) is still, however, needed. We surveyed 201 publications on terrestrial TMSF worldwide, finding that 19.2% of the world's bird species (2049 species) participate in them, including 158 threatened species (including 2 Critically Endangered species, 14 Endangered species, 37 Vulnerable species, and 105 Near Threatened), with tropical species dominating these lists. Of 31 TMSF studies that investigated AD, 22 showed significant declines in some metric, with TMSF in more impacted areas including 1/4 fewer species, and 1/3 fewer individuals. In 13/15 studies, TMSF were more sensitive to AD than the overall bird community. We conceptualized the reasons behind this response: first, AD directly influences drivers of flocking (predation, foraging), and second, AD produces changes in community composition that affect TMSF, such as when the extirpation or reduction of nuclear species affects other species' participation. We ranked nuclear species globally by their consistency of leadership and number of followers, suggested that these species' interactive roles be considered as part of their conservation value and that conserving TMSF provides an efficient mechanism to ensure the protection of many species simultaneously. This work was based on an international collaboration among scientists from Guangdong Institute of Applied Biological Resources, University of Florida, Universidad Nacional de Colombia sede Amazonia, Guangxi University, Sun Yat-sen University and is published in Biological Conservation.

(Zou Fasheng, Guangdong)

The effect of human disturbance on the sex ratio of Reeves’s Pheasant based on camera trapping

Camera trapping is suitable to monitor epigeous pheasants. Although the results based on camera trapping might not be the facts of population of the target species, the results should be suitable to be compared among the environment with a certain gradient. The intensity of human disturbance is one of the important factors to evaluate the quality of wildlife habitats. Reeves’s Pheasant (*Syrmaticus reevesii*) is a terrestrial forest bird. In this study, we selected three areas with different disturbance level as study sites: Liankangshan National Nature Reserve, Henan Province and Santan Scenic Area and Zhonghuashan Bird Nature Reserve, Hubei Province. The human disturbance in Liankangshan National Nature Reserve was the lowest and the highest in Santan Scenic Area. We used infrared cameras to investigate the sex ratio and compared among sites. The 25 cameras at Liankangshan National Nature Reserve photographed 136 times of males and 82 times of females; the 19 cameras at Santan Scenic Area captured 94 times of males and 27 times of females; the 23 cameras at the Zhhonghuashan Bird Nature Reserve recorded 79 times of males and 39 times of females. The results showed that the higher the proportion of male Reeves’s Pheasants was related to the greater human disturbance. .

(Hua Junqin and Xu Jiliang, Bejing)

Habitat-dependent changes in vigilance behaviour of Red-crowned Crane influenced by wildlife tourism

The Endangered Red-crowned Crane (*Grus japonensis*) is one of the most culturally iconic and sought after species by wildlife tourists. We investigate how the presence of tourists influence the vigilance behaviour of cranes foraging in Suaeda salsa salt marshes and S. salsa/Phragmites australis mosaic habitat in the Yellow River Delta, China. We found that both the frequency and duration of crane vigilance increased in the presence of wildlife tourists. Increased frequency in crane vigilance only occurred in the much taller *Suaeda salsa* and *Phragmites australis* mosaic vegetation whereas the duration of vigilance showed no difference between the two habitats. Crane vigilance declined with increasing distance from wildlife tourists in the two habitats, with a minimum distance of disturbance triggering a high degree of vigilance by cranes at 300 m. The presence of wildlife tourists may represent a form of disturbance to foraging cranes, but the effect is habitat dependent. Taller *P. australis* vegetation serves primarily as a visual obstruction to cranes, causing them to increase the frequency of vigilance behaviour. Our findings have important implications for the conservation of the migratory red-crowned crane population that winters in the Yellow River Delta and can help inform visitor management.

(Li Donglai, Sun Xinghai and Wan Dongmei, Liaoning; Liu Yu and Zhang Zhengwang, Beijing; Huw Lloyd, England; Zhu Shuyu and Zhang Shuyan, Shandong)

Inclusive fitness maintains altruism to coexist with non-altruism

Altruism has long puzzled evolutionary biologists ever since Darwin largely because of the paradox that individuals help others at the expense of their own fitness. Obviously, traditional evolutionary theory established by Darwin cannot solve this paradox as it emphasizes that competition among individuals is the evolutionary driver of phenotypes including social behaviors. British evolutionary biologist W.D. Hamilton successfully uncovered the mystery by proposing inclusive fitness theory. Hamilton used an elegant formula $rb > c$ to illustrate his theory — altruistic genotypes will spread against non-altruistic ones if the benefits to the recipients of an altruistic act b, weighted by the relatedness between the social partners r, exceed the costs to the altruists c.

However, Lu and his colleague argues that $rb > c$ only tells part of the story, namely how altruistic genotypes to expand. According to population genetics theory, they predict that altruistic genotypes can persist by coexisting stably with non-altruistic ones relying on $rb = c$, which may let the both genotypes have equal inclusive fitness. Using the data of 12 years of a study on the cooperatively breeding ground tits *Pseudopodoces humilis* endemic to the Tibetan plateau, they provide robust evidence for this prediction.

A major implication of the work is to offer a fundamental support for Hamilton's theory of inclusive fitness. More importantly, their finding highlights that the equal inclusive fitness principle mediated by $rb = c$ is a theoretically and realistically important mechanism to maintain the coexistence of different social polymorphisms.

This work was recently published in Proceedings of the National Academy of Sciences of the United States of America.

(Lu Xin, Wuhan)

Genetic evidence of hybridization of the world's most endangered tern, the Chinese Crested Tern *Thalasseus bernsteini*

We collected multi-locus data to test whether hybridization has occurred between a critically endangered waterbird, the Chinese Crested Tern (*Thalasseus bernsteini*), and the Greater Crested Tern (*Thalasseus bergii*). Phylogenetic analysis shows these two tern species are sister species, having diverged < 1 million years ago. Our findings suggest a grave threat to the survival of the Chinese Crested Tern, and illustrate the need for conservation managers to monitor further hybridization of this endangered tern species.

(Chen Guoling, Guangdong; Yang Jia, Zhejiang)

Are vocal characteristics related to leadership patterns in mixed-species bird flocks?

