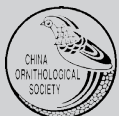




中国鸟类研究简讯

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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目 录

会议报道.....	1
研究动态.....	12
环志简报.....	28
国内外动态.....	31
新书出版.....	40
消息通知.....	42
英文摘要.....	45

Contents

Notes of Meetings	1
Research Reports	12
Bird Banding Report	28
News from China and Abroad	31
Publications	40
News and Notes	42
English Abstracts	45

《中国鸟类研究简讯》编辑委员会

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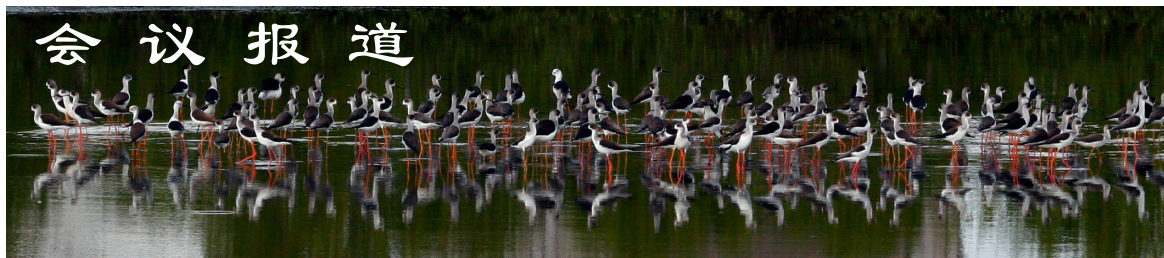
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第十五届中国鸟类学大会在吉林长春召开

2019 年 8 月 8 日至 11 日,“第 15 届中国鸟类学大会”在吉林省长春市东北师范大学本部校区召开。本次会议由中国动物学会鸟类学分会主办,东北师范大学生命科学学院承办,《*Avian Research*》编辑部、东北师范大学科学技术处、华东师范大学、吉林农业大学、吉林省动物学会、世界自然基金会(瑞士)北京代表处协办。来自我国 33 个省、直辖市、自治区和特别行政区及美国、俄罗斯、日本、蒙古等国家近 600 余名代表参会。

开幕式由中国动物学会鸟类学分会秘书长张雁云教授主持,东北师范大学副校长常青研究员代表承办单位讲话;鸟类学分会理事长雷富民研究员致欢迎词。北京师范大学郑光美院士、东北林业大学马建章院士、黑龙江野生动物资源研究所马逸清研究员、台中自然科学博物馆颜重威研究员、东北师范大学宋榆钧教授、广西大学周放教授等老一辈鸟类学家作为大会特邀代表出席了开幕式。

本届大会以“全面发展的新时期鸟类学”为主题,采用多种形式的学术交流,共设 6 个特邀大会报告,2 个青年大会报告,8 个专题报告会,13 个口头报告会,其中包括研究生英文报告专题 2 场,共计 139 个报告;“黄胸鹀的保护”专题圆桌讨论会 1 个,外国学者与研究生面对面交流会 1 场,以及 73 个壁报。会议期间还举办了“中国青年鸟类学家研讨会暨第 15 届翠鸟论坛”。

大会邀请了东北师范大学王海涛教授、中国科学院动物研究所杜卫国研究员、中央研究院生物多样性研究中心沈圣峰研究员、中国科学院动物研究所雷富民研究员、普林斯顿大学 David Wilcove 教授、广西大学 Eben Goodale 教授做了大会特邀报告;中国科学院动物研究所陈嘉妮博士、中国科学院生态环境研究中心王鑫博士做了大会青年报告。王海涛教授基于 16 年的长期研究工作,探讨了洞巢鸟类的繁殖策略和信息利用,从多个角度揭示了洞巢鸟类的生态及其适应性;杜卫国研究员介绍了鸟类和爬行类胚胎的行为热调节以及胚胎对温度变化的响应,这种不同动物类群之间的跨界比较,为鸟类学研究拓展了新思路;沈圣峰研究员的报告强调了环境条件对鸟类合作行为及其种群特征的影响,揭示了环境压力对生物进化的驱动作用;雷富民研究员介绍了鸟类对第三极特殊环境的适应,解析了高原特殊环境下物种多样性的分布格局及物种的形成、适应和维持机制;David Wilcove 教授分享了他在东南亚和南亚地区的研究,介绍了土地利用变化和气候变化对鸟类群落特征的影响;Eben Goodale 教授介绍了他在斯里兰卡、印度和我国南方地区对鸟类混合物种集群行为的研究,探讨鸟类群落稳定性的维持机制,强调了在生物多样性保护工作中维持物种间关系网络的重要性;陈嘉妮博士利用巧妙的控制实验,探讨了鸟类的学习和认知能力对配偶选择的影响,为认识生物的进化开拓了新的视角;王鑫博士分析了多种雁鸭类的迁徙模式,探讨了鸟

类迁徙的驱动机制,挑战了“绿色波浪假说”这一候鸟迁徙中的主流观点。

本届大会学术报告内容涉及领域广泛,涵盖了鸟类学多个研究领域的主题,包括经典的鸟类学研究领域,如鸟类多样性及其调查与监测、栖息地生态、繁殖生态、保护生物学等领域,及近年来新兴的热点领域,如候鸟的迁徙生态、环境变化对鸟类的影响、鸟类的生物地理学研究、鸟类的适应性进化及其机制以及鸟类的个性差异及其生态后果等。所展示的研究成果中,新的方法和新的技术得到了越来越多的应用,如采用卫星跟踪技术精确研究候鸟的迁徙活动和时空特征,利用红外相机技术监测鸟类的活动行为和分布格局等,特别是随着分子生物学技术的快速发展,基因组、转录组、代谢组、表型组等组学的技术和方法在鸟类的生态、进化及适应性研究方面得到了越来越多的应用,新技术新方法的应用推动了研究工作的深入和鸟类学的发展。本届大会学术报告质量高,充分体现了当前我国鸟类学研究全面蓬勃发展的态势。同时,报告呈现了多方位地面向国家需求、服务于我国生态文明建设重大战略的鸟类学研究工作。结合国际鸟类学界近年关注的黄胸鹀种群急剧下降这一问题,大会设置了“黄胸鹀的现状与保护”专题,我会代表与来自俄罗斯、日本和蒙古等国家的学者共同研讨黄胸鹀的受胁现状和保护对策。本次大会参会代表,特别是青年鸟类学者学术思想活跃,交流踊跃,反映出我国鸟类学发展的强大后劲。

2019年8月11日,大会正式落下帷幕。鸟类学分会理事长雷富民研究员主持了闭幕式,鸟类学分会常务理事马志军教授进行了大会学术总结,对本次大会中鸟类学者展现出的研究工作及学术成果予以高度肯定。在闭幕式上,大会公布了评选的鸟类基础研究奖、大会最佳壁报奖、研究生英文报告优秀奖、

翠鸟论坛奖的获奖名单,并由大会特约嘉宾郑光美院士、鸟类学分会名誉理事长周放教授等为获奖代表颁发了证书。

北京爱鸟国际文化传播有限公司、北京地理全景知识产权管理有限责任公司、成都德鲁伊科技有限公司、东北师范大学教务处、广州博观光电科技股份有限公司、湖南环球信士科技有限公司、Lotek Wireless Inc.、上海瑾瑜科学仪器有限公司、《生命世界》、深圳市优威视讯科技股份有限公司、索尼(中国)有限公司、武汉红视热像科技有限公司、中国林业出版社、杭州粤海科技有限公司、中国林业科学研究院湿地研究所等为本次会议提供了支持。

附一:大会报告题目

1. 次级洞巢鸟繁殖对策选择与信息利用(王海涛)
2. 爬行类和鸟类胚胎应对巢温变化的行为和生理对策(杜卫国)
3. Understanding the impacts of land-use change and climate change on birds (David Wilcove)
4. 鸟类合作行为的生态原因与后果(沈圣峰)
5. Mixed-species bird flocks: behavior, community ecology and conservation (Eben Goodale)
6. 鸟类对第三极环境的适应(雷富民)

大会特邀青年报告题目:

1. 鸟类的学习与认知(陈嘉妮)
2. 绿色波浪不是草食性水鸟春季迁徙的普遍驱动因素(王鑫)

附二:获奖名单

研究生英文报告优秀奖:

刘娟 浙江大学

陈泽茹 北京师范大学
林玉英 北京师范大学
余惠响 中国科学院动物研究所
郝 艳 中国科学院动物研究所

鸟类基础研究奖：

一等奖：

陈立军 白眶鸦雀繁殖生态学 中国科学院动物研究所

李万德 褐鸦雀繁殖生态学 西南林业大学和华中师范大学

吴永恒 红翅噪鹛的繁殖生态 新疆农业大学和乐山师范学院

梁 丹 火尾绿鹇繁殖生态学 西南林业大学和中山大学

贾 嘉 黑冠山雀繁殖生态学 中国科学院动物研究所

二等奖：

朱 磊 栗尾姬鹅的新纪录

徐康平 须苇莺的新纪录

最佳壁报奖：

雷维蟠 北京师范大学

柯婉娟 复旦大学

樊倩西 东北师范大学

陈道剑 广西师范大学

刘方远 河北师范大学

巫阳达 中国科学院动物研究所

弓 冶 东北师范大学

侯 丹 北京林业大学

李 末 河北师范大学

熊 鹰 中国科学院动物研究所

Daniel R Gustafsson 广东省生物资源应用研究所

(吉林：王海涛)

中国青年鸟类学家研讨会暨第十五届翠鸟论坛在东北师范大学举办

2019 年 8 月 7 日—8 日，中国青年鸟类学家研讨会暨第十五届翠鸟论坛在吉林省长春市东北师范大学成功召开。本次会议由中国动物学会鸟类学分会主办，东北师范大学生命科学院和吉林省鸟类生态与保护遗传工程实验室共同承办。来自安徽大学、北京林业大学、北京师范大学、东北林业大学、东北师范大学、复旦大学、广东生物资源应用研究所、广西大学、贵州师范大学、海南师范大学、河北师范大学、吉林农业大学、兰州大学、辽宁大学、南昌大学、厦门大学、浙江大学、中国科学院动物研究所、中国林业科学研究院、中山大等 27 个单位的 130 余名研究生参加了本次论坛。中国动物学会鸟类学分会副理事长卢欣教授，中国动物学会鸟类学分会秘书长张雁云教授，中科院动物所屈延华研究员和李欣海副研究员，中山大学刘阳副教授和 Emilio Pagani-Núñez 副研究员等出席并参加了本次论坛的多项活动。

本次论坛分为专家报告、学生报告和学生壁报展示等 3 个单元。来自中科院动物研究所的特邀嘉宾李欣海副研究员做了“关于机器学习与 R 语言操作”报告；中山大学 Emilio Pagani-Núñez 副研究员做了“Stable isotopes in ecological research (稳定同位素在生态学研究中的应用)”报告。来自 20 余所高校 36 名同学进行了口头报告，内容涉及鸟类繁殖对策与适应、性选择、分子进化、迁徙生态、保护生物学等领域，青年鸟类学家和研究生的报告精彩不断，反映了我国鸟类学发展的强大后劲。相信在不远的将来，这些青年人中将会涌现一批具有国际影响力的鸟类学者，成为我国鸟类学研究的中坚力量。另外，本次论坛特别设置了师生交流环节，同学们与卢欣教授、张雁云教授、孙悦华研

究员、马志军教授、屈延华研究员、刘阳副教授和李欣海副研究员等进行了密切的交流。

经参会同学和与会专家共同投票选举, 本届论坛评选出金翠鸟奖 5 名、银翠鸟奖 8 名、优秀短报告奖 5 名和优秀墙报奖 7 名。郑光美院士等在第十五届鸟类学大会闭幕式上为获得金翠鸟奖的 5 位同学颁发了获奖证书。

附：第十五届翠鸟论坛获奖名单：

金翠鸟奖：

董飞（辽宁大学），陈国玲（中山大学），彭杨洋（北京师范大学），郎雪敏（北京林业大学），姜志永（中科院动物研究所）

银翠鸟奖：

范倩西（东北师范大学），张守栋（复旦大学），程亚林（中国科学院动物研究所），叶萍（海南师范大学），赵晓萌（北京师范大学），赵岩岩（中山大学），周闯（四川大学），马东辉（兰州大学）

优秀短报告奖：

王翌（东北师范大学），柏军鹏（南昌大学），魏艳慧（辽宁大学），张静（辽宁大学），张凤玲（安徽大学）

优秀墙报奖：

陈泽茹（北京师范大学），杨森（复旦大学），钟国（贵州师范大学），王子健（北京林业大学），董小兵（包头师范学院），张丽（辽宁大学），张剑（北京师范大学）

（吉林：王海涛）

中国动物学会第十八届全国会员代表大会暨第二十四届学术年会在陕西西安召开

中国动物学会第十八届全国会员代表大会暨第二十四届学术年会于 2019 年 8 月 23 日—25 日在陕西省西安市隆重召开。本次会

议由中国动物学会主办，陕西省动物学会、陕西师范大学、西北大学等单位承办，中国科学院动物研究所协办。来自国内外 1,000 多名会议代表齐聚古城，围绕主题“新时代的动物学：学科交叉，创新引领”，共同探讨动物学领域的新发现、新问题，分享交流新方法、新成果。大会包含 10 个特邀大会报告、6 个大会青年报告和 18 个学术专题。部分与会学术报告充分展示了中国鸟类学的最新研究成果。由复旦大学马志军教授和中国科学院生态环境研究中心曹垒研究员主持的学术专题“迁徙鸟类的研究与保护”包括了 13 个关于鹤类、雁鸭类的学术报告，集中展现了近年来中国迁徙鸟类的保护研究进展。浙江大学周琦教授题为“Sex chromosome evolution in birds and bird-like mammals”的大会青年报告赢得了广泛好评。另外还有 15 个关于鸟类学其他方面的学术报告围绕鸟类行为学、多样性与保护、进化与适应的分子机制、协同进化和生理生态等内容展开了深入的讨论。

（陕西：于晓平 刘丹妮）

2019 年北京动物学会学术研讨会在北京林业大学成功召开

2019 年北京动物学会学术研讨会于 2019 年 10 月 19 日在北京林业大学隆重召开。来自北京、天津、江苏、上海、云南、广东等 6 个省市的 214 名代表以及法国专家、代表共聚一堂，分享动物学科研与教学的最新进展与成功经验。本次学术研讨会为期一天，由北京动物学会主办，北京林业大学承办，中国教研网、北京猛禽救助中心、北京生物多样性保护研究中心、高等教育出版社、北京聚通光达科技有限公司和北京野生动物救护中心共同协办，“中国教研网”进行了网络在线直播。

本届大会以“全面发展的新时期动物学”为主题,设置4个大会报告,8个专题报告会共44个报告以及墙报26个。其中“动物多样性与保护”专题报告6个;“野生动物饲养繁殖与救助”专题报告7个;“动物、环境与健康”专题报告6个;“动物学与基础教育教学”专题报告4个;“动物多样性与保护”专题报告5个;“野生动物疫源疫病”专题报告5个;“保护遗传学与系统演化”专题报告5个;“青年报告专场”报告6个。

本届大会学术报告涉及领域广泛,涵盖了动物学多个研究领域的主题。在这些主题中,既有受到长期关注的经典的研究领域,如多样性及其调查与监测、栖息地生态、繁殖生态等领域,也有近年来一些新兴的热点领域,如环境变化对物种的影响、保护生物学研究、生物地理学研究、物种适应性进化及其机制等,还包括与生活息息相关的领域,如野生动物的救助应用及基础教育教学研究等。

本届大会关于鸟类学的学术报告展现出较高水平。马志军教授揭示了候鸟如何通过形态及行为上的调整来应对迁徙停歇地食物减少带来的不利影响,揭示了动物在自然条件下对环境变化适应空间的有限性;Anders Møller教授通过不同案例从动物行为学的角度来阐明鸟类的认知能力及脑的演化。此外,一些新的方法和新的技术在鸟类学研究中得到了越来越多的应用。例如利用红外相机技术监测物种的活动行为和分布格局等等。特别是随着分子生物学技术的快速发展,基因组、转录组、代谢组、表型组等组学的技术和方法在生态、进化及适应性研究方面得到了越来越多的应用,新技术新方法的应用也推动了研究工作的深入和动物学的发展。

本届大会涉及的领域广泛,学术报告质量高,与会代表参与积极,在会上和会下热烈交流和互动,充分反映了当前我国动物学

研究全面蓬勃发展的态势,国际化水平也进一步提升。

(北京:徐基良 田姗)

第七届国际鸡形目鸟类学术研讨会在越南洞海市成功召开

由世界雉类协会(WPA)主办、越南自然保护协会(VNC)承办的“第七届国际鸡形目鸟类学术研讨会”于2019年9月23日—24日在越南洞海市召开,来自英国、越南、中国、德国、捷克、日本、新加坡、印度等14个国家的科研院所、动物保护管理、饲养繁殖机构及保护地的一百余位代表参加了本次会议。本次研讨会的主题是探讨全球鸡形目鸟类的研究、保护及可持续管理,重点关注珍稀濒危物种及其栖息地的保护。

研讨会设有大会报告、圆桌讨论和墙报等环节。来自中国、尼泊尔、英国、巴基斯坦、印度等国家的19位代表就鸡形目鸟类的野外种群调查、繁殖行为、栖息地选择、进化与谱系地理重建、基因组及遗传多样性、人工繁殖以及监测与观测网络等方面的内容做了报告,并与参会代表进行了热烈讨论。在会议墙报环节,10多张墙报的作者展示了其雉类研究方面的最新成果,并与参会专家进行了深入的交流。本次研讨会还出版了论文摘要集,共收录论文摘要26篇。

会议期间组织召开了2场圆桌会议、一场分组讨论会,分别就绿孔雀和彩雉两个物种的研究和保护以及国际鸡形目鸟类的优先研究领域进行了讨论。其中,9月23日晚上召开了“绿孔雀保护策略及计划”,由IUCN鸡形目专家组主席Simon Dowell博士主持。会议通过视频、PPT等形式,就亚洲当前绿孔雀种群调查监测与保护中面临的困难及可能的解决措施进行了认真交流与讨论。在9

月 24 日下午的“鸡形目鸟类保护优先物种研究”讨论会上, 首先由 Simon Dowell 博士介绍了鸡形目鸟类保护生物学研究的当前最新进展及今后的工作目标及计划, 然后通过分组的形式对鸡形目鸟类保护优先性的评估标准及拟选物种进行了讨论, 最后各小组分享了各自的讨论结果。

本次研讨会充分展示了各国学者在鸡形目鸟类研究与保护方面的最新进展, 代表所属单位涉及高等院校、科研院所、自然保护区管理局及有关机构、非政府组织、动物园、饲养繁殖中心及相近机构。本次会议上, 来自这些机构的代表们对参与交流与展示积极性较高, 且富有激情。在研究内容上, 既有鸡形目物种分布、种群数量动态变化、栖息地选择等经典研究内容, 也有系统进化、基因组学等最新研究方向, 还涉及到珍稀雉类饲养繁育、再引入等传统内容。

我国是世界上雉类资源最丰富的国家, 长期以来雉类研究也在国际上享有盛誉。本次研讨会, 我国共有 23 位专家和研究生参加交流。其中, 中科院动物所孙悦华研究员、北京师范大学张正旺教授、北京林业大学丁长青教授分别主持了大会的学术报告。广东省生物资源应用研究所邹发生研究员、北京林业大学徐基良教授、王楠副教授、中山大

学刘阳副教授、中科院昆明动物研究所董锋副研究员、兰州大学安蓓副教授、北京师范大学王鹏程博士、北京动物园张敬老师、北京林业大学博士生姚红艳等做了大会报告。付义强、田姗、汪珍、杨晓君、邱源等进行了墙报展示。在绿孔雀圆桌会上, 杨晓君研究员介绍了其团队的最新研究成果。我国代表的报告内容丰富, 涉及物种包括雪鸡、白鹇、褐马鸡、白马鸡、绿孔雀、白冠长尾雉、黄腹角雉、灰腹角雉、绿尾虹雉、白眉山鹧鸪、四川山鹧鸪、环颈雉等, 受到了与会代表的高度评价。

9 月 24 日晚上举行的会议闭幕晚宴上, 为此次会议作出贡献的个人颁发了纪念品, 我国代表团的张正旺教授、丁长青教授、孙悦华研究员、徐基良教授等人获得了表彰。

会后, 我国部分与会代表还参观了越南河内动物园, 进行了学术交流, 受到了该动物园副园长等管理人员的欢迎和热情接待。

本次研讨会进一步促进了各国专家的交流和联系, 拓展了我国鸟类学家、动物饲养繁育单位技术人员与世界雉类协会的合作空间, 这必将对我国今后一段时期内鸡形目鸟类的保护管理、科学研究、管理及饲养繁育工作产生积极的推动作用。



第七届国际鸡形目鸟类学术研讨会代表合影

(北京: 徐基良 田姗)

2019年中国鹤类及栖息地保护学术研讨会暨中国野生动物保护协会鹤类联合保护委员会年度工作会议在安徽省池州市召开

2019年11月29日—12月2日,2019年中国鹤类及栖息地保护学术研讨会暨中国野生动物保护协会鹤类联合保护委员会年度工作会议在安徽省池州市顺利召开。中国野生动物保护协会监事长张习文、池州市人民政府副市长方能斌、中国野生动物保护协会副秘书长郭立新、池州市人民政府副秘书长鲍旭东以及国家林草局相关司局、安徽省林业局、国际鹤类基金会、从事鹤类研究的高校和科研院所、来自17个省市的鹤类相关保护区等单位的代表共计200余人出席本次会议。



张习文监事长在开幕式致辞中表示,我国是鹤类资源丰富的国家,全世界有15种鹤,我国就有9种,是世界上拥有鹤的种类最多的国家。中国野生动物保护协会鹤类联合保护委员会作为鹤类保护的科技支撑,在引领鹤类保护技术进步和科学传播、鹤类同步调查,协调鹤类越冬地、停歇地、繁殖地间的联合保护方面发挥了重要作用。

在2019年年会上,钱法文书长介绍了鹤联会2019年工作成果和2020年的工作计划。2019年鹤联会在成果交流和技术培训、推动全国鹤类资源的同步调查、科学研究与科普宣传、国际交流与合作、完善组织机构建设几个方面开展工作,主办了“第二届从

呼伦贝尔到渤海湾迁徙鹤类和水鸟同步调查培训会”,协办“第七届黑颈鹤网络年会暨国际重要湿地监测管理研讨会”、“中国荣成大天鹅保护国际学术交流会”,并在“东亚六国鹤类保护国际研讨会”上介绍了鹤联会的工作内容和工作宗旨。2020年鹤联会将继续在鹤类保护的科普宣传和科技交流、鹤类同步调查等方面开展工作,特别是办好中国鹤年相关活动。鹤联会还新设立“鹤文化与生态摄影工作组”,并增补15家成员单位和新增6名委员。

此次研讨会共有6个大会报告和16个专题报告。安徽大学周立志教授、东北林业大学邹红菲教授、全国鸟类环志中心江红星研究员、昆明学院孔德军副教授、东北林业大学田秀华教授、江苏盐城保护区张亚楠女士分别从鹤类生态学保护、栖息地管理与保护和迁徙路线等方面进行了大会报告。南京林业大学鲁长虎教授等16名代表就鹤类现状及栖息地、鹤类生态与救护进行了专题报告。报告从鹤类的种群现状、栖息地利用、迁徙、越冬、迁地保护、救助管理等多个方面,充分展示了近年来我国鹤类的研究和保护的最新进展。

鹤联会主任委员、北京师范大学教授张正旺主持了闭幕式。会议表彰了全国鹤类保护先进会员单位、会议优秀墙报获奖者和2019年中国鹤类摄影大赛获奖者。会议决定将继续开展2019—2020年全国鹤类资源同步调查,并进行了相关技术培训;下届鹤联会年会定于2020年在黑龙江龙安桥国家湿地公园举行。与会代表还观看了我国第一部展现中国九种鹤自然史的专题片《天是鹤家乡》,并实地考察了安徽升金湖国家级自然保护区。

本次会议由中国野生动物保护协会鹤类联合保护委员会、安徽省池州市人民政府联合主办,安徽大学湿地保护与修复安徽省重点实验室承办,安徽省池州市林业局、安徽

升金湖国家级自然保护区管理处、安徽省动物学会、安徽省野生动植物保护协会、自然影像中国、安徽引力波科教设备有限公司、

安徽天立泰科技股份有限公司、湖南环球信士科技有限公司协办。

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

安徽·池州 2019.11.29-12.3



(鹤联合会秘书处)

第七届黑颈鹤网络年会在甘肃尕斯库勒国家级自然保护区召开

第七届黑颈鹤保护网络年会暨国际重要湿地监测管理研讨会于2019年7月31日至8月2日在甘肃尕斯库勒国家级自然保护区召开，会议由甘肃省林业和草原局、全国鸟类环志中心、国际鹤类基金会、中国科学院昆明动物研究所主办，碌曲县人民政府、甘肃尕斯库勒国家级自然保护区管理局承办，中国野生动物保护协会鹤类联合保护委员会和兰州大学生命科学院协办。这是黑颈鹤网络成立9年来的第七届年会。来自美国、印度、不丹以及国内12个省区57个单位的118名科研、教学、管理、社团、志愿者、爱好者等参加。32位代表在会议上交流了涉及黑颈鹤的现状和保护、黑颈鹤及湿地保护、黑颈鹤与栖息地、黑颈鹤生态生物学、黑颈鹤及其保护、保护管理经验和宣传教育的33个报告，对黑颈鹤保护行动计划、进一步加强中国、印度和不丹三个黑颈鹤分布国家的合作和协调等相关工作作了讨论。让我们了解到了有黑颈鹤分布的3个国家的黑颈鹤现状，

我们欣喜的看到，黑颈鹤的种群数量还在增加，通过西藏、不丹、印度的报告，将有关的地点相加，黑颈鹤的种群数量已经达到了14,000只左右。除学术交流外，代表们在会后还实地考察了甘肃尕斯库勒国家级自然保护区。

(云南：杨晓君；北京：钱法文；国际鹤类基金会：李凤山)

中国动物学会动物行为学分会第三届学术年会暨全国动物行为学第七次研讨会在海口市召开

中国动物学会动物行为学分会第三届学术年会暨全国动物行为学第七次研讨会，于2019年11月15—18日在海南省海口市召开。本次会议由动物行为学分会主办，热带岛屿生态学教育部重点实验室、海南师范大学生命科学学院和海南省动物学会承办。会议主题为“快速发展的中国动物行为学”。来自全国31个省份的288名代表(含学生代表105名)参加了本届学术盛会。此外，新加坡大

学李代芹、日本筑波大学 Sonoko Ogawa 和北京师范大学特聘教授、法国巴黎大学 Anders Pape Møller 等也参加了大会。

会议开幕式由中国科学院动物研究所张健旭研究员主持，海南师范大学史海涛副校长、动物行为学分会主任委员蒋志刚研究员、中国动物学会张希武监事长等先后致辞。

本届会议安排了 8 个大会特邀报告。鸟类学分会理事杨灿朝（海南师范大学）、陈嘉妮（兰州大学）分别作了杜鹃巢寄生行为和鸟类性选择行为的大会报告。杨灿朝研究员和西北大学齐晓光教授获首届“诺达思动物

行为学杰出贡献奖”。

会议选举产生了中国动物学会动物行为学分会第二届委员会委员。其中鸟类学分会副理事长梁伟教授当选动物行为学分会第二届委员会副主任委员，鸟类学分会会员李忠秋、陈嘉妮当选动物行为学分会第二届委员会常务委员。

中国动物学会动物行为学分会成立于 2015 年 10 月，首届主任委员为中国科学院动物研究所蒋志刚研究员。本届（第二届）主任委员为中国科学院动物研究所张健旭研究员。



大会开幕式（从左至右分别为：张健旭、史海涛、蒋志刚、张希武、邵发道和贾志云）



全体与会代表合影留念

（海南：梁伟 汪继超）

第十五届全国野生动物生态与资源保护学术研讨会在海口市召开

第十五届全国野生动物生态与资源保护学术研讨会于2019年11月17日—20日在海南省海口市顺利召开。会议由中国生态学会动物生态专业委员会、中国动物学会兽类学分会、中国野生动物保护协会科技委员会、国际动物学会和海南省动物学会联合主办；热带岛屿生态学教育部重点实验室（海南师范大学）、海南师范大学生命科学学院承办；中国科学院动物研究所动物生态与保护生物学院重点实验室协办。来自全国的112个单位、近570名从事野生动物生态和资源保护的代表参加本次学术研讨会。兽类学家胡锦涛先生、汪松先生也亲临大会。

大会开幕式由中国动物学会兽类学分会秘书长胡义波研究员主持。中国科学院院士、中国动物学会秘书长、兽类学分会主任委员魏辅文研究员，中国野生动物保护协会副会长兼科技委员会主任蒋志刚研究员，海南省林业局党组成员周绪梅女士，海南省科学技术协会副主席郑红女士，海南师范大学党委

副书记、纪委书记、热带岛屿生态学教育部重点实验室主任刁晓平教授，分别代表会议主办和承办单位致辞。中国野生动物保护协会副会长、中国动物学会监事长张希武研究员，海南师范大学副校长史海涛教授也到会进行指导交流。

会议特别邀请了5个大会报告，分别是中国科学院动物研究所魏辅文院士的“天人合一——2020后生物多样性保护愿景与框架”、西北工业大学王文研究员的“反刍动物及其独特特征的进化系统生物学研究”、海南师范大学史海涛教授的“中国龟鳖类的研究与保护”、中国科学院昆明动物研究所赖仞研究员的“动物毒液与生存适应”、中国科学院动物研究所詹祥江研究员的“隼形目鸟类的进化与保护”。

本次大会一共设置9个专题报告会。鸟类学分会马志军、徐基良、斯幸峰3人作为专题召集人主持了专题报告。大会评选出南京师范大学黄铮、海南师范大学丁利、安徽大学李春林（鸟类学分会）、西华师范大学韩茵、兰州大学李欢等5位青年学者为本届“优秀青年动物生态学工作者”获奖者。



开幕式现场

（海南：梁伟）

第 11 届国际整合动物学研讨会在新西兰召开

2019 年 12 月 2 日至 7 日, 第 11 届国际整合动物学研讨会在新西兰奥克兰梅西大学举办, 会议的主题是保护动物学研究, 内容主要包括动物行为保护及生态学、林业和农业对动物种群的影响、生活在边缘 - 极端环境中动物的适应性、无脊椎动物的进化及生态学、人与野生生物的相互作用、动物疾病对动物保护的影响、植物 - 动物相互作用和协同进化等。参会代表有来自美国普林斯顿大学、加利福尼亚大学、密苏里大学, 澳大利亚昆士兰大学, 新西兰奥克兰大学、梅西大学, 韩国檀国大学, 南非比勒陀利亚大学以及中国、英国、德国、俄罗斯、波兰等国家和地区的专家学者 200 多人, 中国鸟类学会由理事长雷富民先生带队, 成员有来自中科院动物研究所、四川大学、厦门大学等 10 余人, 专题报告有中科院动物研究所宋刚博士的 “Genetic structure and gene flow routes among geographical populations of a recent distribution range expanding bird, light-vented bulbul”、李欣海博士的 “New R tools for studying bird

migration”、詹祥江研究员的 “Evolutionary conservation biology of saker falcons”、罗静的 “Influenza A virus surveillance in wild birds in China”, 上海自然博物馆杨刚博士的 “The influence of vegetation structure on bird guilds and their niches in urban area”, 厦门大学黄智君的 “Home range and habitat use at pre-migratory stage in the vulnerable Chinese egret (*Egretta eulophotes*) revealed by GPS tracking”, 阿拉善 SEE 基金会张琼的 “Free Flying Wings - protects endangered shorebirds and their habitats in China”, 乐山师范学院文陇英教授主持了专题 “Living on the edge – Animals in extreme environment”, 同时做了专题报告 “The adaptation of the blood pheasant (*Ithaginis cruentus*) under cold stress”, 首都师范大学张子慧教授做了墙报 “Ontogenetic changes of trabecular bone in the femoral head of pigeon”, 李言阔做了墙报 “Abundance variation and population trends of waterbirds in relation to water level fluctuation in Poyang Lake” 等学术报告。本次会议内容丰富, 学术交流氛围浓厚。

(四川: 文陇英)



鹬类食物特征的个体差异与取食器官无关

鸟类所利用的食物特征与觅食器官或食物处理器官的特征密切相关。喙是重要的觅食器官和食物处理器官，因此，很多鸟类所摄取的食物特征与喙部形态有关。这也是自然史研究发现的鸟类喙部形态特征适应食物变化而发生的演化的基础。鹬类的主要食物是具有坚硬外壳的软体动物，它们的食物处理方式比较特殊，通常是将食物整个吞下，利用强大的肌胃将软体动物的外壳压碎后再进行食物消化。因此，食物的处理过程主要发生在消化道内。它们的食物特征是受喙部特征的影响，还是受肌胃特征的影响呢？本研究利用野外获取的被滩涂上的渔网缠住无法脱身而溺水死亡的大滨鹬为研究对象，首次从个体水平阐述了鹬类的食物特征。

研究表明，在个体水平上，大滨鹬的食物特征与喙长无关，而与肌胃大小有关。肌胃大小与所摄取的外壳坚硬的托氏昌螺的数量比例呈显著正相关。肌胃越大，食物中托氏昌螺的比例越高，同时大型托氏昌螺（外壳硬度更高）的比例也越高。肌胃中底栖动物外壳的干重与喙长没有显著相关性，但与肌胃大小呈显著的正相关。另外，肌胃中食物的平均硬度也与喙长没有显著相关性，但与肌胃大小呈显著的正相关。

喙是一个形态固定的觅食器官，而肌胃是一个具有表型弹性的器官，其大小可以在较短的时间内发生快速变化从而改变消化能

力。肌胃具有表型弹性这一特征使得大滨鹬可以对食物硬度的变化做出快速响应。本研究指出，肌胃的这种调节能力有利于大滨鹬等迁徙鹬类快速适应食物的季节变化和地点差异。

相关研究详见：Zhang, S.D., Ma, Z.J., Feng, C.C., et al. 2019. Individual diet differences in a molluscivore shorebird are associated with the size of body instruments for internal processing rather than for feeding. *Journal of Avian Biology*, e02255. doi: 10.1111/jav.02255.