What structures the organization of mixed-species bird flocks, so that some ‘nuclear’ species lead the flocks, and others follow? Previous research has shown that species actively listen to each other, and that leaders are gregarious; such gregarious species tend to make contact calls and hence may be vocally conspicuous. We investigated whether vocal characteristics were associated with leadership, using a global dataset of mixed-species flock studies and recordings from sound archives. We first asked whether leaders were different from following or occasional species in flocks in the proportion of the recordings that contain calls (n = 58 flock studies, 145 species), and especially alarm calls (n = 111 species). We found that leaders tended to have a higher proportion of their vocalizations that were classied as calls than occasional species, and both leaders and following species had a higher proportion of their calls rated as alarms compared to occasional species. Next, we investigated the acoustic characteristics of flock participants’ calls, hypothesizing that leaders would make more calls, and have less silence on the recordings. We also hypothesized that leaders' calls would be simple acoustically, as contact calls tend to be, and thus similar to each other, as well as being detectable, in being low frequency and with high frequence bandwidth. The analysis (*n* = 45 species, 169 recordings) showed that only one of these predictions was supported: leading species were less often silent than following or occasional species. Unexpectedly, leaders' calls were less similar to each other than occasional species. The greater amount of information available and the greater variety of that information support the hypothesis that leadership in flocks is related to vocal communication. We highlight the use of sound archives to ask questions about behavioral and community ecology, while acknowledging some limitations of such studies.

(Emilio Pagani-Núñez, Guangzhou； Xia Xue, Guangxi & Yunnan)

Breeding ecology of Ural Owl in natural nest holes

Ural Owl (*Strix uralensis*) widely distributed in the Palaearctic coniferous forest, mixed coniferous broad-leaved forest. Ural owl is the top predator in the local forests and has a vital role for the regulation of the bird community structure. We studied the breeding ecology of Ural Owl in Yongji County, Jilin Province in 2014–2016. The results showed that the density of Ural Owl in the study area was 0.15 pairs/km^2 (18 pairs/117 km^2) on average in 2015, but the the highest density could reach 1.72 pairs/km^2 (7 pairs/4.08 km^2). The closest distance between two nests was only 559 m. Ural Owl's active defened territory radius was 358.8 m (*n* = 6) based on song playbacks. The main nest trees were *Salix pierotii* (69%) and *Quercus liaotungensis* (25%, Figure1). The most common nests were tree holes (82%), however, an old goshawk nest, a tree stump-nest and a ground-nest were found. The most common tree holes were up-opening (64%), followed by the side-opening (36%). Ural Owl preferred lower holes with larger opening and lager hole area.

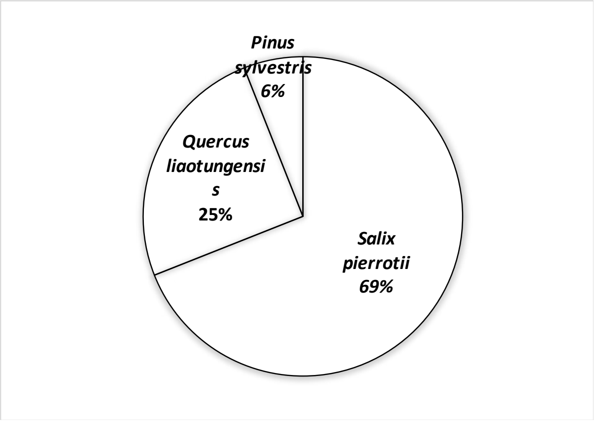


Figure 1. The proportion of nest tree species of Ural owl

Ural Owl laid eggs from March 14 - April 15, females produce one egg every 2-3 days and began to incubate after laying the first egg. The average clutch size was 2.94 (47/16, $n = 16$), the clutch size varied from 2-4. Eggs were white. The egg surface was rough with samll kicks. Eggs weighted 39.93 ± 0.72g ($n = 28$). The long diameter of the eggs was 48.09 ± 0.30 m ($n = 28$) and the short diameter was 40.01 ± 0.15 mm ($n = 28$). Females incubated the eggs, males defended territory and delivered food. Hatching date was April 23 - May 22. Hatchability rate was 61.7% (29/47, $n = 47$), the average number of nestlings was 1.81 (29/16), the average incubation duration was 32d ($n = 5$). No predation was detected during the incubation period,but egg picking by people,, weather conditions, and other unknown interference caused 38.5% (6/16, $n = 16$) reproductive failure. All reproductive failure occurredduring the incubation period. Hatchability rate by nest was 100% ($n = 29$), excluding failed nest; and the average number of nestlings was 2.9 (29/10). Chicks mortality rate was 10.3% (3/29, $n = 29$), with the nestlings surviving rate of 89.7% (26/29, $n = 29$), the average fledgling was 1.63 per nest (29/16, $n = 16$). The real fledgling rate was 2.6 (26/10, $n = 10$). Adult Birds brooded from April 23 - June 18, the chicks left nests from May 22 - June 19, the average age when nestling left the nest was 27.4 d ($n = 17$).

We found that the wrist carpal metacarpal distance to the wing tips, the headto beak, the wrist carpal metacarpal to the maximum length of the feathers when wing was folded, flight feathers, body mass, beak length, tarsus length followed linear growth pattenwith $R^2 > 0.9$. The R^2 of the distance from wing tip to the wrist carpal metacarpal distance reached 0.98. Flight feathers sheath, crude tarsus, tail sheath followed the logarithmic growth pattern, and the tail followed a non-linear growth curve with R^2 between 0.69-0.85, which was different from linear fit R^2 ($P < 0.05$) (Table 1). For the nests with clutch size greater than or equal to 3 birds, the average weight of the first hatched chicks was 411.3 ± 29.2 g, and was 365.4 ± 12.8 g of the last hatched chicks; they were not different ($U = 8.000$, $p = 0.421$). The average age of the fly was 26.8 ± 0.6 d, and 23.6 ± 1.5 d , respectively for these two group birds, and was not different ($U = 4.50$, $p = 0.09$).

The owls' food including Ussuri White-toothed Shrew (*Crocidura lasiura*), Grey Red-backed Vole (*Myodes rufocanus*), Korean Field Mouse (*Apodemus peninsulae*), Striped Field Mouse (*Apodemus agrarius*), Hazel Grouse (*Tetrastes bonasia*), Great Spotted Woodpecker *(Dendrocopos major*), and Red-tailed Thrush (*Turdus naumanni*).