（上海：张守栋 马志军）

人工管理的芦苇沼泽可以成为鸟类高质量的繁殖栖息地

有着茂密植被的沼泽湿地为很多雀形目鸟类提供了繁殖栖息地。但由于受到大规模高强度开发活动的影响，全球自然沼泽湿地的面积不断减少，这导致了很多鸟类栖息地丧失，种群数量下降。与此同时，全球一些地区开展了湿地修复活动，人工湿地的面积不断增加并吸引很多鸟类栖息。但目前关于人工湿地对鸟类的支持作用主要关注水鸟类群，仍不清楚人工沼泽湿地是否可以像自然沼泽湿地一样成为一些鸟类（特别是雀形目鸟类）的繁殖地，从而减缓自然沼泽面积减少对繁殖的雀形目鸟类带来的不利影响。本研究比较了位于长江口崇明东滩鸟类自然

保护区的自然芦苇沼泽和人工管理的芦苇沼泽中常见鸟类东方大苇莺 (*Acrocephalus orientalis*) 的繁殖栖息地特征 (植被和食物特征) 以及繁殖成功率。该区域的人工芦苇沼泽是通过实施互花米草控制和鸟类栖息地优化生态工程而形成的。研究结果表明, 与自然芦苇沼泽相比, 人工管理的芦苇沼泽植被密度更高, 鸟类在繁殖期的食物资源 (节肢动物) 更丰富。人工芦苇沼泽中东方大苇莺的领域密度、巢密度、窝卵数、卵大小和出飞雏鸟数均不低于自然芦苇沼泽。人工芦苇沼泽中巢的被捕食率较低, 这是导致人工芦苇沼泽中鸟类繁殖成功率较高的主要原因。但人工芦苇沼泽中巢址的位置较高, 这使得鸟巢相对不稳定, 遇到强风时鸟巢容易被破坏。总之, 人工芦苇沼泽比自然芦苇沼泽中东方大苇莺的繁殖成效更高, 其主要原因是人工芦苇沼泽通过管理在繁殖期一直保持着高而稳定的水位, 这有助于芦苇生长和节肢动物的繁殖, 不仅为鸟类提供了食物资源, 而且高的水位可以减少陆生捕食者的活动; 茂密的植被也有助于提高鸟巢的隐藏度, 从而使得鸟巢难以被捕食者发现。此外, 人工芦苇沼泽附近的人类活动可能在一定程度上也减少了捕食者的活动。本研究结果说明了人工管理的芦苇沼泽可以为东方大苇莺提供高质量的繁殖栖息地, 从而在一定程度上弥补自然沼泽湿地丧失对繁殖鸟类带来的不利影响。本研究强调了保持人工芦苇沼泽维持一定高度的稳定水位有助于提高鸟类的繁殖成功率。

具体研究结果见: Wang J.Y., Zhou Q.Y., Wu W., Liang W., Ma Q., Ma Z.J. 2019. Managed marshes can be good alternatives to natural marshes as breeding habitats for birds. *Ecological Engineering*, 139: 105584.

(上海: 马志军)

发现树麻雀适应青藏高原特殊环境的新机制

物种如何快速、有效地适应变化的自然环境, 是其生存和种群拓殖的必要条件。被称为地球“第三极”的青藏高原代表着世界上最严酷的高原环境之一, 然而这里却孕育着一群独特的动物区系。以往对鸟类、其他动物和人类高原适应的研究主要集中在表型分化后期的高分化群体, 很少有人关注高原适应过程的初始阶段。通过对身边最为常见的一种小鸟, 树麻雀 (*Passer montanus*) 的群体基因组研究, 结合转录组、心肌、飞行肌组织形态特征分析, 发现了树麻雀对高原环境的早期适应机制。

种群遗传结构、历史动态及全基因组性状 - 基因关联分析, 发现树麻雀在青藏高原高海拔地区农耕文明发展之后 (大约 3,600 年之前), 才拓殖到青藏高原。在短短几千年里, 它们的心肌、飞行肌首当其冲发生了明显变化, 这些性状变化与低氧、低温环境的适应能力密切相关。通过对树麻雀高、低海拔种群群体基因组比较研究, 发现它们的遗传分歧非常微弱, 这与其表型的高度分化显著不同。为探讨这种遗传与表型变化的差异是否缘于表型性状的可塑性? 特别是短期应激下高原树麻雀表型改变, 研究人员对低海拔树麻雀进行了为期一个月的低氧习服试验, 发现低氧习服实验处理树麻雀的心肌、飞行肌的相关性状并未呈现出短期应激变化, 可见, 表型的可塑性未能解释高原适应的主要表型变化。研究人员进一步比较了树麻雀高、低海拔种群的群体基因组, 发现全基因组上一系列和高原适应性性状相关的基因 (如肌肉发育相关的基因) 相对于基因组背景有着较高的遗传分化, 而多个与表型性状密切相关的基因位点同时出现频率改变, 由此推测, 树麻雀肌肉等表型性状的快速高原适应

是多基因联合驱动的结果，即多基因适应 (polygenic adaptation)。

该研究开创了领域内的诸多第一，研究团队在全球范围内第一次阐述了高原适应过程的早期阶段，为物种对特殊环境的适应提出了一种新的动态机制。研究人员首次发现高原适应背景下物种的多基因适应机制，大大拓宽了物种适应新环境研究的视野和角度，为我们理解物种在极端环境下的适应和演化提供了新的范例。该研究以“Rapid phenotypic evolution with shallow genomic differentiation during the early stage of high elevation adaptation in Eurasian Tree Sparrows”为题在线发表于 *National Science Review* (<https://academic.oup.com/nsr/advance-article/doi/10.1093/nsr/nwz138/5567447?guestAccessKey=908825cb-b298-4e7b-8526-99bbf40e9e0c>)。

(北京：屈延华)

捕获和笼养刺激对繁殖期树麻雀血浆皮质酮和代谢物水平的影响

野生动物由自然生境转移到人工笼养环境的过程会经历捕获和笼养应激，此时动物下丘脑 - 垂体 - 肾上腺轴 (HPA 轴) 被激活，进而导致机体产生一系列生理和行为变化。对野生鸟类而言，尽管捕获和笼养刺激后血浆皮质酮 (Corticosterone, CORT) 水平升高在调节机体生理和行为响应中发挥了重要作用，应激发生后血浆代谢物的变化仍不清楚。本研究以繁殖期野生树麻雀 (*Passer montanus*) 为对象，探究了捕获刺激和 24-h 笼养刺激对树麻雀体重、身体状况、血浆 CORT 和血浆代谢物 (葡萄糖, glucose, Glu; 总甘油三酯, triglyceride, TG; 总胆固醇, total cholesterol, TC; 尿酸, uric acid, UA) 的影响。结果显示，经历捕获刺激后，树麻雀血浆 CORT 和

Glu 含量显著升高，而 TC 和 UA 含量显著降低；笼养 24-h 后，树麻雀体重、身体状况相比本底状态显著下降，但血浆 CORT、Glu 和 UA 水平显著上升；雄鸟血浆 TG 含量捕获刺激和 24-h 笼养刺激后均显著低于雌鸟。相关性分析结果显示，CORT 与血浆代谢物间相关性存在性别差异。以上结果说明捕获和笼养刺激可显著改变树麻雀代谢状态，本研究为更好地理解应激所引发的性别依赖的能量动员提供了基础资料。本研究已在 *Avian Research* 上发表 (2019, 10: 16)。

(河北：李末 朱伟伟 汪洋 孙砚峰 李巨勇
刘雪路 吴跃峰 李东明；陕西：高学斌)

雀形目鸟类形态和运动学参数的种内变异与飞行性能关系

尽管在鸟类中更强壮的飞行肌肉、更大的翅膀，更高的振翅频率和更大的振翅幅度会增强扑翼飞行中的动力输出，但目前仍不清楚这些参数中究竟哪些因素是重要的限制因子。为探索这一科学问题，本研究以非迁徙雀形目鸟类——树麻雀 (*Passer montanus*) 为对象，研究其与飞行相关的 13 个形态学和运动学变量。我们假设更大的翅膀将与更高的振翅频率、更大的飞行肌会增强飞行动力输出，同时更大的心脏和肺可增强代谢能力和能量供应相关，而且相对较小的消化器官有利于减轻自重。我们发现较大的飞行肌和较大的翅膀、较大的胃、但更短的喙是提升飞行动力能力的重要因素，而振翅频率，振翅幅度以及心脏、肺和消化器官的质量和相对大小却不是影响飞行动力能力的重要因素。结构方程模型结果表明载荷能力增加与飞行肌质量、翅膀面积和胃重呈显著正相关，但与喙长度呈显著负相关。野生雀形目鸟类飞行性能在种内水平表现出形态学和生理学特

征之间的相互作用效应,与以往发现的种间特征的结果有所不同。本研究已在 *PeerJ* 上发表 (2019; 7: e8048)。

(河北:汪洋 殷源 葛仕勇 李末 张谦
李巨勇 吴跃峰 李东明;美国:
Robert Dudley)

野生树麻雀的喙部白化现象:形态和生理描述

相比其它类群而言,大多报道发现鸟类体表颜色异常更为普遍。尽管有证据显示体色异常可能与形态和生理特征存在一定关联,但目前在野生动物中的相关研究仍非常缺乏。本研究报道了一只羽色正常,但喙部白化的野生树麻雀 (*Passer montanus*) 个体,并进一步比较了该个体与其它正常个体在形态和生理上的差异,包括体重、身体状况 (body condition index, BCI)、喙长、跗跖长、翅长,以及内核温度、血比容 (hematocrit, Hct)、本底状态下血浆葡萄糖 (glucose, Glu)、总蛋白 (total protein, TP)、尿酸 (uric acid, UA)、总胆固醇 (total cholesterol, TC)、总甘油三酯 (triglycerides, TG)、游离脂肪酸 (free fatty acid, FFA)、 β -羟丁酸 (β -hydroxybutyrate, β -HB)、高密度脂蛋白 (high density lipoprotein cholesterol, HDL-C)、低密度脂蛋白 (low density lipoprotein cholesterol, LDL-C)、乳酸脱氢酶 (lactate dehydrogenase, LDH)、碱性磷酸酶 (alkaline phosphatase, ALP) 和肌酐 (creatinine, CREA)。结果显示:白化树麻雀跗跖长度显著短于正常个体,但翅长显著长于正常个体。此外,白化个体内核温度显著高于正常个体,而血浆 TP、UA、LDL-C、ALP 和 CREA 水平均显著低于正常个体。上述结果表明喙部颜色异常会导致形态和生理特征发生变化,尤其是在机体热

调节和蛋白代谢等方面,但不影响机体身体状况和其它血浆代谢物和代谢酶水平。本研究已发表在 *Wilson Journal of Ornithology* 上 (2019, 131: 553-560)。

(河北:李末 张谦 高小涵 孙砚峰 曹嘉欣
李贺 吴跃峰 李东明)

基于幼鸟营养和生理状态预测物种受物候错配威胁的敏感性

气候变化引起的雏鸟出生高峰与其最佳食物资源高峰期的错配正在威胁许多鸟类物种的生存。判断物种对物候错配的敏感性十分重要,因此有必要建立一种更可靠的方法来预测鸟类物种的脆弱性。以内蒙古草原分布的短趾百灵 (*Calandrella cheleensis*) 为例,我们评估雏鸟是否能从不同的食谱中吸收同等水平的营养并保持同等的生理状态来预测这种脆弱性。通过比较两个繁殖季节不同适宜食物 (蝗虫若虫) 丰度条件下孵化雏鸟的食谱、血浆营养成分、血浆胰岛素样生长因子 (IGF-1)、体重和成活率,发现:1) 中、低蝗虫若虫丰度条件下孵化的雏鸟血浆单糖、氨基酸、三羧酸循环代谢产物、部分脂肪酸、IGF-1、体重和成活率均显著低于高蝗虫若虫丰度条件下孵化的雏鸟;2) 血浆氨基酸、单糖、TCA 循环代谢产物和脂肪酸的相对丰度与 IGF-1 水平呈显著正相关,与雏鸟体重呈正相关。我们的研究表明,低适宜食物比例的食谱的营养功能低于高适宜食物比例的食谱,对雏鸟生长有抑制作用。短趾百灵等物种由于替代食物不足而难以满足雏鸟的营养需求,容易受到物候错配引起的营养威胁。

原文:Zhang S, Zhao L, Zhang X, Liang W (2019) Predicting the vulnerability of birds to trophic threat posed by phenological mismatch

based on nutritional and physiological status of nestlings. *Conservation Physiology* 7: cozo96 (doi:10.1093/conphys/cozo96).

(北京: 张淑萍; 海南: 梁伟)

一样的巢寄生, 不一样的威胁: 不同大小的杜鹃对不同宿主的威胁不同

以往由于欧洲主要只分布有大杜鹃 (*Cuculus canorus*) 一种寄生性鸟类, 因此关于不同大小的寄生性杜鹃对不同宿主的威胁很少有人研究。我们通过标本展示和录音回放实验, 分别在贵州宽阔水 (分布有 11 种不同大小的寄生性杜鹃) 和吉林左家 (仅分布有 4 种大小相似的寄生性杜鹃) 对绿背山雀 (*Parus monticolus*) 和大山雀 (*P. cinereus*) 进行了比较。结果发现, 北方的大山雀对翠金鹃 (*Chrysococcyx maculatus*) 和大杜鹃均无行为反应; 但南方的绿背山雀则对翠金鹃和大杜鹃的行为反应显著不同。绿背山雀对翠金鹃的反应强烈, 而且该行为与对洞巢鸟类的主要捕食者花鼠 (*Tamias sibiricus*) 的行为一致。我们的研究表明, 绿背山雀对体型较大的巢寄生者 (如大杜鹃) 没有反应, 但却视体型较小、能自由出入其巢洞的翠金鹃为一种威胁。这说明, 杜鹃与宿主的协同进化, 在单一杜鹃寄生系统 (如欧洲) 和多杜鹃寄生系统 (如亚洲和中国) 里会有很大的不同。研究结果发表在 *Current Zoology* 上。

(吉林: 于江萍 鄂明鞠 王海涛;

海南: 梁伟; 法国:

Anders Pape Møller)

狐假虎威? 5种山雀科鸟类的吓唬叫声 (hissing call) 比较

许多山雀科鸟类在洞巢繁殖遇到危险的时候, 常发出类似蛇类咆哮的吓唬叫声。一般认为这是一种有效的驱赶捕食者的方式。但这种叫声在山雀科鸟类中是否具有普遍性, 以及这种叫声是否与捕食压力有关, 尚未有研究。我们在河北塞罕坝、辽宁仙人洞对 5 种山雀科鸟类即大山雀 (*Parus cinereus*), 沼泽山雀 (*Poecile palustris*), 杂色山雀 (*Sittiparus varius*), 褐头山雀 (*Poecile montanus*) 和煤山雀 (*Periparus ater*) 的吓唬叫声进行了比较。我们的结果表明, 所研究的 5 种山雀在孵卵期均表现出种间、种内不同程度差异的吓唬叫行为, 但该行为与其窝卵数、繁殖成效和当地的巢捕食风险没有相关性。这一工作发表在 *Behavioral Processes* 上。

(辽宁: 张丽 张雷 万冬梅;

海南: 刘建平 梁伟;

法国: Anders Pape Møller)

灰鹤越冬地的改变与全球气候变化的对应关系

最近几年, 一些水禽越冬地向北偏移。以灰鹤为例, 过去迁徙至我国的灰鹤 (*Grus grus*) 越冬地主要是在长江以南及云南、贵州、江西等地, 但近年来却发现在新疆塔里木盆地周围地区有灰鹤越冬, 主要地点在拜城县、乌什县、墨玉县、民丰县、皮山县等区域。

2016 年, 首次发现数千只灰鹤种群在新疆越冬, 对此持续跟踪观察, 探讨气候变化的影响。2019 年 10—12 月, 环绕南疆调查, 初步统计到灰鹤上万只。这可能是中亚最北的越冬地, 距离原来的越冬地大大向北偏移 (直线距离 1,800~2,100 km, 纬度相差 8~12

度), 类似情况在欧洲也出现了, 繁殖地与越冬地之间的距离缩短。这与全球气候变化密

切相关, 同时也与食物有关系, 如种植种类改变和收割方式机械化等。



照片1 新疆和田越冬灰鹤 (马鸣摄)



照片2 新疆墨玉县越冬灰鹤数量超过千只 (马鸣摄)

(新疆: 马鸣)

睾酮对杂色山雀繁殖的影响

类固醇激素睾酮 (testosterone, T) 是影响鸟类繁殖最重要的性激素之一, 与鸟类的繁殖行为的各个方面息息相关。杂色山雀是社会性单配制鸟类, 双亲共同抚育后代。2019年3月—7月间, 我们收集并测量了繁殖前期 (筑巢期) 与繁殖后期 (育雏期) 杂色山雀血浆睾酮水平, 探究睾酮浓度对其繁殖的影响。结果显示, 筑巢期, 杂色山雀雌雄亲鸟睾酮浓度显著升高; 雄性亲鸟睾酮水平与其窝卵数呈显著正相关关系; 育雏期雌雄配偶对间睾酮水平显著正相关。但个体睾酮浓度与体征参数、雌性睾酮浓度与繁殖参

数间均无相关性。总的来说, 自然状态下, 睾酮水平对雄性杂色山雀窝卵数具有调节作用, 睾酮浓度高的个体窝卵数高; 但睾酮水平对雌性繁殖的影响仍需要进一步实验探究。

(沈阳: 王娟 万冬梅)

黄喉雉鹑基因组研究

黄喉雉鹑 (*Tetraophasis szechenyii*) 又名四川雉鹑, 隶属于雉鹑属 (*Tetraophasis*), 为我国特有种, 国家 I 级重点保护野生动物。主要分布于西藏东南部、青海东南部、云南省西北部和四川省西部等地。栖息在海拔

3,350~4,600 m 的针叶林、高山灌丛、草甸及林线以上的岩石苔原地带。黄喉雉鹑生活在高海拔环境中,这种环境相对于低海拔地区来说具有高紫外辐射和氧气浓度低的特点。为了进一步了解黄喉雉鹑高海拔适应的分子机制,本研究从头组装了黄喉雉鹑的全基因组并进行了比较基因组学研究。论文已发表在 *Molecular Genetics and Genomics* (Zhou et al. 2019, <https://doi.org/10.1007/s00438-019-01601-8>)。

测序原始数据经质量控制过滤后共获得 68.45 Gb 的二代测序数据,覆盖深度大约为 61 \times 。基于 k-mer 分析评估的基因组大小约为 1.12 Gb,通过 de novo 组装得到 1.02 Gb,其中 scaffold N50 大小为 3.69 Mb。线性分析展示了黄喉雉鹑和红原鸡保守的基因组结构,通过 BUSCO 评估的基因组单拷贝基因完整性为 89.8%。黄喉雉鹑基因组的 GC 含量大约为 41.43%,和已测的海南山鹧鸪 (*Arborophila ardens*)、四川山鹧鸪 (*A. rufipectus*) 以及红原鸡 (*Gallus gallus*) 等鸟类的基因组相似。黄喉雉鹑基因组重复序列大小为 97.60 Mb,约占基因组的 9.60%,包括长散在重复序列 (LINEs, 70,552,303 bp),长末端重复序列 (LTR elements, 13,395,851 bp),短散在重复序列 (SINEs, 685,340) 以及 DNA 转座子 (DNA elements, 11,857,820 bp)。此外,黄喉雉鹑基因组中包含了 307,213 个完美微卫星,其中:单碱基 223,389 个;二碱基 21,571 个;三碱基 18,877 个;四碱基 29,196 个;五碱基 11,807 个;六碱基 2,373 个。本研究共预测到 15,798 个蛋白编码基因,其中 92.71% 的蛋白编码基因能被公共数据库 (TrEMBL, Swissprot, Nr, InterPro, GO 和 KEGG) 支持。

从 12 种鸟的全基因组中鉴定出的 4,886 个 1:1 直系同源基因用于系统进化树的构建,结果展示了雉鹑属和虹雉属 (*Lophophorus*) 的姐妹关系。基于构建的系统进化树和 1:1 直

系同源基因,我们进行了正选择分析。通过比较基因组学分析,本研究发现分布在 HIF-1 信号通路 (map04066),对低氧的响应 (response to hypoxia) (GO: 0001666),对含氧化化合物的响应 (response to oxygen-containing compound) (GO:1901700),三磷酸腺苷结合 (ATP binding) (GO:0005524) 和血管形成 (angiogenesis) (GO:0001525) 通路和高海拔适应相关的一些基因在黄喉雉鹑中受到了正选择作用。在黄喉雉鹑受到正选择作用的基因中,本研究发现在线粒体离子肽酶 1 (LONP1) 中含有一个黄喉雉鹑特有的氨基酸非同义突变,该突变被 PolyPhen-2 评估为损伤性突变。此外,对黄喉雉鹑受到正选择作用的基因进行富集分析发现这些基因能显著富集到 DNA 损伤修复的细胞反应 (cellular response to DNA damage stimulus) (corrected p-value: 0.028006) 和 DNA 修复 (corrected p-value: 0.044549) 通路,这很可能与黄喉雉鹑应对高紫外辐射有关。通过与其他一些鸟类基因组比较,本研究发现与内固醇激素受体活性 (steroid hormone receptor activity) 相关的基因发生了扩张,而与免疫和嗅觉相关的基因发生了收缩。本研究中的基因组数据及发现将有助于了解雉科鸟类的进化历史,同时为进一步了解黄喉雉鹑的高海拔适应分子机制奠定了基础。

(四川:周闯 孟杨 岳碧松)

大湖和小湖的差异:越冬鸭类在中国最大的湖停留时间更长且利用更单一的栖息地

近年来,越冬水鸟在长江中下游湿地两个大湖明显集中,即东洞庭湖 (湖南省, 29°20'N, 113°E) 和鄱阳湖 (江西省, 29°N, 116°20'E)。其他湖泊虽然建立了保护区,但

并未改变水鸟的集中趋势。该趋势可能是由于大湖栖息地人类干扰较小,但我们对该趋势对个体行为影响的驱动因素了解甚少。通过使用 GPS 追踪器追踪了三种鸭(赤颈鸭(*Mareca penelope*), 罗纹鸭(*M. falcata*)和针尾鸭(*Anas acuta*))在越冬期的运动,从三个方面比较了两个大湖和其他小湖差异,即鸭类的栖息地使用、在每个湖泊的停留时间、以及被追踪的鸭类在这些地点每天运动的距离。结果显示,赤颈鸭和罗纹鸭在两个大湖停留的时间比在较小的湖泊停留的时间多 5 倍,且几乎完全使用自然栖息地(占全部栖息地利用的 91~95%)。而在小湖(不包括捕获地点),它们平均停留 28~33 天,栖息地利用也更为多样(包括大约 50% 的湖外栖息地)。本研究首次表明,鸭类在小湖区的短时间停留和多样性栖息地利用,可能有助于解释近年来此类物种在大湖的区域性集中趋势。与之相比,它们在小湖的丰度下降,则可能与小湖栖息地丧失和退化更为明显有关。

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(北京: 孟凡娟 曹垒)

蒙古繁殖翘鼻麻鸭的秋季分散迁徙: 多样性栖息地利用下的一致性选择偏好

许多鸟类种群的迁徙都有较为固定的狭窄迁徙通道,但有些物种或种群会利用分布广泛的停歇地,且在繁殖地和越冬地之间采用的迁徙路线也大相径庭。目前,关于这种迁徙路线差异的原因研究很少。本调查结合

了 GPS 追踪的迁徙数据和遥感数据,对在蒙古繁育的翘鼻麻鸭(*Tadorna tadorna*)在秋季迁徙过程中在内陆停歇地的栖息地选择进行了研究,以解释该种群分散迁徙的原因。通过使用广义线性混合模型,我们分析了种群层次和停歇地层次的栖息地选择。种群层次模型表明,水面年际重现性对鸟类停歇地选择具有的正向效应最大,而耕地和草地覆盖类型具有的负向效应最大,其他土地覆盖类型对鸟类停歇地利用具有弱负向效应。水面季节性和人类活动具有不显著的弱正向效应。尽管停歇地层次模型显示的变量数值存在差异,但方差分解和交叉预测 AUC 评分表明,在秋季分散迁徙中,翘鼻麻鸭不同个体在内陆停歇地的栖息地选择具有高度一致性。这表明,该物种秋季分散迁徙的原因,是适宜栖息地的广泛而分散的分布,而非灵活的栖息地选择。

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(北京: 孟凡娟 曹垒)

近 20 年大别山区人类基础设施的发展加速白冠长尾雉适宜栖息地的减少

在过去 20 年里,中国的人类基础设施发展尤其迅速。这些区域恰好与 IUCN 红色名录的易危物种白冠长尾雉(*Syrnaticus reevesii*)的一个重要分布区域相吻合。作为国家重点保护动物,它是我国中部山区的旗舰物种,在某种程度上对维持天然森林资源

具有重要意义。如果不加以控制,基础设施快速发展将威胁到这种珍稀野生动物的生存。了解白冠长尾雉对生境变化的时空响应,将有助于对土地利用资源的使用和改善生境质量提供基础信息。

为了阐明 2001—2002 年至 2018—2019 年期间人类基础设施发展对白冠长尾雉潜在栖息地的影响,我们比较了三种不同的分布模型:一个具有地形和土地覆盖变量的模型,一个具有地形和人类基础设施发展的模型,以及一个具有所有变量的模型。然后,我们通过 CA-Markov 分析,估计了土地利用/土地覆盖 (LULC) 因素对这些变化的相对强度。最后,我们评估了这两个时期潜在分布范围的破碎化程度。

我们发现,2001—2002 年至 2018—2019 年间,白冠长尾雉的潜在适宜分布范围有所减少。此外,分布范围的方向分布更加拉长,平均中心向东南移动,更接近大别山的最高峰。2000—2015 年,耕地和草地土地类型面积减少,人工表面土地类型面积增加。对 LULC 变化的详细研究表明,荒漠化现象也有发生。破碎化功能分类显示,从 2001—2019 年,白冠长尾雉潜在分布范围中所有不同栖息地类型的面积都有所下降。随着白冠长尾雉可能迁移到更高的海拔,人类基础设施的发展和环境保护需同时加以考虑,以确保这个受胁物种的生存。

(北京:田珊 徐基良;美国:王勇)

基于MaxEnt模型预测白琵鹭 (*Platalea leucorodia*) 在中国东北地区的适宜分布区

运用 MaxEnt 模型与 GIS 空间技术对东北地区白琵鹭的生境适宜性开展了研究。通过分析环境因子如何影响白琵鹭的繁殖生境

适宜性以及这些预测因子的重要性排序,评价白琵鹭在东北地区的适宜生境,预测它的潜在繁殖栖息地。研究发现了白琵鹭适宜生境在东北地区的分布,认为白琵鹭喜好的栖息地都是靠近水源、有植被覆盖、海拔较低的地方,对气候变化也有一定的选择,而人为干扰、距河流距离和土地覆盖对白琵鹭分布影响力较弱。

(北京:李敏 钱法文)

山东荣成越冬大天鹅 (*Cygnus cygnus*) 迁徙路线及重要中途停歇地研究

运用卫星跟踪技术对在山东荣成大天鹅国家级自然保护区越冬的大天鹅进行了跟踪研究。发现山东荣成越冬的大天鹅迁徙途经天津、辽宁、河北、吉林、山西和内蒙古,有 5 条明显的迁徙路线;其度夏地主要位于中国内蒙古、蒙古国及俄罗斯境内;迁徙路线上有多个停歇地,重要的停歇地有辽宁的白石水库、内蒙古的老哈河和西拉木伦河等;还发现大天鹅春季迁徙时间和迁徙距离比秋季的要长。本研究揭示了荣成越冬大天鹅的迁徙路线和迁徙规律,对大天鹅及其栖息地保护管理有重要的科学价值。

(北京:武爱明 钱法文)

鄱阳湖越冬水鸟丰富度变化及其与水位变化的关系

鄱阳湖地处长江南岸,江西省北部,是我国最大的淡水湖,也是全球重要的水鸟越冬地。每年在此越冬的水鸟超过 40 万只,是白鹤 (*Grus leucogeranus*)、东方白鹳 (*Ciconia boyciana*) 和小天鹅 (*Cygnus columbianus*)

等珍稀濒危鸟类的重要越冬地。世界上约 99% 的白鹤和 80% 以上的东方白鹤在鄱阳湖越冬。近年来,受气候变化和三峡工程的影响,鄱阳湖水位发生了明显的改变,丰水期水位抬升,枯水期提前,使鄱阳湖越冬水鸟的生存条件更加复杂多变。在上述背景下,我们分析了 2001—2016 年鄱阳湖越冬水鸟丰富度的变化特征。根据水鸟的生态习性将鄱阳湖越冬水鸟分成游禽 (waterfowl)、涉禽 (wading bird)、岸禽 (shorebird) 和开阔水域鸟类 (open water bird) 共 4 个功能群,以及鹤类、雁类、鸭类、天鹅、鸬鹚类、琵鹭、鸥类和其它等 8 个类群,分别从功能群、类群和种群水平分析了 16 年间越冬水鸟丰富度是否存在显著的变化趋势,并分析了水鸟丰富度变化与鄱阳湖水位变化的相关性。研究结果表明:在同步调查过程中共记录到越冬水鸟 111 种,分属 7 目 18 科。年平均数量为 $426,707 \pm 150,170$ 只,最大值为 725,760,出现在 2005 年;最小值为 264,859,出现在 2012 年。水鸟丰富度存在明显的年际波动,但是总丰富度没有显著的趋势性变化。在 4 个功能群中,游禽和开阔水域水鸟表现出增长趋势,但是并没有达到统计上的显著性。趋势性变化主要发生在种群水平上:在涉禽中,灰鹤 (*Grus grus*) 和东方白鹤显著增加;在游禽中,豆雁 (*Anser fabalis*) 表现出显著的指数增长趋势,赤膀鸭 (*Anas strepera*) 和针尾鸭 (*A. acuta*) 数量显著减少;岸禽中仅有红脚鹬 (*Tringa totanus*) 种群显著减小;开阔水域水鸟中的小鸕鶿 (*Tachybaptus ruficollis*) 和凤头鸕鶿 (*Podiceps cristatus*) 显著增加。水鸟数量与夏季水位表现出显著的相关性,譬如小天鹅丰富度与八月平均水位显著负相关,鸭类丰富度与五月、六月、七月平均水位均显著负相关。雁鸭类是鄱阳湖优势水鸟类群,其主要食物(苦草)的生长受鄱阳湖夏季水位的显著影响,平均水位超过 17.5 m 时,苦草密

度出现崩溃式下降,导致植食性水鸟越冬食物短缺。近年来,受气候变化和三峡工程的影响,鄱阳湖丰水期水位被抬升,丰水期平均水位超过 17.5 m 的频次越来越高,这意味着冬季越冬候鸟食物短缺的概率增大,候鸟向稻田和藕塘等人工湿地扩散有可能会成为新常态。

具体研究结果见: Yankuo Li, Fawen Qian, Janet Silbernagel, Hannah Larson. community structure, abundance variation and population trends of waterbirds in relation to water level fluctuation in Poyang Lake, *Journal of Great Lakes Research*, 2019, 45(5): 976–985.