Table 1. The average growth parameters of Ural Owl nestlings in different ages

Day	Wing length (mm)	Weight (g)	Head-beak length (mm)	Beak length (mm)	tarsus length (mm)	Crude tarsus (mm)	Tail sheath (mm)	Tail (mm)	Flight feather sheat (mm)	Flight feather (mm)
1	14.77	29.4	34.38	15.55	14.04	2.76				
2	15.92	28.8	33.97	15.65	14.13	2.35				
3	17.93	41.9	35.93	17.01	15.81	2.99				
4	19.67	63.0	38.93	18.04	18.72	3.83				
5	20.06	60.3	38.50	18.58	16.08	3.34				
6	23.23	83.8	42.36	20.88	19.92	4.40				
7	24.92	101.4	42.92	20.88	22.06	4.62				
8	26.45	112.9	44.33	22.05	21.05	4.48			3.48	
9	31.35	162.5	48.12	23.08	26.08	5.59	2.06		7.86	
10	31.26	141.5	46.11	23.54	23.47	4.93			5.12	
11	34.84	192.0	50.33	23.86	28.85	6.05	1.65		15.94	
12	36.65	215.0	52.66	24.38	28.46	6.07	2.04		14.17	
13	41.31	214.9	52.45	25.99	30.84	6.21			21.55	
14	45.64	273.3	56.10	25.94	33.66	7.20	6.80		27.06	33.49
15	43.61	248.4	55.53	25.94	33.48	6.27	2.72		26.58	35.20
16	48.62	284.0	58.02	27.31	35.54	6.95	3.52		31.65	44.56
17	50.66	299.9	58.41	27.89	34.95	6.40	2.14		34.44	41.81
18	55.06	348.2	61.31	28.30	37.50	7.38	5.11		40.64	58.32
19	53.13	326.4	59.67	28.27	35.13	6.54	2.72	6.30	37.68	48.28
20	57.41	386.8	63.03	29.21	36.36	7.15	7.24	7.95	44.85	68.55
21	58.58	357.2	63.88	29.47	38.07	6.92	9.17	9.93	45.73	66.93
22	62.11	357.9	64.00	30.12	39.22	6.59	10.83	18.57	45.65	73.59
23	67.34	365.9	65.98	30.65	39.88	6.75	11.95	18.33	50.63	83.11
24	66.40	408.3	65.85	30.37	40.25	7.36	13.77	21.68	48.05	88.49
25	69.07	360.4	66.97	30.41	40.41	6.40	18.09	27.22	43.70	95.36
26	70.19	412.9	66.98	31.37	42.38	6.80	19.50	29.49	48.94	99.06
27	70.51	381.3	68.69	30.67	41.07	6.90	19.00	27.67	45.36	100.10
28	74.21	420.3	69.10	31.72	41.40	7.04	24.11	39.64	44.19	108.85
29		395.0		32.63	40.27	5.85	23.41	34.73	47.52	108.32
30	72.30	408.0	71.22	32.94	40.41	7.16	23.37	41.97	41.63	120.01

(Wenhong Deng, Beijing)

Glossy Ibis (*Plegadis falcinellus*) found in Mujiu Lake, Tibet

On June 26th at Mujiu Lake (31°00′19″N，89°4′7.6″E, ASL 4673 m), Shenzha County, Tibet, we found a medium sized wader with dark plumage, resting half-hidden in vegetation. The following day the bird was found again several hundred meters from its previous location and filmed. The body length of the bird was approximately 60 cm, pale colored bill was long and curved downward, streaked white at its base. Plumage from head to upper back was thick chestnut, glinting with crimson, rest part of the body was blackish with green metallic luster. Feet were dark

(Fig. 1). We identified the bird as Glossy ibis (*Plegadis falcinellus*), within the Threskiornithidae family, Pelecaniformes order. When found, the ibis was foraging among emergent aquatic plants, and was vigilant of human approach. Its wing beat was vigorous, interrupted by intervals of hawk-like gliding. Other birds, including *Grus nigricollis*, *Anser indicus* and *Sterna hirundo* were also observed at the habitat.

Fig. 1 *Plegadis falcinellus*

Glossy ibiss breeds globally (www.hbw.com) exception in Antarctica, with even greater migration distribution. In China, the species's vagrant ranges is from East to Southwest China and Xinjiang (Zheng 2017), no confirmed record was reported in Tibet. Our discovery of this species solidifies its distribution at Tibet plateau above 15331 ft, and suggest wetlands rich in vegetation may be utilized as breeding area in north Tibet.

(Yang Le, Liu Sishan, Gao Yi and Yixiduoji, Tibet)

Research advances of Galliformes since 1990 and future prospects

Galliformes are widely distributed throughout the world and economically important to humans as domesticated animals or gamebirds. They are at a unique position for advancing knowledge and techniques of wildlife conservation as the barometer of the status of applied ecology. Populations of many galliform species have declined mainly due to habitat loss and over-hunting. An assessment of knowledge of galliformes could help to provide guidelines for future research and conservation strategies.

Using the Web of Science search engine, we conducted a literature review of galliform-related articles published from 1990 to 2016. We used the "research area" option to filter articles focused on the zoology, environmental sciences ecology, biodiversity conservation, forestry, behavioral sciences, reproductive biology, biochemistry molecular biology, cell biology, genetics heredity, evolutionary biology, physiology and developmental biology. We then checked duplication based on the title, abstract and full text. In addition, we examined the reference lists of selected studies to include related reviews and analyses.

We retained 1874 articles related to the galliformes from the initial 243,128 publications. About 91.4% focused on one or two species, and 85.0% were conducted within a short duration, typically one to two years. The majority of the articles concentrated on macroscopic ecology (55.5%), mainly focusing on habitat selection or habitat use. With recent advances of molecular biology, the studies of taxonomy and phylogenetic rose quickly in last two decades. The study of physiology and biochemistry was no longer limited to simple description but expanded to the mechanisms of phenotype and micro-evolutionary potential. An additional area receiving increasing attention is the conservation of galliformes, with the assessment of the conservation status and conservation management effectiveness of galliformes (e.g. species diversity and genetic diversity) becoming the focus.

The studies on galliformes have made great achievements since 1990, but there are still gaps, particularly in macroscopic ecology, molecular genetics, and conservation. There is an urgent need to enhance long-term monitoring and analysis of population dynamics, and applying different disciplines to galliform conservation. Moreover, life history information of many galliform species is still lacking, which has hindered conservation efforts and effectiveness. In addition, multidiscipline studies and new technologies are not common for galliform studies, and should be encouraged.