(江西:李言阔)

红头长尾山雀 (*Aegithalos concinnus*) 的偏性扩散模式可能因地理尺度而异

动物扩散行为一直是进化生物学和行为生态学的研究热点。近年来对少数物种的研究发现,研究的地理尺度可能会影响对动物偏性扩散模式的分析结果。我们在河南董寨国家级自然保护区对红头长尾山雀 (*Aegithalos concinnus*) 的偏性扩散行为进行了研究,发现在 300 m 空间范围内的红头长尾山雀雄性个体之间的亲缘关系要显著高于随机的两个个体间的亲缘关系,但雌性不存在这样的现象,说明在一定地理尺度内雄性红头长尾山雀具有显著的空间遗传结构,而原因可能在于红头长尾山雀存在偏雌扩散的现象。对重捕的环志个体的分析也发现,雌性后代的平均出生扩散距离要显著远于雄性后代 (1,240 m vs. 289 m),也支持红头长尾山雀的偏雌扩散的结论。但该结果与 Dai et al. (2002) 研究发现的我国红头长尾山雀不同种群间存在雄性基因流(即偏雄扩散)的结果相反。由于我们研究过程中曾有两只雄

性个体在距原捕捉地约 4.8 km 的地方被重捕, 是发现的雌性扩散最远距离的两倍, 我们推测上述关于该物种偏性扩散模式的截然不同的研究结果可能与研究的地理尺度有关。在我们研究的地理尺度 (单一种群) 上, 红头长尾山雀可能以雌性扩散为主, 但在更大的地理尺度 (分布区尺度), 雄性个体可能存在比雌性更长距离的扩散行为, 从而对种群间的基因流贡献大于雌性, 导致种群间偏雄性的基因流。虽然上述猜测有待进一步证实, 但是这些结果说明在研究动物的扩散模式时, 地理尺度可能是一个很重要的因素需要予以考虑。上述结果详见 Li et al. (2013) Sex-biased dispersal patterns of a social passerine: complementary approaches and evidence for a role of spatial scale. *Biological Journal of the Linnean Society*, 128(3): 592–602.

(北京: 李建强 张正旺)

研究生论文选登

鸭绿江口湿地食物变化对迁徙鹬类的影响

黄渤海区域的滨海滩涂湿地为东亚 - 澳大利西亚候鸟迁飞区鸻鹬类提供了重要的迁徙停歇地。由于人类活动的影响, 黄渤海区域滨海滩涂湿地快速丧失和退化并导致东亚 - 澳大利西亚候鸟迁飞区很多鸻鹬类种群数量快速下降。大量研究关注于迁徙停歇地丧失对鸻鹬类种群的影响。然而, 黄渤海区域滩涂上鸻鹬类的食物变化对鸻鹬类的影响长期未受到关注。鸭绿江口湿地是黄渤海区域鸻鹬类最重要的迁徙停歇地之一, 支持着该区域已知数量最大的斑尾塍鹬 (*Limosa lapponica*) 和大滨鹬 (*Calidris tenuirostris*) 迁徙种群, 为两种鹬类提供了关键的能量补

给地。本研究以鸭绿江口湿地为研究地点, 以大滨鹬和斑尾塍鹬两种鹬类为研究对象, 采用大型底栖动物调查、鸟类数量调查、粪便及呕吐物分析、觅食行为分析、形态测量等方法, 从种群动态、食物生态位分化、生理和行为特征等方面探讨了鹬类对迁徙停歇地食物减少的响应, 并通过人为食物补充实验, 分析了人为干预对迁徙鹬类保护的作用。主要结论如下:

1) 2011 至 2016 年, 鸭绿江口湿地大型底栖生物的生物量急剧减少, 主要是由于光滑河蓝蛤 (*Potamocorbula laevis*) 数量减少导致的, 而其他类群的底栖动物在研究期间无显著变化。光滑河蓝蛤是斑尾塍鹬和大滨鹬的主要食物, 其密度在 2011 年至 2016 年下降了 99%。鸟类调查结果表明, 斑尾塍鹬 *baueri* 亚种和大滨鹬的高峰数量一直维持相对稳定, 但迁徙期相对较晚的斑尾塍鹬 *menzbieri* 亚种在鸭绿江口湿地的高峰数量下降了 91%。

2) 两种鹬类均采取改变食物组成、增加食物生态位宽度、取食更多食物种类的方式来应对高质量食物光滑河蓝蛤的减少。大滨鹬食谱宽度指数由 2011 年的 0.001 增加到 2018 年的 0.093, 斑尾塍鹬的食谱宽度指数由 2011 年的 0.053 增加到 2018 年的 0.15。食物减少后, 虽然斑尾塍鹬雌雄个体间的食物生态位重叠度并无显著降低, 但是斑尾塍鹬和大滨鹬种间的食物生态位重叠度降低显著。在食物匮乏的年份 (2016—2018), 斑尾塍鹬和大滨鹬种间的食物生态位重叠度由停歇早期的 0.63 下降至晚期的 0.07。尽管有 25% 的大滨鹬和 52% 的斑尾塍鹬在食物匮乏的年份放弃利用鸭绿江口湿地, 仍利用鸭绿江口湿地的两种鹬类个体的食物摄入速率均显著下降。

3) 大滨鹬在 2011—2012 年主要以外壳较薄的光滑河蓝蛤为食, 在 2016—2017

年主要以外壳坚硬的托氏昌螺 (*Umbonium thomasi*) 为食。大滨鹑的觅食方式是将带壳的软体动物整个吞下, 靠肌胃将软体动物的壳压碎以进一步消化食物。与 2011—2012 年相比, 大滨鹑在 2016—2017 年肌胃需要 3~11 倍的力量才能将所取食的食物外壳压碎。2016—2017 年大滨鹑的肌胃平均重量与 2011—2012 年相比增加了 15%, 这使得它们处理食物的速率增加了 32%。在行为方面, 大滨鹑在 2016—2017 年将托氏昌螺不能被消化的实心钙质螺旋部分以呕吐物的形式排出体外, 而不是通过粪便的形式经消化道排出体外。虽然大滨鹑面对食物数量减少和质量降低在形态和行为上做出调整, 但是与 2011—2012 年相比, 食物摄入速率仍然下降了 85%。

4) 在个体水平上, 大滨鹑的食物组成与喙长无关, 而与肌胃重量有关。肌胃重量与托氏昌螺的数量比例呈显著正相关。肌胃重量和小型托氏昌螺的数量比例呈显著负相关, 与大型托氏昌螺的数量比例呈显著正相关。肌胃越大, 食物中具有坚硬外壳的托氏昌螺比例越高, 大型托氏昌螺占的比例也越高。肌胃中壳碎片干重和与喙长没有显著相关性, 但与肌胃重量呈显著正相关关系。喙长与肌胃中食物的平均压碎力量没有显著相关性, 但与肌胃重量呈显著正相关。

5) 为了探究在食物匮乏的情况下开展人工补充食物的方法并评估食物补充的效果, 本研究开展了大滨鹑食物补充实验。超过鸭绿江口湿地总数量 40% 的大滨鹑集中在投放光滑河蓝蛤的区域觅食。大滨鹑在投食区主要取食投放的光滑河蓝蛤, 在未投食的对照区域主要取食托氏昌螺。大滨鹑在投食区的食物摄取速率是在对照区域的 4.2 倍。大滨鹑在对照区拒绝摄取搜索到的食物的频率是投食区的 2.2 倍; 对食物的平均处理时间是投食区的 5.5 倍。

综合上述研究结果, 本研究发现: (1) 能量补给地的食物不足可能是导致东亚 - 澳大利西亚候鸟迁飞区鹑类种群数量下降的一个重要但被忽略的因素。对迁徙鸟类保护来讲, 维持关键能量补给地的栖息地质量与确保栖息地面积不减少同样重要。(2) 在食物丰富的年份, 大滨鹑和斑尾塍鹑可以共同利用丰富的高质量食物。在食物匮乏的年份, 大滨鹑和斑尾塍鹑通过增加各自的食物生态位宽度、减小食物生态位重叠度的方式减小种间竞争。(3) 尽管鸟类可以通过生理、形态、觅食行为等方面的适应性调整来应对食物匮乏, 但并不能完全抵消食物下降对能量积累速率的不利影响。这可能会使候鸟无法完成迁徙活动并最终导致种群数量下降。(4) 人为补充适宜的食物能够显著提高鸟类的能量积累速率, 对于临时解决候鸟的食物短缺问题有重要作用。但为了从根本上解决食物短缺的问题, 需要查明食物减少的原因并采取恢复食物的自然供给。

本研究结果揭示了迁徙停歇地食物减少对鹑类的种群数量以及生理、生态、行为等方面的多重影响, 对于进一步认识生物对环境变化的适应以及适应程度的有限性提供了重要依据。

(复旦大学博士生: 张守栋, 导师: 马志军)

鹑类和雉物种多样性格局形成和维持机制研究

随着人口的增长和气候变暖, 全球的生态系统遭受了严重的破坏, 使得生物多样性正面临日益严重的威胁。研究物种的分布格局, 可以确定物种的多样性中心, 有助于在制定生物多样性保护计划时划定保护优先区。研究物种多样性格局的形成和维持机制, 可以了解物种多样性对环境的响应, 从而预测

未来的环境变化对物种多样性的影响,从而提前制定合理的保护计划。中国 - 喜马拉雅山区包含了全球 10% 的脊椎动物和 8% 的植物,是全球最重要的生物多样性热点地区之一。虽然已有一些研究尝试解释该地区物种多样性格局的形成机制,但是该地区作为生物多样性热点的成因,以及维持该地区极高的物种多样性的机制尚不清楚。我们以两个不同演化时间 (evolutionary time, *EvolTime*) 的鸟类类群: 雉类 (古老类群, 起源于始新世末期 - 渐新世早期) 和 鹇类 (年轻类群, 起源于中新世早期) 为研究对象, 从生态、演化和功能多样性的角度出发, 探讨了物种多样性格局的形成和维持机制, 以揭示中国 - 喜马拉雅山区成为物种多样性中心的成因。本论文主要包括以下四部分研究内容: (1) 鹇类的系统发育分析和分类修订; (2) 演化时间、多样化速率 (diversification rate, *DivRate*) 和扩散对鹇类物种多样性格局的影响; (3) 生态过程和演化过程对雉类物种多样性格局的影响; (4) 功能特征分化对鹇类物种共存的影响。

鹇类是一个分类十分混乱的类群, 曾被称为分类上的“烂摊子”, 目前还没有研究基于广泛的采样去分析它们的系统发育树和修订分类系统。为了解决这一问题, 我们基于 12 个基因标记, 并用多个时间校正点, 构建了包括 89% 的全部鹇类物种的系统发育分歧时间树, 并对该类群作了分类修订。结果表明, 鹇类大约起源于 22 百万年前 (million years ago, Ma) (95% highest posterior densities, HPD: 26.4~18.6 Ma), 主要包括 7 个演化支, 大部分属都是并系属。根据该系统发育树的结果, 我们对鹇类的分类进行了修订, 建议将鹇类划分为 7 个科, 包括鸢鹇科 *Sylviidae*, 绣眼鸟科 *Zosteropidae*, 鸦雀科 *Paradoxornithidae*, 鹇科 *Timaliidae*, 幽鹇科 *Pellorneidae*, 雀鹇科 *Alcippeidae* 和噪鹇科

Leiothrichidae; 此外, 我们比较了属级阶元间的形态和生态相似性, 参考 10 Ma 的阈值, 大致将鹇类划分为 64 属。该分类修订提出了一个新科 (雀鹇科 *Alcippeidae*) 和一个新属 (领凤鹇属 *Parayuhina*)。该部分的研究为后面鹇类的生物地理学、物种多样性格局和物种共存研究提供了数据基础。

鹇类的分布并不均匀, 中国 - 喜马拉雅山区物种多样性最高, 而在全球其他地区物种多样性较低。中国 - 喜马拉雅山区物种多样性较高可能是较高的多样化速率、多次扩散和较长的演化时间累积更多物种这三个演化过程直接作用的结果。在该部分研究中, 我们基于较为完整的鹇类系统发育树, 旨在验证多样化速率、扩散和演化时间这三个演化因子对全球鹇类物种多样性格局的影响, 以探究中国 - 喜马拉雅山区作为鹇类物种多样性热点的成因。首先, 我们基于 13 个地理区, 重建鹇类的祖先分布区, 推断鹇类的起源和扩散路径, 并估算每个地理区内的扩散事件和最早拓殖时间。然后我们分析了 7 个地理区内物种家系累积随时间的变化; 鹇类各支系的分化速率随着时间的变化; 以及中国 - 喜马拉雅山区与其他地区和大陆与岛屿间的成种速率、灭绝速率和扩散速率的差异。最后, 我们用一般线性模型检验了 13 个地理区内的物种多样性与多样化速率、首次拓殖时间以及扩散事件数量之间的相关性。我们的研究结果发现, 鹇类在中新世早期起源于中国 - 喜马拉雅山区, 而后扩散到其他地区, 表明鹇类在中国 - 喜马拉雅山区物种累积的时间最长。分化速率分析表明, 鹇类的成种速率在 2.5 Ma 时快速增加, 这与绣眼鸟属 *Zosterops* 在海洋岛屿的快速成种有关, 该时间与第四纪冰期循环导致的海平面升降的时间吻合。一般线性回归分析表明, 鹇类物种多样性与首次拓殖时间相关, 与扩散事件的次数和多样化速率无关。根据以上结果,

我们可以得到以下结论：(1) 鵑类的物种多样性格局主要受到“时间-成种效应”的影响,即中国-喜马拉雅山区是鵑类的起源中心,鵑类在该地区物种多样性高是长时间演化的结果,而与多次扩散和多样化速率无关；(2) 海洋岛屿是鵑类的分化中心,这主要与第四纪冰期导致的海平面下降有关：海平面下降使得浅海地区形成新的陆地,物种从大陆扩散进入这些空白生态位,随后间冰期海平面上升,使得各种群在岛屿上隔离成种。

中国-喜马拉雅山区比临近的低地拥有更高的物种多样性,为了解释这一格局,学者们曾提出多种生态和演化假说,主要包括生态约束假说、能量约束假说、多样化速率假说、拓殖频率假说和“时间-成种效应”假说。在该部分研究中,我们以雉类作为研究对象,旨在验证以上5种假说对中国-喜马拉雅山区物种多样性格局形成的直接影响和间接影响,以探讨物种多样性格局的形成机制。基于物种分布模型预测的雉类分布区、多基因构建和多个化石校正的雉类系统发育分歧时间树、雉类的功能特征和气候数据,我们使用皮尔斯相关性分析和结构方程检验了初级净生产力 (net primary productivity, NPP)、生态位多样性 (niche diversity, NicheDiv)、多样化速率、演化时间和拓殖频率对物种多样性的影响。同时,我们重建了雉类的祖先分布区,分析了系统发育树基部类群和衍生类群的分布格局,以更好的理解物种多样性格局的形成机制。研究结果发现,雉类可能在渐新世早期 (33 Ma, 95% HPD : 28.7~38.2 Ma) 起源于非洲,随后扩散到中国-喜马拉雅山区以及全球其他地区。在中国-喜马拉雅山区,物种多样性与多样化速率、初级净生产力、生态位多样性和拓殖频率高度相关,与演化时间没有相关性。结构方程表明,多样化速率和生态位多样性对物种多样性的直接影响比初级净生产力和演化时间的直接影

响更强。初级净生产力主要通过多样性速率间接地影响物种多样性,而生态位多样性通过多样化速率对物种多样性的间接影响力较弱。我们的研究表明,可用生态位空间的增加,快速分化和多次拓殖是造成中国-喜马拉雅山区物种多样性高于临近低地的直接因素；初级生产力对物种多样性格局的形成也有重要的影响,但主要通过改变多样化速率影响物种多样性。因此,中国-喜马拉雅山区物种多样性高是生态和演化机制共同作用的结果。

鵑类物种丰富,形态和行为差异大,在中国-喜马拉雅山区高度同域分布,是研究物种共存机制的最佳类群。通常认为,同域分布的物种为了避免激烈的种间竞争,需要在生态、食性或觅食层等一个或多个维度上存在差异；而对于同域分布的近缘种,还需要在羽色和鸣声等与性选择相关的特征上发生分化,以避免种间杂交的发生。同域物种间的特征分化可能由两种不同的过程导致：(1) 快速成种导致物种间的特征分化；(2) 长时间演化导致物种间的特征存在差异。然而,目前关于特征分化与物种共存之间关系的研究较少,其内在机制也尚不清楚。该部分研究旨在分析物种形态、食性、鸣声和羽色等生态和性选择特征的分化对物种共存的影响,同时检验多样化速率和演化时间对特征分化的影响,以揭示物种多样性的维持机制。研究发现,共存物种的数量与鸣声和羽色等相关的社会性特征和性选择特征的功能分散指数 (代表特征分化) 显著相关,而与形态和食性功能分散指数没有相关性。结构方程的结果表明,共存物种的数量主要与性选择特征的分化直接相关,这一过程受到演化时间的影响,而与多样性速率无关。因此,在中国-喜马拉雅山区,鵑类高度同域分布是长时间演化导致的性选择特征分化的结果,这种性选择特征的分化可能促进物种间的生

殖隔离,使得同域分布种稳定共存。

基于以上几个研究,我们发现中国 - 喜马拉雅山区物种多样性热点的形成机制不同:对于年轻类群(鹇类)来说,中国 - 喜马拉雅山区物种多样性高是长时间演化、积累更多物种的结果;对于古老类群(雉类)来说,中国 - 喜马拉雅山区物种多样性高是快速分化和多次扩散的结果。也就是说,中国 - 喜马拉雅山区是鹇类的起源中心,是雉类的扩散中心和分化中心。中国 - 喜马拉雅山区不同类群物种多样性格局的形成机制存在差异可能与该地区的地质历史有关:青藏高原大约在渐新世早期达到 4,000 米,因此在雉类形成的早期,中国 - 喜马拉雅地区尚不能为雉类提供适宜的栖息地,随着后来中国 - 喜马拉雅山区栖息地的形成,才逐渐为雉类提供了适宜生境,成为雉类的扩散中心和分化中心;但是鹇类形成于中新世早期,在这个时期,中国 - 喜马拉雅山区大部分地区已形成现有格局(横断山除外),可以为鹇类的祖先种提供适宜的栖息地,使得鹇类在该地区长时间分化和积累更多的物种。因此,我们在理解一个地区多样性格局的形成机制时,不仅需要综合分析不同类群的生态和演化历史去探究物种多样性格局的形成过程,而且需要考虑该地区的地质和气候历史。最后,我们发现中国 - 喜马拉雅山区物种多样性的维持机制具有一致性:(1) 在雉类中,物种多样性与生态位多样性(相当于功能多样性)相关;(2) 在鹇类中,共存物种数量与性选择相关的功能特征多样性相关。这一结果表明共存物种功能特征的分化可能是维持物种共存的主要途径。

(中科院动物所博士生:蔡天龙,导师:
雷富民)

山雀科鸟类的进化历史及其高海拔环境的适应机制

自然选择是适应进化的主要驱动力,进化过程中环境变化所驱动的强烈选择压力使生命体产生生理、表型或遗传的适应性改变,并在它们的基因组中烙有适应性变异的遗传印迹。由于青藏高原的隆升导致了区域性的气候变冷、氧含量降低和生境开放等环境的剧烈变化,显著影响了当地生物的分布与生存,使青藏高原成为了现今适应性进化研究的热点区域。起源于中国 - 喜马拉雅地区的山雀科(Aves: Paridae)鸟类是一类具有丰富研究基础的小型雀形目鸟类,不仅具有广泛的水平分布且具有长跨度的垂直海拔分布,是研究高海拔环境适应的理想模式系统。本研究共获得 19 个高低海拔山雀科物种的 87 号样本的全基因组重测序数据,以及地山雀(*Pseudopodoces humilis*)和大山雀(*Parus major*)胚胎上喙的转录组数据,结合系统发育学、种群遗传学、形态学、进化发育学、比较基因组学和比较转录组学的研究方法,对山雀科鸟类的进化历史、高海拔低氧适应机制、以及青藏高原腹地开放性生境适应机制三部分内容进行了探讨,得到以下结果。

(1) 基于全基因组 SNPs 位点的最大似然树和物种树显示了完全一致的拓扑结构,基本支持了现有的山雀科物种的系统发育关系,但确证了颇有争议的地山雀分类地位,明确了地山雀与 *Machlolophus* 属的亲缘关系最近;证实了黑胸山雀(*Poecile palustris hypermelaenus*)是沼泽山雀(*Poecile palustris*)的亚种,而并非褐头山雀(*Poecile montanus*)的姐妹种。

(2) 发现储食与不储食进化分枝之间的遗传分化主要发生在与外部或非生物因子刺激响应相关的基因组区域。这些高分化区域所蕴含的基因被注释到与大脑和海马体的发

育以及对光或声音刺激的感知显著相关, 这从遗传上进一步证明了储食与不储食分枝间的分化与储食行为和鸣声有关。

(3) 发现山雀科起源于渐新世 (24.8 Mya), 不支持之前提出的中新世起源假说, 与青藏高原南部地区的隆升时间 (约 35~20 Mya) 一致。随后的山雀科分枝多样化发生在晚中新世 (8.8~5.1 Mya), 与青藏高原横断山区最后的隆升时间 (约 10 Mya 至今) 相符。

(4) 核苷酸多样性的分析发现, 相对于其它鸟类 (10^{-3} ~ 10^{-2}), 山雀科鸟类的遗传多样性非常低 (0.073×10^{-3} ~ 1.77×10^{-3})。遗传多样性地理分布图显示, 西部高海拔山区的山雀的遗传多样性明显低于东亚低海拔地区山雀的遗传多样性。

(5) 种群历史动态推断结果显示, 大多数的山雀科物种在更新世期间经历了显著的种群波动。且发现了与遗传多样性和第四纪冰川一致的地理分布模式, 即大多数西部高海拔山区物种在末次冰期经历了剧烈的种群收缩, 而东亚低海拔地区物种却经历了种群的扩张。然而, 少数几个物种的种群动态不受冰期活动的影响, 结合遗传多样性和残留的分布区, 我们推测它们不同的历史种群动态可能是由分布区改变所导致的。

(6) 分别从核苷酸、基因和生物学功能水平对山雀科低氧适应机制进行了探讨, 通过不同的 Fst 分析发现, 高海拔山雀之间没有趋同的核苷酸替代, 虽然发现 HBA 基因簇在高海拔山雀中具有高度的分化, 但并不是所有物种的 HBA 基因簇中都具有一致性的适应性氨基酸突变。然而, 所有高海拔山雀都

发现了共性的, 许多与呼吸、循环、肌肉以及能量系统相关的低氧适应性基因, 尤为与能量系统中的脂代谢相关的基因最多, 其中 PLB1 在多数高海拔山雀中具有最多的非同义突变的固定位点。

(7) 形态特征分析显示, 地山雀长而弯曲的喙是青藏高原腹地开放生境的最适应表型。地山雀和大山雀 HH28/29 胚胎上喙的基因表达差异分析发现了 17 个与骨骼发育与形态发生相关的基因, RT-qPCR、原位杂交以及鸡胚的功能试验都验证了 FGF13 和 ITGB3 可能通过调节成骨细胞和破骨细胞的分化而影响地山雀喙的形态发生。此外, Fst 和 PMT 分析检测到了 7 个基因与骨骼形态发生与重塑相关, 但中性检验和功能预测发现只有高度保守的 COL27A1 基因在地山雀中遭受了强烈的正选择, 且其功能域的 R1493Q 和 P1501L 突变被预测可能导致其蛋白功能的改变。

综上所述, 青藏高原隆升不仅影响山雀科鸟类的起源与多样化, 且通过其驱动的环境变化影响山雀科鸟类的地理分布及其内在的基因组印记, 使高海拔山雀具有与低海拔山雀完全不同的种群历史, 使高海拔山雀产生生物学功能水平趋同的低氧适应机制, 也使高原特有种地山雀形成特化的多基因、多水平调控的喙型。进化历史和自然选择的综合作用最终导致了山雀科鸟类低水平的遗传多样性。

(中科院动物所博士生: 程亚林, 导师: 雷富民)

环志简报



2019年全国秋季鸟类环志培训班在抚远举办

9月23—28日,全国鸟类环志中心在黑龙江省抚远市举办“2019年全国秋季鸟类环志培训班”,参加培训班的学员分别来自全国各鸟类环志站新参加环志工作的人员,共计27个单位40余人。

培训主要采取室内授课与野外实践相结合。培训班上,全国鸟类环志中心相关领导专家分别总结介绍了《野生动物保护法》以及鸟类环志管理、全国鸟类环志概况、鸟类学基础知识、鸟类环志技术规程、鸟类识别与分类、佩戴和迁徙鸟类追踪等相关技术以及环志技术野外操作等内容。

培训期间,各环志站相互交流了环志情况、经验以及对出现的问题所采取的解决办法。培训最后还通过试卷考试以及野外实践考核的方式考核培训人员,基本全部考核通过。

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

本次培训班得到黑龙江三江国家级自然保护区管理局的大力支持和帮助。

(北京:陈丽霞 王毅花)

2019年董寨保护区鸟类环志简报

2019年董寨保护区共开展环志10余次,共环志鸟类5,581只,隶属于6目23科77种。其中重捕2目10科17种计146只。

另外捕获归家鸟类黄喉鹀1只,红胁蓝尾鸲3只,发冠卷尾1只,白眉姬鹀1只,红翅凤头鹀1只。重捕黄喉鹀1只,环号为B120-0223。

本年度捕获蓝喉仙鹩1只,据文献显示为董寨鸟类新记录。捕获栗耳凤鹛88只,据文献显示为河南省鸟类新记录。

2012年董寨环志站被全国鸟类环志中心批准为全国候鸟监测网络15个地点之一。结合本站点资源状况,确定每年定期于夏季5月10日—26日和冬季11月10日—26日各进行一次候鸟监测。根据全国候鸟监测任务目标,环志站即时组织人员分春夏季和冬季按时完成本年度的候鸟监测任务。

(河南:溪波 杜志勇 张俊峰)

2019年新青鸟类环志站环志简讯

2019年共环志鸟类7目24科65种30,164只,其中:重捕553只,归家244只,新增鸟种2种,分别为H03-2548丘鹑(*Scolopax rusticola*)、F09-3677小田鸡(*Porzana pusilla*)。异地环志本地回收1只:4月17日在新青南山网场回收KANKYOSHO2AK JAPAN93827黄喉鹀(日本石川县株洲市内

浦纳戈于2018年10月31日环志)

今年的优势鸟种依然是白腰朱顶雀 (*Carduelis flammea*) 7,421 只、田鸫 (*Emberiza rustica*) 5,470 只、灰头鹀 (*Emberiza spodocephala*) 4,208 只、红喉歌鸲 (*Luscinala calliope*) 2,041 只、燕雀 (*Fringilla montifringilla*) 1,715 只、锡嘴雀 (*Coccothraustes coccothraustes*) 1,258 只。

自2007年环志以来,新青鸟类环志站在本区共记录18目46科223种,已环志14目41科193种453,872只。

(黑龙江:侯林祥 李红伟)

青峰鸟类保护环志站2019年秋季环志工作简讯

黑龙江省兴隆林业局青峰鸟类保护环志站 (E128°10'00", N46°21'42"), 2019年秋季环志工作在8月15日开始,于11月15日结束。共计环志鸟类4目19科67种8,993只,其中归家10种34只,重捕8种33只。

今年秋季途经青峰迁徙的候鸟数量相比,雀形目为最多,环志了16科61种8,941只,占总环志量的99.4%,非雀形目环志了3目3科6种52只,占总环志量的0.6%;雀科环志数量最大,环志了9种3,993只,占总环志量的44.4%;其次是鹀科环志10种3,459只,占总环志量的38.5%;鹁科环志8种343只,占总环志量的3.8%;莺科环志9种230只,占总环志量的2.6%;岩鹳科环志1种322只,占总环志量的3.6%;绣眼鸟科环志1种18只,占总环志量的0.2%;鹡科环志4种39只,占总环志量的0.4%;鹁鹁科4种21只,占总环志量的0.2%;伯劳科环志2种7只,占总环志量的0.1%等。

今年秋季的环志种类数量和去年秋季相比,种类一样,数量比去年多了将近两千只,

在同等人数和下网数量相同的情况下,分析其原因是因为今年朱顶雀数量突然增多,去年一只也没有发现,今年却环志了两千多只,这是特别值得欣喜的。

(黑龙江:阳艳岚)

黑龙江双河国家级自然保护区2019年鸟类环志简讯

2019年黑龙江双河国家级自然保护区开展鸟类环志,并且在保护区领导的支持下与疫源疫病监测同步进行。

春季,2019年4月11日进驻双河保护区中心站开展环志工作,根据环志站周边情况,因地制宜选出4块网场,清除网场内的杂草、树木,布设粘网6片。由于天气干旱等一些客观原因截止到5月10日共环志300余只鸟,23种。

秋季,通过对网场的调换,确定环志时间,进一步摸清环志规律,增加了张网数量。9月20日至10月18日,在中心站开展了秋季鸟类环志工作,使秋季环志数量有了很大的提升,共布设粘网8片,环志1,047只,23种。

疫源疫病采样方面我们通过实践经验总结出不伤鸟的办法,用肛式采样法对小鸟的伤害比较大,我们采取的是通过环志完把每种鸟分开,放到不同的鸟笼里,等小鸟便出粪便在采集放到容器中,并做好记录。2019年共完成采集鸟粪便150多份。

(黑龙江:陈鹏)

为哀牢山候鸟迁徙保驾护航

哀牢山连绵起伏,纵贯南北,座座群山成为候鸟迁徙的道道屏障,金山丫口是大量候鸟翻越哀牢山的必经之路。

2019 年 8 月下旬，哀牢山新平金山丫口鸟类监测环志站工作人员正式入住环志站开展秋冬季鸟类监测环志工作。同时广东省生物资源应用研究所的赵雪冰博士依托新平环志站，在鸟类环志期间开展了“不同波长光对夜间迁徙候鸟影响研究”，通过几个月的实验研究，取得了良好的成效，达到了预期的目的。截止目前环志已圆满结束，共捕获鸟类 3,337 只，环志鸟类 3,299 只，原地重捕

38 只，共 12 目 22 科 129 种，其中国家Ⅱ级保护鸟类 6 种，与往年鸟类环志相比新增鸟类记录为 14 种，环志的鸟类是近五年来数量最多、种数最多、新增记录最多的一年。