(Tian Shan, Xu Jiliang, Li Jianqiang and Zhang Zhengwang, Beijing; Wang Yong, USA)

Ph.D Thesis

Bioaccumulation of environmental heavy metals in tree sparrow via food and its exposure risk assessment

Heavy metals are introduced to soil, water and atmosphere via industry, agriculture and people's daily life, influencing animals and plants in such polluted environment in varied degrees. Birds, an important part of ecosystem, are vital to maintain the balance of ecosystem. However, environmental heavy metals could enter and accumulate in different parts of birds via soil, water and food. Excessive heavy metals will bring some adverse effects to birds, including limitations of their growth, development, reproduction or even survival. To provide suggestions for establishing thresholds of heavy metal exposure risks to birds, tree sparrow *(Passer montanus*), a passerine widely spread over Eurasia, was chosen as study subject fr this study, and Liangzhuang village in Baiyin District (BY, a mineral resources depleted city in China) was chosen as the heavy metal polluted sample area, Weichuan Village in Liujiaxia District (LJX, a relative unpolluted scenic spot in China) as the control, to investigate copper (Cu), zinc (Zn), lead (Pb) and cadmium (Cd) accumulations in adult tree sparrows and their exposure risks to tree sparrow nestlings, juveniles and adults.

The main results are shown as follows:

1. Heavy metal concentrations in soils and waters of LJX and BY. Heavy metal concentrations in soils and waters in two areas were determined because heavy metals can be consumed by birds via soils and waters. Concentrations of Cd in soils from BY surpassed the threshold of environmental quality standards for soils (GB 15618-1995) indicating a moderate pollution, while Cu, Zn and Pb concentrations in soils from BY were below the thresholds. Lead and Cd concentrations in water from BY surpassed the thresholds of standards for drinking water (GB 5749-2006) while Cu and Zn concentrations were below the thresholds. Heavy metal concentrations in both soils and water from LJX were below the thresholds. Higher heavy metal concentrations were found in soils and water from BY compared to those from LJX ($p < 0.01$), indicating LJX can be a control sample area.

2. Body parameters of tree sparrow juveniles and adults from LJX and BY. For juveniles and adults, there was no significant difference between LJX and BY for body weights, body lengths, tail lengths, wing lengths, tarsus lengths and beak lengths ($p > 0.05$), indicating there is no significant effect of heavy metal pollution on body parameters of tree sparrow juveniles and adults from BY.

3. Heavy metal concentrations in different parts and faeces of tree sparrow adults from LJX and

BY. High heavy metal concentrations were found in primary feather, tail feather, breast feather and back feather of tree sparrow adult. Zinc and Pb were found in tarsometatarsu with high concentrations. High heavy metal concentrations were found in liver, kidney and faece, while low concentrations were found in muscle and blood. Heavy metal concentrations in primary feather, blood and faece of tree sparrow adult from BY were higher than those from LJX ($p < 0.05$), so they can be indicators of heavy metal pollution.

4. Diet compositions of tree sparrow nestlings, juveniles and adults. SIAR was employed to investigate diet compositions of tree sparrows from both LJX and BY. For nestlings, non-phytophagous invertebrates (nph-in) had the biggest contribution to diet compositions, while maize and C4 plants belonging to Gramineae (C4-Gra) contributed lowest. With few exceptions, maize had the biggest contribution to diet compositions of juveniles and adults. Nestlings from both LJX and BY consumed animal food most, while juveniles and adults consumed plant food most.

5. Heavy metal concentrations in food of tree sparrows from both LJX and BY. Highest heavy metal concentrations were found in nph-in among different food sources, while the lowest were found in maize. With few exceptions, food sources from BY were found with higher heavy metal concentrations than those from LJX ($p < 0.05$). Food of nestlings had the highest average heavy metal concentrations (AC values) followed by food of adult (summer). Tree sparrows from BY had higher AC values than those from LJX, indicating tree sparrows from BY consumed more heavy metals.

6. Biomagnification of heavy metals from food to tree sparrows. With few exceptions, biomagnification factors (BMF values) were all above 1.0, indicating a biomagnification of heavy metals from food to tree sparrows. Lead concentrations were biomagnified by 2.29 to 7.08 times with the highest biomagnification. A significant linear relationship was found between heavy metal concentrations and $\delta^{15}N$ values of tree sparrows' food and primary feathers from LJX and BY ($R^2 \geq 0.33$, $p < 0.05$). Moreover, trophic magnification factors (TMF values) of heavy metals were all above 1.0, indicating a biomagnification of heavy metals as the trophic level increased. In a word, Cu, Zn, Pb and Cd concentrations were found biomagnified from foods to tree sparrows from LJX and BY, and they increased with the trophic levels.

7. Heavy metal intake levels of tree sparrows from LJX and BY. Nestlings had the highest heavy metal daily intake (MDI values) and heavy metal daily intake per unit of body weight (MDIBW values) followed by adult (summer). MDI and MDIBW values of juveniles and adult (winter) were comparable. MDI and MDIBW values of tree sparrows from BY were higher than those from LJX ($p < 0.05$), indicating heavy metal pollution can increase the exposure levels of heavy metals.

Besides, different food sources had different contributions to MDI values. Invertebrates were found positively correlated with MDI values, while crops showed the opposite trend. Heavy metal intake levels of nestlings, juveniles and adults of tree sparrow from BY were higher than those from LJX, and nestlings had the highest intake levels among tree sparrows at different life stages.

8. Exposure levels and risks of tree sparrows. Exposure level (EL value), hazard quotient (HQ value) and hazard index (HI value) of tree sparrows via soil, water and food were calculated, we found that nestlings had the highest values followed by adult (summer), while juveniles and adult (winter) had the comparable values. For tree sparrow nestlings, juveniles and adults from both LJX and BY, HQ and HI values of Zn and Pb were above 3.0, indicating a high risk to tree sparrows. In addition, EL, HQ and HI values of BY were higher than those of LJX ($p < 0.05$). In a word, exposure levels and risks of tree sparrows from BY were higher than those from LJX and nestlings had high exposure risks.

In conclusion, Cu, Zn, Pb and Cd concentrations of primary feathers, blood and faeces of tree sparrow from BY were higher than those from LJX, indicating they can be indicators for biological effects of long-term heavy metal pollution. Nestlings consumed invertebrates most, while juveniles and adults consumed crops and grass seeds more often. Invertebrates had higher concentrations than crops and grass seeds, so nestlings had higher MDI values and exposure risks than juveniles and adults. Copper, Zn, Pb and Cd concentrations of soil, water and food from BY were higher than those from LJX. Higher exposure risks were found to tree sparrows from BY than those from LJX. In addition, there was an obvious biomagnification of heavy metals from food to tree sparrows, indicating there is a significant biomagnification effect of heavy metals from food to tree sparrows which aggravates the exposure risks of tree sparrows, even if they live in the habitats with low environmental heavy metal concentrations for a long time.