哀牢山新平管护局将不忘初心，牢记使命，为候鸟保驾护航，增加候鸟越过哀牢山的安全感，同时为我县生态文明建设做出应有的贡献。

（云南：普秀）



Avian Research 入选中国科技期刊卓越行动计划“梯队期刊”建设项目

2019年11月，中国科技期刊卓越行动计划办公室公布了入选计划的期刊，由中国动物学会鸟类学分会和北京林业大学共同主办的 *Avian Research* 入选了该计划的“梯队期刊”项目。

为深入贯彻落实中央关于培育世界一流科技期刊的重要指示精神，认真落实《关于深化改革 培育世界一流科技期刊的意见》，推动我国科技期刊高质量发展，加快建设世界一流科技期刊，夯实进军世界科技强国的科技与文化基础，中国科协、财政部、教育部、科学技术部、国家新闻出版署、中国科学院、中国工程院等七部门联合实施了中国科技期刊卓越行动计划。该计划2019年9月开始分领军期刊、重点期刊、梯队期刊、高起点新刊、集群化试点等5个子项目进行申报，11月初完成答辩评估。全国共有近860多份期刊进行了申报，经过资格审查、定量评价、答辩评审和世界一流科技期刊建设专家委员会复核，最终产生了入选项目共计285项（英文期刊180项，中文期刊100项，集群化试点5项）。由中国动物学会鸟类学分会和北京林业大学共同主办的 *Avian Research* 经激烈竞争，入选“梯队期刊”项目，将获得由该计划40万元/年的经费支持，项目建设期5年。

项目建设期间，期刊编辑部将在立足自身功能定位的基础上，进一步提升办刊专业化和国际化水平，加强传播能力和服务能力

等方面的建设，力争期刊的国际影响力再上一个新台阶。希望广大会员多多关注和支持期刊的发展，积极贡献高质量的稿件。

（北京：程朋军）

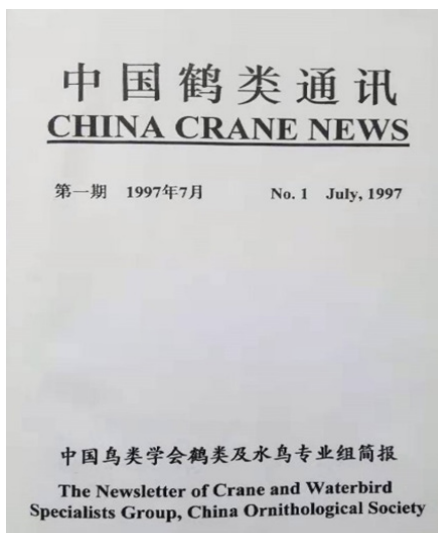
《中国鹤类通讯》走过23年——略述国际鹤类基金会与中国鸟类学会的合作出版《中国鹤类通讯》

1997年，《中国鹤类通讯》创刊了，这也开启了国际鹤类基金会与中国鸟类学会20多年的合作。《中国鹤类通讯》是由国际鹤类基金会资助、中国鸟类学会鹤类和水鸟专家组主办的刊物。中国鸟类学奠基人郑作新院士特为本创刊题了词，中国鸟类学会理事长郑光美撰写发刊词。

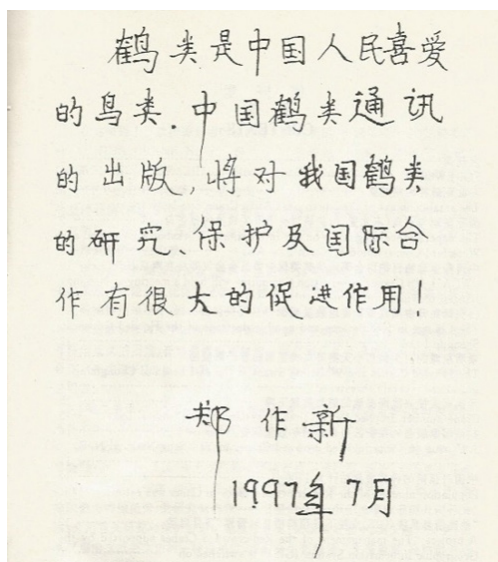
《中国鹤类通讯》为中英文内部刊物，主要报道中国鹤类与水鸟的研究、保护、饲养、管理和宣传教育等工作的动态和阶段成果，也报道国外鹤类研究动态及其它水鸟有关信息，旨在促进鹤类与水鸟信息交流。自创刊以来，《中国鹤类通讯》共计出版23卷39期，内容涵盖鹤类研究监测、保护管理、迁徙、环境教育、饲养繁殖等，也大量报道了其他水鸟的研究保护工作。其中2015年为鄱阳湖和黑颈鹤两个专刊。

在此感谢《中国鹤类通讯》历任主编王岐山（1997—2010）、苏立英（2010）、丁长青（2011—2012）、邹红菲（2011—2019）。感谢中国科学院动物研究所徐延恭老师、马

逸清、杨兆芬、马志军、韩联宪、金杰锋、吴庆明、周立志、马蕊、李峰、张有瑜、张智、王卉、郑昕、胡雅滨、王丽君、李丁男、蒋一婷、丁伊真、董海燕等为《中国鹤类通讯》所做的筹稿、编辑和翻译工作。



《中国鹤类通讯》首期



郑作新院士为《中国鹤类通讯》创刊的题词



《中国鹤类通讯》封面

主办国际鹤类学术研讨会

除了出版《中国鹤类通讯》外，国际鹤类基金会与中国鸟类学会也开展了其他的合作。

2002 年在北京共同举办了国际鹤类研讨会，来自 12 国家 86 名中外代表参加了会议，就区域性鹤类研究和保护、鹤类与环境、鹤类的饲养与繁殖生物学、鹤类环志与迁徙、鹤类研究与保护展望五个议题进行了广泛交流与讨论。在 2002 年北京召开的国际鹤类学术研讨会上，国际鹤类基金会为安徽大学王岐山教授在中国鹤类及其他鸟类的研究保护所做的杰出贡献，颁发了荣誉证书。在 2002 年鹤类研讨会上，中国国家林业局保护司王伟副司长代表东北亚鹤类网络为黑龙江兴凯湖、山东黄河三角洲、江苏盐城、江西鄱阳湖、黑龙江三江、黑龙江扎龙、吉林向海、辽宁双台河口、安徽升金湖、贵州草海等共 10 个鹤类自然保护区颁发了东北亚鹤类网络成员证书。

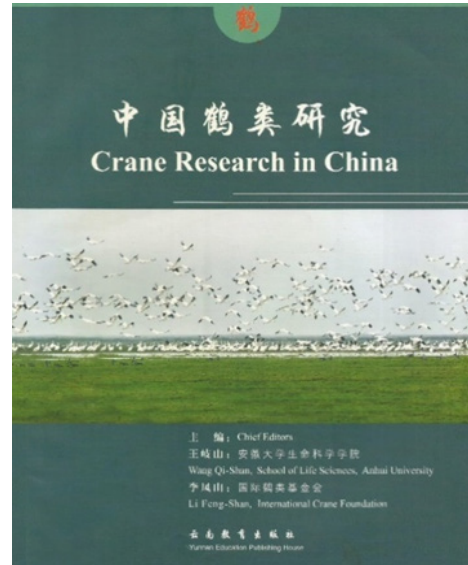


安徽大学王岐山教授为一直从事中国鹤类研究和保护工作，其中包括多年负责征稿和编辑《中国鹤类通讯》。这是在 2002 年国际鹤类学术研讨会上，国际鹤类基金会主席 Jim Harris 为王岐山先生颁发荣誉证书

《中国鹤类通讯》于 2002 年为迎接国际鹤类学术研讨会在北京召开专门出版了一个增刊。



《中国鹤类通讯》第 6 卷增刊 - 国际鹤类学术研讨会
论文摘要集



2005 年出版的《中国鹤类研究》，汇集了自 1990 年
《国际鹤类保护与研究》出版以来中国鹤类研究的多
项成果

出版鹤类书籍

2005 年,《中国鹤类研究》(云南教育出版社)和《中国鹤类研究文献题录》(安徽大学出版社)出版。《中国鹤类研究》收录了 28 篇科学研究文章,汇集了当时有关中国鹤类现阶段的主要研究成果,涵盖鹤类研究综述、数量分布、栖息地、繁殖、迁徙、食物、行为、生化、疾病防治和谱系分析,在一定程度上反映了该阶段鹤类研究内容和学术水平。《中国鹤类研究文献题录》收录了中国鹤类研究的文献共 1,000 余条,包括中国人做的中国鹤类的研究工作,以及外国人在中国做的有关中国鹤类的研究工作。一些在中国动物园开展的国外鹤类物种的饲养和繁殖工作也收录在内。可以说此书在当时是一本鹤类文献索引大全。

设立中国鹤类研究基金

中国鹤类研究基金于 1999 年设立,为小额基金项目,重点面向从事中国鹤类野外研究工作的研究生和基层科研人员,每年资助 1~3 项,每项资助额度为 1,500 美元。为了更好地管理中国鹤类研究基金,中国鸟类学会鹤类和水鸟专家组组成了鹤类研究基金管理小组,定期组织基金申请评审和成果评估。在 1999—2008 年期间,本基金为国内 20 名鹤类研究人员,21 个鹤类小型科研项目提供了资助。鹤类研究基金虽然额度较小,但也为年轻的和基层的鹤类研究人员创造了机会,极大地调动了他们的积极性。

回顾国际鹤类基金会与中国鸟类学会水鸟专业组这 23 年的合作,确实开展了很多落在实处并且卓有成效的工作,推动了中国鹤类的研究和保护事业。感谢以下单位和个人为此项合作提供资助: Cracid Breeding and Conservation Center、Felburn Foundation、Peter Jay Sharp Discretionary Fund、中国海外学术交流协会以及国际鹤类基金会会员。

(国际鹤类基金会: 李凤山)

河南民权发现青头潜鸭重要繁殖地

2019年9月7日,中国青头潜鸭保护与监测工作组与河南商丘市政府联合举办新闻发布会,公布北京林业大学与河南民权黄河故道国家湿地公园的合作调查监测结果,在河南民权发现青头潜鸭重要栖息地和繁殖地。

青头潜鸭(*Aythya baeri*)于2012年被世界自然保护联盟(IUCN)列为极危物种(CR),全球数量不足1,000只。民权黄河故道国家湿地公园青头潜鸭最大统计数量达155只,占全球种群的15%以上且常年稳定,是我国青头潜鸭的重要栖息地。2019年,在阿拉善SEE任鸟飞项目的支持下,中国青头潜鸭保护与监测工作组与河南民权黄河故道国家湿地公园管理局合作开展繁殖期专项调查,于2019年5月首次发现青头潜鸭繁殖巢,记录并拍摄到成功繁殖的雏鸭和亚成体,证实民权黄河故道是青头潜鸭的重要繁殖地。

东亚澳大利西亚迁飞路线伙伴关系青头潜鸭工作组主席、中国青头潜鸭保护与监测工作组组长、北京林业大学教授丁长青在本次发布会上公布了青头潜鸭筑巢、孵卵、育雏及亚成体潜水捕食的视频、图片(见本期封底)和调查数据,并针对主要威胁因素提出保护建议。2019年在民权监测到的青头潜鸭繁殖成功率仅约20%,未孵化成功的原因包括人为捡蛋、弃巢和天敌捕食。此外,青头潜鸭的巢距离水面较近,繁殖期暴雨或水库、池塘蓄水也会导致巢被淹没。

为保护青头潜鸭在内的各种野生鸟类,在中国青头潜鸭保护工作组的技术支持下,民权湿地公园管理中心增加了监测和巡护频率,控制繁殖期水位,对主要栖息地加强管控,在今后将进一步加强青头潜鸭保护宣传,推动栖息地改善、繁殖地生产经营方式扭转、繁殖期威胁因素管控等工作。中国青头潜鸭保护工作组将继续针对青头潜鸭的繁殖生

态、栖息地选择、主要威胁因素等开展科学研究,并协助民权黄河故道国家湿地公园申报加入“东亚—澳大拉西亚迁飞区保护网络(EAAFP-FSN)”和“国际重要湿地”,守护好这片珍贵的青头潜鸭重要栖息地。

(北京:李露 马富光 丁长青)

一种自动的人工巢箱亲鸟捕捉器

基于人工巢箱结构的捕鸟器目前已有许多类型,但在捕捉效率、故障率和自动触发与否等方面却差异很大。辽宁大学万冬梅教授研究组研发出一种更为先进的捕鸟器,当亲鸟进入巢箱后会自动触发,且磁铁结构能有效防止被困亲鸟逃跑。在2014—2016年繁殖季研究中,使用这种装置捕捉了包括杂色山雀(*Sittiparus varius*)、大山雀(*Parus cinereus*)、沼泽山雀(*Poecile palustris*)在内的177只山雀类,装置触发率达到92.2%,捕捉率达到100%,单只亲鸟平均抓捕时间仅为 22.5 ± 19.6 min。另外,没有亲鸟受伤或弃巢的状况发生。该装置轻便、易安装、高捕捉效率的特点能够有效提高野外工作中的数据收集效率,且可在多种类型人工巢箱及鸟种中应用。

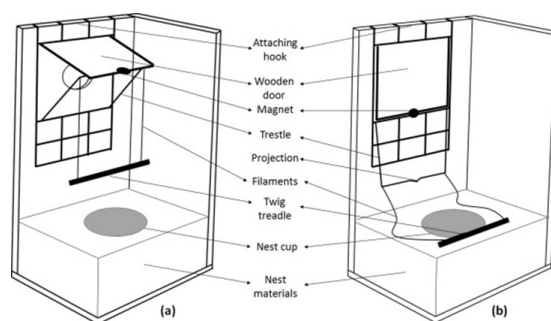


Fig.1 View of the trap set within a nest box. (a) Details when the trap is activated, (b) Details when the trap is triggered

装置具体结构及研究结果见: Lei Zhang, Juan Wang, Congying Zhang, Xuotong Shu, Jiangxia Yin, Dongmei Wan. An improved automatic trap for capturing birds in nest boxes, *Ethology Ecology & Evolution*. 2019, 31(3): 277-282. DOI: 10.1080/03949370.2018.1553799.