(Ai Shiwei and Zhang Yingmei, Gansu)

A new insight into the classification of dusky thrush complex: bearings on the phylogenetic relationships within the Turdidae

Dusky thrush complex comprises of two sister species breeding in SC Siberia, which is the member of thrush Turdus from Turdidae. The phylogenetic resolution of Dusky Thrush complex remains controversial, and a detailed research is still necessary. In this research, we determined the complete mtDNAs of both species, and estimated phylogenetic trees based on the mtDNA alignment of these and 21 other Turdidae species, to clarify the taxa status of the Dusky Thrush complex. The squenced lengths of these three mitochondrial genomes were 16,737, 16,788 and 16,750 bp. The mtDNAs are circular molecules, containing the 37 typical genes, with an identical gene order and arrangement as those of other Turdidae. The ATG and TAA, respectively, are observed the most commonly start and stop codon. Most of the tRNA could be folded into the canonical cloverleaf secondary structure except for tRNASer (AGY) and tRNALeu (CUN), which lose 'DHU' arm. The control region presented a higher A+T content than the average value for the whole mitogenome. The phylogenetic trees reconstructed by the concatenated nucleotide sequences of mtDNA genes (Cyt b, ND2 and COI) indicate the Dusky Thrush complex cannot be divided into two species, but the relationships between Dusky thrush subspecies still need additional study. This study improves our understanding of mitogenomic structure and evolution of the Dusky Thrush complex, which can provide further insights into our understanding of phylogeny and taxonomy in Turdidae.

(Dong Yuanqiu, Li Bo and Zhou Lizhi, Anhui)

Does DNA barcoding gap exist in the Passerine birds of East Asia?

The taxonomy is fundamental to the biological science. Only when we have the full knowledge of how to identify the species correctly, could biological research be carried out properly. Accurate and rapid identification of species has become a hot topic in the taxonomy community for years. DNA barcoding technique, as a new method for rapid identification for biological species, has been widely used since 2003. Ideal barcodes are standardized DNA sequences, sufficiently variable, and easily amplified. For birds, the study on 260 species of North American suggested a 648 bp region of cytochrome c oxidase I (CO1) in the mitochondrial DNA (mtDNA), might serve as DNA barcode for birds. Nevertheless, birds of East Asia and North American have very different evolutionary history. Whether the "standardized DNA barcode" generated from North America, could also work for the birds in East Asian, is a question worth exploring.

The passerine birds are rich in species, accounting for more than half of the whole number of bird species. The group is an important part of the world's wildlife resources and for the protection of global biodiversity. Many comprehensive studies have been conducted on the breeding, singing, ecology, and behavior of passerine birds. However, due to the large number of species, the differences in the morphology of some species are small, passerine birds are often difficult to identify. The morphological variation is significant. Therefore, the species identification, taxonomic status, and phylogenetic relationships of many birds in the passerine form have attracted much attention and have caused much controversy. Therefore, it is of great significance to explore whether DNA barcodes can be used for species identification of passerine birds in East Asia. The research aims to answer two questions: 1) does the barcoding gap exists in birds of east Asia? 2) how reliable is the DNA barcodes used to identify the bird species in east Asia?

We chose Passeriformes as the subjects of study. Bardcode sequences were explored and selected from NCBI (www.ncbi.nlm.nih.gov) and BOLD (www.barcodinglife.org), and additional samples were sequenced in our lab. All the sequences were analyzed on the interspecific and intraspecific category to calculate the genetic divergence at different taxonomic levels.

We collected 4,525 barcode sequences of 427 species, belonging to 156 genus, 48 families. Moreover, 275 new barcode sequences were added to the database, involving 72 species in 52 genus, 19 families. Results showed that the mean intraspecific genetic divergence was 1.355%, variation range was 0-17.5%, 77.8% of the distances was below 2%. However, the mean interspecific genetic divergence was 10.557% with a range between 0 and 18.8%, 92.2% of the genetic distances were from 5-16%. The barcode differences between species were, on average, 7.79 times higher than that of the differences within species.

Barcoding gap does not exist in Passeriformes of East Asia. The "Barcoding gap" is an artifact of insufficient sampling across taxa. Compared with North American results, interspecific and intraspecific CO1 distances in Passeriformes of East Asia are greater which is consistent with the evolution history of birds in East Asia. Due to the different evolutionary history, the thresholds that apply to North America could not be applied to the identification of passerine birds in East Asia. We propose a threshold of 4.9%. Under this threshold, the identification success rate of birds in East Asia is the highest, 94.2%. We suggest that DNA barcoding can be used to identify most species of the Passeriformes of East Asia, but not for recently diverged species. The intraspecific distance of birds in East Asia is much higher than that of birds in North America. The pattern suggests that the protection of birds in East Asia should not only focus on the protection of species, but also on the geographic populations.

(Chen Xi and Luo Xu, Yunnan)

Nest site selection and its implications for conservation of the threatened Oriental White Stork (*Ciconia boyciana*) in the Yellow River Delta, China

Avian nest selection is crucial for understanding the breeding adaptability and implementing the conservation of threatened birds. We investigated the population dynamics, nest and breeding habitat selection, offspring numbers and reproductive success of oriental white storks from February to June 2017 in the Yellow River Delta National Reserve (YRD NNR), Shandong, China. We measured the variables of 32 randomly selected control plots and 62 nest plots, including 40 power pole nests, 14 artificial nests and 8 pylon nests. We used conditional logistic regression with model-averaging and PCA to quantify variables affecting nest site selection. Our results showed that density of the electric power transmission line and human disturbance were two main negative factors affecting oriental nest selection of white stocks using power poles as nest location. Meanwhile, distance from the highway and the suitable foraging habitat were the most important variables in the selection of artificial nest. Distances from the nearest conspecific nest and from sightseeing sites were the main variablescontributed to selection of pylon nest. PCA revealed that vegetation and disturbance were factors that influenced nest height selection. We recommend reducing human disturbance in nest site area and recovering wetland vegetation for suitable habitat and nest sites to promote conservation of this species.

(Cheng Lei and Zhou Lizhi, Anhui)

The effects of human activities on diurnal energy expenditure of Tundra Swan (*Cygnus columbianus*) foraging in paddy field during the late wintering period

Energy expenditure strategy of birds with human disturbance is interesting because of potential effect on birds' fitness, influenced by daily activities budget and habitats characteristics of birds. Paddy field is becoming important habitat for waterbirds over the world, adjust energetic response to human disturbrance is important for migratory waterbirds inhabiting this habitat. To better understand the energy expenditure in disturbed environmental conditions, using Tundra Swan (*Cygnus columbianus*) wintering in a paddy field of Shengjin Lake, China, we employed a focal sampling approach to record their responses and calculate the diurnal energy expenditure (DEE). The percent of time being vigilant and its energetic cost ($P_{\text{alerting time}} = 0.00$, $P_{\text{energetic cost}} = 0.00$), vigilance bout and frequency ($P_{\text{vigilance bout}}=0.03$, $P_{\text{vigilance frequency}} = 0.00$), swimming frequency ($P = 0.04$) under the human disturbance were significant longer than that under the undisturbed situation. The energetic costs of alert increased with the interference time and decreased with interference distance. Due to disturbance reduced high-cost feeding and increased low-cost alerting, the DEE of swans under disturbrance was less than that under undisturbed condition ($t = -2.22$， $P = 0.04$).

(Yu Chao Zhou Lizhi and Song Yunwei, Anhui)

Range-wide phylogeography of the Common Pheasant (*Phasianus colchicus*) in continental Asia

The Common Pheasant is an exemplary species with a large geographical range in the Palearctic region and prominent intra-specific divergence in plumage patterns and coloration. Thirty recognized subspecies categorized into five subspecies groups have been defined mainly on the basis of biogeography and morphology. The phenotypic variation is widespread in populations in the Asian continent. The species also has a long history of captivity and being introduced as a common game species in Western Europe, North America and Australia.

To build a comprehensive understanding of the phylogeography of the common pheasant, we increased sampling coverage (102 locations) from East Asia to Mid- and West Asia to test the regional lineage diversifications and demographic dynamics in response to past climatic oscillations across the Asian continent. We sequenced a set of neutral genetic markers including seven introns and two mitochondrial loci, and genotyped 13 autosomal microsatellites derived from 278 individual covering 22 known subspecies. We used RAD-seq approach based on the next generation sequencing to generate genome-wide single nucleotide polymorphisms (SNPs) from 110 individuals, covering 9 relevant subspecies or populations in China.

Our results showed that populations within common pheasants were highly structured, corresponding to seven evolutionary linages with major splits located through Asian monsoon and continental climatic zones: Hengduan Mountain linage, from Southeast of Qinghai-Tibet Plateau, was the basal clade consisted of P.c.elegans, diverging from 1.35mya. Common pheasants from East Asia formed the largest clades, diverged into two linages at around 0.7mya, Eastern East-Asian group and Central East-Asian group. Tarim group from Tarim Basin and Kirghiz group from Kazakhstan and Xinjiang were two monophyletic clades, sister to common pheasants from Central Asia (Central Asian group and Caucasus group, diverging since about 0.7-1 mya). The results of Extended Bayesian Skyline Plot suggested that during the dispersal process, five groups of common pheasant underwent a recent population and range expansion, apart from Kirghiz group and Tarimensis group with stable population size. Populations from Qinghai, Gansu, Mongolia and Hengduan Mountain were isolated by multiple geographical barriers, such as mountains, deserts or water bodies. However we did find evidence of population admixture occurring among continuous and contiguous populations in Eastern East Asian pheasants. Migration rates from Eastern to Central East Asia was significant.

According to the divergence time and spread routes, we inferred common pheasants originated from subtropical forests of Southwest China and dispersed from early Pleistocene. The uplift of Qinghai-Tibet Plateau formed the arid regions in Asian continent as well as monsoon areas in East Asia and South Asia, which led to climatic vicariance, resulting in reduction of gene flow. Patchy distributions in Central Asia caused by Caucasus Mountains and expansion of deserts contributed to divergence of inland populations. Our study highlighted both historical geographical events and climatic changes in continental Asia strongly influenced geographical distribution patterns, genetic diversity and demographic of common pheasants.

（Liu Simin and Liu Yang, Guangdong）

Continental island effect of the Sichuan Basin—based on morphological variation and genetic structure of the tree sparrow

To test the continental island effect in the Sichuan Basin, the morphological characteristics and genetic structure of the tree sparrow (*Passer montanus*) inside and outside the Sichuan Basin was studied.

We collected 7 morphological characteristics of 558 tree sparrow samples in Sichuan Basin and surrounding areas. The samples were divided into 3 groups based on different altitudes: Sichuan Basin (219-725 m), Central China Plain (46-784 m) and mountains surrounding outside of Sichuan Basin (807-4472 m). The results indicated that the body mass, wing length, tail length and tarsus length were extreme significantly different ($P < 0.01$), while the body mass was greater in mountains surrounding outside of Sichuan Basin than those of Sichuan Basin and Central China Plain (ANOVA $P < 0.05$ or $P < 0.01$). However, no difference in body mass, body length, tail length, tarsus length, culmen length and rictus was observed between Sichuan Basin and Central China Plain ($P > 0.05$). The body size increased with the increase of altitude, which indicated that the morphology variation was correlated with altitude, and was consistent with Bergman's rule.

Using mitochondrial genes (12srRNA, Cytb, Dloop, COI) and nuclear gene (Myo) of the tree sparrows of 172 individuals in 29 geographical populations. The population dynamics and genetic structure inside and outside the Sichuan Basin were obtained based on nucleotide diversity, genetic distance, phylogenetic tree and haplotype net map. The main results as follows:

(1) Most of populations showed lower genetic diversity ($Pi < 0.01$). The overall genetic diversity displayed an increasing trend from the Sichuan Basin to the surrounding mountainous (Western Sichuan Plateau and Yunnan-Guizhou Plateau).
(2) The genetic variation mainly comes from the mountain population around the basin. There were gene exchange between the populations in the basin and the outside the basin.
(3) The population was expanded from the basin outwards the northwest of the Sichuan Basin.

Based on the above results, we concluded that mountains surrounding the Sichuan Basin created certain isolation to the tree sparrows between inside and outside the basin. It indicated that the continental island effect was occurred in the Sichuan Basin to some extent.

(Zhao Wenhai, Liu Fangqin and Wen Longying, Sichuan)

Drivers of waterbird communities and their declines on Yangtze River floodplain lakes

The seasonally flooded Yangtze Valley Floodplain wetlands of China are globally important for wintering waterbirds in the East Asian-Australasian Flyway. These birds have declined in the last 60 years; understanding factors shaping waterbird distribution and abundance patterns is critical for their conservation. We applied linear mixed models to investigate the effects of climate, winter water area and inundation area (the difference between maximum flooded and winter dry season water area) on waterbird abundance and diversity at 72 lakes of 2005 and 2016. Neither winter water area nor climate featured was selected for the the best models, rather inundation area was the key determinant of waterbird abundance and diversity. Future water abstraction and land claim will therefore have greater impacts on waterbird abundance and diversity than likely climate change effects. Significant declines in waterbird abundance and diversity between 2005 and 2016 were not explained by variables in the models, and there was no reduction in wetland inundation areas to explain these declines, confirming other factors might be responsible for. These factors potentially include declining wetland quality affecting carrying capacity (e.g. flooding phenology, disturbance, habitat loss and degradation, declining water quality caused by eutrophication and pollution) and/or factors limiting migratory waterbird populations at other stages in their life cycle elsewhere. The Yangtze lakes in this study are amongst the best for wintering waterbirds; and many are protected for their biodiversity, suggesting such protection cannot fully safeguard these internationally shared populations when threatened by other, currently unknown factors. This confirms the urgent need for more research to safeguard these ephemeral lake systems for their global biodiversity significance.

(Qiang Jia, Xin Wang, Lei Cao, Beijing; Yong Zhang, Jiangsu; Anthony David Fox, Denmark)

Comparison of counteradatations in four sympatric host species to defense against cuckoo parasitism

This study investigated the characteristics of life-history and anti-parasitic strategies in four sympatric host species of common cuckoos (*Cuculus canorus*), namely Oriental reed warbler (*Acrocephalus orientalis*), blunt-winged warbler (*Acrocephalus concinens*), reed parrotbill (*Paradoxornis heudei*) and vinous-throated parrotbill (*Sinosuthora webbiana*), to explore the co-evolutionary interactions between cuckoos and their hosts. The main results and conclusions are as follows:

The four sympatric hosts breed within the same reeds, they differed in breeding phenology and nest-site microenvironment. Floods had disastrous effects on breeding birds, and reed parrotbills demonstrated behavioral plasticity in nest-site choice. The main factors that affected breeding success of four breeding species were nest predation and bad weather; cuckoo parasitism was also an important factor reducing breeding success of Oriental reed warblers. There was no significant variation of parasitism rate between two years for different hosts, but the parasitism rate of different hosts was distinct which could not completely support for the habitat imprinting hypothesis. All the four hosts had egg recognition ability suggesting a coevolution between them and cuckoos. Both Oriental reed warbler and vinous-throated parrotbill could reject the experimental eggs up to 100%, but the rest two hosts only have intermediate egg recognition ability. The attack rate of Oriental reed warblers against common cuckoos was 100% and neighboring individuals participated in up to 87.1% of such attacks indicating social defense behavior. Cooperative defense probably evolved in Oriental reed warblers as an anti-parasitic strategy through long-term coevolution with common cuckoos, which could reduce parasitism risk effectively for aggressive host.

(Ma Laikun and Liang Wei, Hainan)

On the correlation between bird diversity and cuckoo diversity

In recent years, the common cuckoo (*Cuculus canorus*) as a reliable indicator of bird diversity has become a research hotspot. However, most previous studies focused on Europe system where there are only two cuckoo species, while there were 17 species of parasitic cuckoo species in China. The present study investigated the correlation between bird diversity and cuckoo diversity, and focused on the effective indicators of the cuckoos for bird diversity in China. The species of cuckoos in all surveyed sites decreased gradually from south to north. Homogenization of forest bird species was higher than that of urban bird species at small scale, while on large scale the homogenization of urban bird species was higher than that of forest bird species. The species number and dispersion, Shannon-Weiner index, and evenness index of urban birds were lower than those of forest birds, indicating that the species richness of urban birds was more conservative than that of forest birds. The average bird diversity of the samples with cuckoos was higher than that of the samples without cuckoos. The average bird diversity of the area with cuckoo occurance was higher than that of the area without. There was a significant positive correlation between the bird diversity and the abundance and richness of cuckoos.

(Zhou Bo and Liang Wei, Hainan)

Studies of vocal evolution and species divergence in Cettiidae and *Cuculus canorus*

Songs and calls are important means of communication in birds, the richenss of vocal diversity is a representation of and an important part of avian diversity. The evolution of vocalization could occur at different levels such as individuals, populations and species. In the mean time, many factors may affect song evolution, such as natural seltion, sexual selection, cultural drift, evolutionary history, and interactions among species. It is benefitial to study vocal evolution at different scales and with different factors and in different systems to gain a more comprehensive understanding of vocal evolution. Birds use songs and calls as important cues of species recognition, therefore vocalization serves as an important mechanism of reproductive isolation between avian species. Acoustic data along with gentic and morphological data could be used to study integrative taxonmony and delimit species boundary, and gain more understanding of species divergence process and species diversity in the nature. In the current study, we seek to understand the song evolution in Cettiidae both in phylogenetic and population scales across a large geographical distribution. We discussed level of divergence and species status of taxa in the Browinish-flanked Bush Warbler Horornis fortipes complex. Apart from passerines systems, we also studied vocal divergence in a non-passerine common cuckoo (*Cuculus canorus*). The main finding and conclusion of our studies are as follows:

1. we studied evolutionary trajectrory of song frequency and song length of Cettiidae, and factors that might affect song evolution in this group. We studied associtations between song of Cettiidae and ecological factors such as body size, breeding latitude as well as migration status, and try to understand the evolution origin of the association, using a Cettiidae phylogeny. We found that the song frequency was negatively correlated with body size, and song length increased with latitude. This was consistent with some other studies. In the mean time, we also found that the accosiation between song length and latitude existed only in the nonmigrators but was absent in the migrators. We confirmed that it was breeding latitude, not migration, affected song length. We also found that the associtation between song frequency and body size arised early, and they were more evolutionary conservative. On the other hand, the correlation between song length and latitude arose later in the evolution and both variables were more labile. We infered that the associaiton between song length and latitude was driven by the association between sexual seletion and latitude.

2. There are many studies that addressed the factors that might affect evolution of song repertoire size and song verse complexity. We hypothesized that the repertoire size and song verse complexity should be a trade-off between the two because of the limited learning ability, and such association should result in a negative correlation between these two factors in a geographical scale. We sampled most part of the distribution of *Horornis fortipes* and tested this hypothesis. We found that the reportorie size had an increasing trend from west to east, while the song verse complexity had an opposite trend. The two variables showed a negative correlation geographically. With Mantel test and partial Mantel test, we ruled out the effect of special auto correlation and other confounding factors such as climate. Our results indicated that there was

a trade-off between repertoire size and song verse complexity, and the association drived the geographical pattern. The study offered some new insight into song evolution.

3. Species is a basic unit in many areas of biological study, thefore studies of species limits are the underlining foundation of related research. However, because the lack of study, the species diversity in Asia, especially in species-rich Sino-Himalayas area, could be underestimated. Previous studies have hintet that there may be multiple independent species in Horornis fortipes complex. However, previous studies offered limited evidence as their samples sizes were relatives small. In the current study, we did a relative comprehensive sampling, and we used multiple genetic methods, especially with multiple species coalescent method to test the species limit of *Horornis fortipes*, a wide spread species complex in Asia. We also analysed the song and morphometric difference to see if there was any diagnosable difference which might further support the species limit. The genetic analysis comformed that there were at least three independent evolutionary lineages in the complex. We also found that the song and morphometric difference were small among taxa. We concluded that the lineages in the *Horornis fortipes* complex were incipient species, in the early stage of species divergence. We argue that there may be more unrecognized species diversity in Sino-Himalayan region, and further studies are needed.

4. The geographical variation of calls of common cuckoo *Cuculus canorus* has not been studied in a continental scale. In the current study, we studied geographical variation of common cuckoos across Eurasia.We discussed potential impact of factors such as isolation by distance, subspecies divergence, climate and altitude on cuckoo vocal variation. We found that common cuckoos differed in calls. The calls of subtelphonus had higher frequency than that of other subspecies and had high classification sucess. We also found that vocal difference was associated with geographical distance, but not with climate or altitude. We also confirmed that the calls of common cuckoos in central China varied by among habitats. We conclude that isolation by distance and subspecies divergence are the main reason for call divergence in large geographical scale, while in the smaller scale, habitat difference plays an important role.

(Wei Chentao, Zhang Yanyun and Trevor Price, Beijing)

The role of personality in sexual selection, parental care and nest-site selection of Chestnut Thrush

In recent years, with the increased interest of adaptive individual differences within a single population, animal personality has become one of the most active research areas in animal behavior. Animal personality is the consistent behaviours that vary among individuals of the same species over time and across contexts. Personality traits linked to a range of life history traits can have important fitness consequences and may therefore be subject to natural and sexual selection.

We used simple cage and handling stress tests to examine the personality traits of a wild Chestnut Thrush (*Turdus rubrocanus*) population in the Lianhuashan Natural Reserve during the breeding seasons 2015–2016. We found that individuals differed consistently in their activity and breathing rate, but not in neophobia over time. Boldness was correlated with activeness, which suggested that activity and boldness were two personality traits in this population. In addition, Chestnut Thrush mated preferentially with a partner of similar boldness.

There was no correlation between provisioning rate and boldness of parents. However the mating pairs with more similar boldness had higher provision rates and raised their offspring better (i.e., with higher weights) than pairs with dissimilar boldness. Under the nature condition, assortative mating based on boldness modulated the conflict over parental care, as those parents with similar boldness would also have similar provision rates. In the parent removal experiment, males always reduced their parental care, while females showed divergent decisions depending on the boldness similarity with her partner. Females compensated through provisioning more frequently and providing better quality food items within pairs of similar boldness, but reduced their parental care investment within non-similar pairs.

Degree of horizontal concealment, cover of plant, distance to the road and distance to the farmland were the main factor in nest-site selection of Chestnut Thrush. Bold females tended to choose nest-sites with more horizontal concealment and in the area with lower nest density. The patterns of nest distribution, affected by personality, varied between years, these differences might be caused by the fluctuation of food resource. In 2015, the nest-site of Chestnut Thrush assorted by boldness during the breeding season. Bold females in low nest density area had higher rate of nest success, while shy females in high nest density area had higher rate of nest success. However, the nest-site of Chestnut Thrush did not assort by boldness in 2016. Bold females in high nest density area had higher nest success, and shy females in low nest density area had higher nest success.

(Lou Yingqiang and Sun Yuehua, Beijing)

Annoucements

VII International Conference on Black Stork

The feasibility to organize the VII International Conference on Black Stork at Donana National Park (Andalusia Region, Spain) from 28th to 30th November 2018 with the support of the Biological Station of Donana and Region of Andalusia has been explored.

The Biological Station of Donana would facilitate accommodation for 25 participants as well as conference room. The Station will try to arrange the conference room for a maximun of 30 people.

The cost for the registration is estimated to be around 40-50 Euros for the whole conference with the arrangement of a simple meals, transportation, etc. Hopefully this fee would be affordable for everybody. The organizer is very interested in having participants from China; applicants from China will have the priority to replace registered person who cannot make the trip to attend the conference.

Please, do not hesitate to write to: Dr. Luis Santiago Cano (Co-chair): catuche.gallego@gmail.com

(Ma Ming, Xinjiang)

The 4th International Conference on Malaria and Related Haemosporidian Parasites of Wildlife will be held in Beijing

The conference will take place in Beijing, China, from November 1-5, 2018, and will be hosted by the Beijing Normal University, Beijing Zoo and China Zoological Society.

During the past 10 years, much research has been done, and remarkable discoveries have been made in various fields of research regarding wildlife malaria parasites (*Plasmodium*, Plasmodiidae) and related haemosporidians (Haemosporida), the agents of infections which affect all major groups of terrestrial vertebrates. The conference will promote international exchanges and enhance collaborations across the world for wildlife malaria research and the conservation and health of terrestrial vertebrates. Your participation would contribute to the success of this rare event in wildlife malariology, and we invite you to join us.

Beijing, the capital of China, is an international metropolis combining both modern and traditional cultures. With its beautiful ancient Forbidden City, magnificent Great Wall and surrounding mountains, lakes and forests, Beijing is a gateway into a rich and historic past, and a modern Asian capital. The various activities around the conference, and the mild autumn setting, will make your journey an enjoyable and memorable experience.

The conference will include invited plenary lectures, oral presentations and posters. Information on the conference program, registration, student travel grants, and other details are now available on the website. The information about abstract submission, accommodation, social programs and travel will be available soon.

More detailed information: www.malariaconference2018.com

(Dong Lu, Beijing)

Publications

Recently, the story of the black stork has been published by China Forestry Publishing House. As a peer reviewer, I recommend this popular science book. Black stork is a nationally protected species (in the list of the first class), which has some distribution and population in China, but lacks research data. The authors of the book are mostly from the Lingqiu Nature Reserve for Black Storks in Shanxi Province. They presented the habitat, morphology, distribution, breeding ecology, migration, behavior, foraging, over-wintering, protection and management of the black stork based on the field observations. The Forestry Publishing House has published more than ten books in this category. These books not only promote the science popularization, but also have the value for the researchers.

(Ma Ming, Xinjiang)