(沈阳: 张雷)

“丝路上的鹤类迁徙研究及中国鹤文化传播”二期圆满落幕

2019年11—12月, 北京林业大学生态与自然保护学院在执行“丝路上的鹤类迁徙研究及中国鹤文化传播”项目中邀请了来自俄罗斯、蒙古、哈萨克斯坦和尼泊尔四国的17位鸟类学专家, 从北京出发, 途经黄河口、盐城、长江口、杭州湾, 与迁徙的鹤同行, 访问了9个自然保护区, 参观了中国丝绸博物馆, 签署了“鹤类保护与研究合作备忘录”。一路行进一步交流, 还在首都师范大学、上海自然博物馆等地举办了四场跟鹤类研究及鹤文化相关的国际交流研讨活动。最后还组织了5支国际观鸟队助力由江西省政府、中国野生动物保护协会主办, 江西省林业局等单位承办的2019鄱阳湖国际观鸟周活动。

参与“丝路上的鹤类迁徙研究及中国鹤文化传播”二期活动的外籍专家通过实地考察, 现场体验了中国野生动物保护的成就, 颠覆了他们将区域性生物多样性降低的原因归咎于中国的错误观点, 学习了中国优秀的传统生态理念, 听到了更多的中国声音, 也体验了各样的中国速度, 对与中国专家的合作充满期待。

(北京: 蒲真 郭玉民)

三峡库区蓄水后首次发现越冬小天鹅

小天鹅 (*Cygnus columbianus*) 隶属于雁形目 (Anseriformes) 鸭科 (Anatidae), IUCN 将其列为无危物种 (LC), 我国将其列为国家 II 级保护物种。根据郑光美 (2017) 记载, 小天鹅在我国主要分布于除重庆、海南、陕西、青海、西藏、香港、澳门以外的省市。江西的鄱阳湖是我国小天鹅最大的越冬地, 据最新统计数据, 在我国江西鄱阳湖越冬的小天鹅数量达 11 万余只。

2019年12月11日, 我们在开展三峡库区陆生野生动物调查时, 于重庆市巫山县龙溪镇 (31°18'14"N, 109°41'35"E, 海拔 170 m) 的大宁河上发现了在此越冬的小天鹅 (图 1)。三峡库区蓄水前, 在重庆市长寿区的长寿湖有分布记录, 但时间和数量不详。我们此次调查发现的小天鹅为三峡库区蓄水后的鸟类新纪录。此次发现的小天鹅为一家庭群, 2 只成体和 1 只幼鸟。

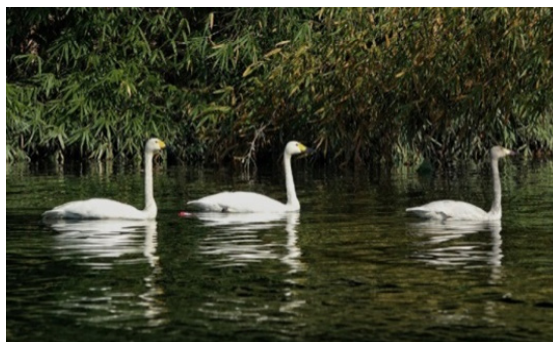


图 1 三峡库区发现的小天鹅 (刘富国摄)

(北京: 李秀明 刘富国 钱法文 刘小云)

江西鄱阳湖国际观鸟周放飞救护鸟类

2019年12月8日上午, 来自北京、天津、黑龙江、江西、广东的野生动物救护中心的工作人员于鄱阳湖国家级自然保护区的大湖

池放飞了救护的 237 只鸟类,包括鸿雁 (*Anser cygnoid*) 5 只、赤麻鸭 (*Tadorna ferruginea*) 1 只、绿头鸭 (*Anas platyrhynchos*) 3 只、豆雁 (*Anser fabalis*) 2 只、斑头雁 (*Anser indicus*) 1 只、东方白鹳 (*Ciconia boyciana*) 7 只、白枕鹤 (*Grus vipio*) 4 只、灰雁 (*Anser anser*) 1 只、黑水鸡 (*Gallinula chloropus*) 200 只、小天鹅 (*Cygnus columbianus*) 3 只、斑嘴鸭 (*Anas zonorhyncha*) 10 只,隶属 3 目 4 科 11 种。

这些鸟类主要来自各地救护或执法罚没的野生鸟类,经过精心治疗和饲养后,均已达到放归野外的标准。为帮助受救助候鸟跟上已经飞抵鄱阳湖越冬的候鸟大部队,各地野生动物救护中心将它们直接送到鄱阳湖进行集体放飞。

放飞前,江西省野生动物救护中心和全国鸟类环志中心的工作人员对其中的 33 只鸟类进行了环志并佩戴了追踪器。其中包括斑嘴鸭 10 只、赤麻鸭 1 只、绿头鸭 3 只、鸿雁 4 只、豆雁 3 只、斑头雁 1 只、小天鹅 3 只、东方白鹳 4 只、白枕鹤 4 只。

(北京: 盘凯筠 钱法文)

Daniel R. Gustafsson 博士 2019 年发表 SCI 论文 17 篇

Daniel R. Gustafsson 博士,瑞典籍,从事鸟类寄生虫分类与进化研究专家,2017 年通过广东省科学院专项人才计划引进全职到广东省生物资源应用研究所工作。Daniel R. Gustafsson 博士热爱中国、热爱自己的工作与专业,积极到野外开展采集样本工作,然后分类鉴定、撰写论文,并经常帮助同事和研究生修改英文稿件等。2019 年共发表 SCI 论文 17 篇,其中第一作者 12 篇,描述并发表 2 个新属、42 个新种,修订 18 个已经命名的

种。在中国,鸟类羽虱研究非常缺乏, Daniel R. Gustafsson 博士首次系统开展羽虱的分类研究,目前已经整理中国羽 170 多种,科研工作成绩斐然。2019 年获“广东省珠江人才计划-青年拔尖人才”资助。

鸟类的羽虱寄生具有种的特异性,如各位同行对所研究鸟种的羽虱有兴趣,请在野外采集和环志时,注意收集羽虱标本并与我们联系,电话: 18675885773, Email 地址: zoufs@giabr.gd.cn or kotatsu@fripost.org, 我们乐于合作并给予经济补偿。



(广东: 邹发生)

国家自然科学基金国际(地区)合作与交流项目

2019 年我会会员邹发生研究员获国家自然科学基金委员会和美国国家自然科学基金会生物多样性合作项目资助,研究题目为“Dimensions 合作研究项目: 羽虱的生命乐

章 - 雀形目鸟类 - 羽虱 - 细菌共生关系的维持机制”。美国合作者是来自 University of Utah 的 Dale Clayton 教授、Colin Dale 教授、Sarah Bush 副教授, 以及 Illinois Natural History Survey 的 Kevin Johnson 教授。该项目以中国种类较多、而国际上关注较少的噪鹛科和幽鹛科鸟类、羽虱 *Brueelia* 属复合种和 *Sodalis* 属共生细菌为研究对象, 通过协同进化研究, 比较鸟类物种多样性分布模式与羽虱物种多样性分布模式的异同, 探讨羽虱的寄生对鸟类物种多样性形成格局的影响; 通过羽虱共生细菌的功能基因组研究, 揭示细菌对羽虱寄生的作用; 通过对鸟类、羽虱、共生细菌的研究, 从物种多样性、遗传多样性和功能多样性三方面阐明生命共同体如何共存与演化。

(广东: 邹发生)

任鸟飞——搭建民间网络, 守护候鸟家园

阿拉善 SEE 任鸟飞项目是由阿拉善 SEE 基金会与红树林 (MCF) 于 2016 年共同发起, 是以超过 100 个亟待保护的湿地和 24 种珍稀濒危水鸟为优先保护对象, 通过民间机构发起、企业投入、社会公众参与的“社会化参与”模式开展积极的湿地保护工作, 搭建与官方自然保护体系互补的民间保护网络, 建立保护示范基地, 进而撬动政府、社会的相关投入, 共同守护中国最濒危水鸟及其栖息地。自 2017 年项目实施以来, 任鸟飞资助了 62 家民间环保组织, 守护了 86 个保护空缺的重要水鸟栖息地。

2019 年任鸟飞民间保护网络守护湿地由 50 个增加至 58 个; 保护超过 2000 km² 水鸟栖息地, 开展湿地巡护和鸟类调查 2,390 多次, 提交鸟类记录 8 万条; 开展自然教育 345 次, 累计覆盖 5.4 万人次。推动湖北武汉府河青头

潜鸭保护小区和广西防城港山心沙岛保护小区的建立, 持续运营上海崇明东滩自然教育基地和天津北大港自然教育基地。

开展青头潜鸭、遗鸥等鸟种专项, 通过 2018—19 年冬季调查监测后的统计发现青头潜鸭种群数量超过 800 只, 在河南民权发现青头潜鸭重要繁殖地; 遗鸥越冬调查监测到在以天津沿海为主的中国黄渤海区域沿海滩涂越冬的遗鸥数量超过 16,600 只, 繁殖地记录到超过 8,600 个繁殖巢, 获得 2 种受胁鸟类种群及栖息地保护现状的一手资料。

任鸟飞项目资助中科院地理资源所于秀波研究员完成了《中国沿海湿地保护绿皮书 2019》的编写。项目实施过程中广泛发动公众参与“最值得关注十大滨海湿地”评选活动, 梳理了 2 年来中国沿海湿地保护中的热点; 评估了我国沿海各类型湿地的生态系统服务价值, 以及沿海 35 个国家级自然保护区的生态系统服务价值, 是由民间机构资助的对我国沿海湿地健康状况和生态系统服务价值进行评估。

项目组与国家林草局湿地管理司和自然保护区形成稳定的合作, 通过湿地公园管理能力建设培训和湿地开发监督利用管理机制研究项目, 提升一线湿地工作者的能力, 搭建民间环保组织与主管部门的沟通桥梁。与自然保护地司达成合作, 希望在黄渤海候鸟栖息地世界遗产 (二期) 申报中发挥环保公益组织的力量, 保护好中国滨海湿地。积极参加国际国内各项鸟类和湿地保护会议, 与科研和保护学面的专家共同探讨“社会化参与”的湿地保护模式。

(阿拉善 SEE 基金会任鸟飞项目: 张琼)

江西举办“2019 鄱阳湖国际观鸟周”

2019 年 12 月 6 日至 10 日, “2019 鄱阳

湖国际观鸟周”活动在南昌、九江、上饶三地举行，来自国内外各界领导、院士、专家学者、国际组织代表等共1,000余人参加。本次活动由国家林业和草原局指导，江西省人民政府和中国野生动物保护协会主办，江西省林业局、江西省文化和旅游厅、南昌市人民政府、九江市人民政府、上饶市人民政府承办，联合国粮农组织、北京林业大学、世界自然基金会、国际鹤类基金会协办。

江西省委、省政府，国家林业和草原局主要领导出席活动开幕式并致辞。江西省委书记刘奇，国家林业和草原局局长张建龙，江西省长易炼红，中国野生动物保护协会会长陈凤学，国际鹤类基金会副总裁斯派克·米林顿共同启动开幕仪式。开幕式还观看了鄱阳湖越冬候鸟实时监控视频，播放了观鸟周

宣传片，志愿者和小学生代表共同宣读《鄱阳湖爱鸟宣言》。活动期间召开了美丽中国“江西样板”院士论坛、鄱阳湖湿地和候鸟保护国际论坛、国际白鹤论坛，开展了鄱阳湖国际观鸟比赛、嘉宾观鸟、救助候鸟放飞、鄱阳湖候鸟国际摄影展、公众自然教育等活动，向评选为优秀湿地暨候鸟保护志愿者（组织）颁奖，江西省林业局与阿拉善SEE基金会共同签订《鄱阳湖保护和发展合作框架协议》，各国代表就加强湿地与候鸟保护达成共识，共同发布《湿地与候鸟保护南昌宣言》。

（江西：俞长好）

安徽淮河流域出现越冬大鸨

2020年3月1日在安徽蚌埠怀远县淮



a 在麦地里觅食



b 在休耕地里觅食



c 飞翔中的大鸨



d 脱落的羽毛

图版：淮河流域越冬大鸨（摄影：张建平）

河支流的茨河岸边张圩村 (116°52'21.01"E, 33°01'22.31"N) 发现越冬大鸨 (*Otis tarda*), 3 月 1—4 日通过实地观测和走访村民的方法对其分布地点进行了调查, 结果表明大鸨在本地越冬时间约一个月, 栖息地位于河流附近开阔的滩地、小麦地、休耕地等, 常在小麦地觅食。调查期间三次见到大鸨并拍摄到

大鸨活动照片, 每次仅见到一只个体, 此间, 还在其越冬觅食地拾到该鸟脱落羽毛五枚。新冠病毒肺炎防控限行大幅度减少人为活动可能是大鸨在传统栖息地重新出现的重要原因。

(安徽: 张建平 周立志)

新书出版

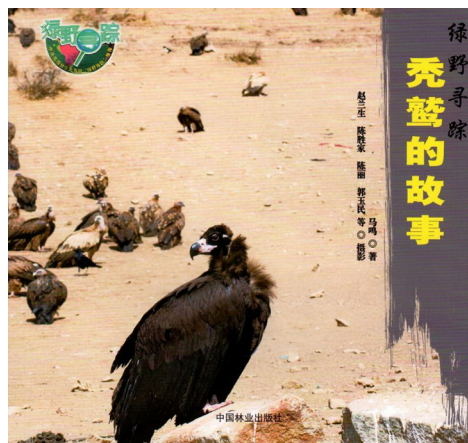
猛禽新书《秃鹫的故事》和《猎隼的故事》出版介绍

由中国科学院新疆生态与地理研究所马鸣研究员主编的图书《秃鹫的故事》和《猎隼的故事》在 2019 年底正式出版。该书属于中国林业出版社“绿野寻踪”系列丛书，图文并茂，各选录 200 余幅图片，合计 20 万字，定价均为 28 元。

秃鹫 (*Aegypius monachus*) 被认为是自然界的清道夫，喜食腐尸，俗称为“座山雕”。其体型甚大，体长可达 1.1 米，翼展达 3 米，为我国猛禽中体型最大者。秃鹫主要栖息于高山陡崖、开阔草原及耕作地区，飞翔能力强，可长时间翱翔空中。作为生态系统中的终极消费者，秃鹫位于食物链的顶端，对维持生态平衡有一定的作用，具有较高的生态与经济价值。由于兽药滥用、栖息地丧失、过度放牧、农药化肥残留、重金属污染（中毒）、高压电网电击、碰撞风电塔架及人为干扰等诸多因素的直接影响，世界鹫类多处于濒危状态，很多物种的地理分布区发生变化，有的物种已处于极危或濒危状态。因此，世界鹫类的保护和研究成为鸟类研究中的热点。在我国约有 8 种鹫类，占世界鹫类的三分之一，中国政府已将所有鹫类列为国家重点保护野生动物。

猎隼 (*Falco cherrug*) 为中型珍稀猛禽，因为非法捕捉和驯养而数量锐减，已被拟定为国家一级保护动物（新版待公布）。其性情凶猛，身形矫健，飞行迅捷。它们善于在高

速飞行中追捕猎物，其俯冲速度极快，时速可达 200~300 公里，完全称得上是疾飞如箭，俯冲似闪电，是最优秀的“飞行猎手”。过去，猎隼的分布面积很广，遍布整个欧亚大陆的森林草原带、荒漠与稀树草原带，从匈牙利穿越中亚直抵中国大部分地区。近年猎隼栖息地受到严重破坏，加上非法捕捉、驯养、贸易（走私）的影响，如今它们的数量正急剧减少，濒危级别不断提升。



中科院马鸣课题组近年来主要从事西部猛禽的野外种群生态调查与研究，持之以恒，先后获得了针对猎隼、金雕、高山兀鹫和秃

鹭等多个国家自然科学基金项目资助。课题组成员翻越阿尔泰山、天山、昆仑山，横穿塔克拉玛干沙漠、青藏高原及羌塘地区，足迹遍布中国西部的山山水水。掌握大量第一手资料，他们最先使用无人机寻找大型鹭巢，最早开始利用红外相机监测猛禽繁殖行为，在国内较早使用卫星跟踪器研究猛禽的迁徙。经过 20 多年野外考察，积累了近百万张生态图片（包括红外自动拍摄）。项目组还征集到国内外上百位作者的摄影作品，两本新书浓缩了其中精华。

（新疆：猛禽研究小组）

《六盘山鸟类图谱》出版

六盘山国家级自然保护区位于宁夏回族自治区最南端，地处北纬 $35^{\circ}15' \sim 35^{\circ}41'$ ，东经 $106^{\circ}09' \sim 106^{\circ}30'$ ，总面积 $90,071 \text{ hm}^2$ 。处于我国中温带半湿润向半干旱气候过度地带，同时也是森林植被向草原植被过度地带，是我国西部黄土高原重要的水源涵养林基地。

因其独特的地理位置、相对湿润的气候环境，使得这里的生物资源丰富。自 2016 年起，兰州大学、宁夏观鸟会和六盘山国家级自然保护区管理局联合开展六盘山鸟类资源调查，历时三年，调查成果由王双贵、宋森、袁海龙以图文并茂的方式编写成《六盘山鸟类图谱》一书。该书已于 2019 年 11 月由宁夏黄河出版传媒集团的阳光出版社出版发行。全书记录了在宁夏六盘山国家级自然保护区境内拍摄到的鸟类 17 目 46 科 200 种，其中宁夏新记录鸟种 16 种：黄臀鹌、白头鹌、斑背噪鹛、灰翅鹌、棕腹柳莺、橙斑翅柳莺、灰喉柳莺、冕柳莺、比氏鹌、画眉、普通鹌、绣胸蓝姬鹌、棕胸岩鹌、长尾雀、蓝鹌、大鹰鹌。书中对各鸟种的形态特征、生态习性、居留类型和保护状况进行了较为详细的描述，每种鸟都有精美的图片作参照。该书为今后研究和保护六盘山鸟类的科研工作者、鸟类爱好者与管护人员提供了基础资料，对了解六盘山保护区以及宁夏回族自治区的鸟类现状具有重要参考价值。

（甘肃：宋森）

消息通知

杨岚研究员不幸去世

我国著名鸟类学家、中国科学院昆明动物研究所杨岚研究员因病于 2019 年 9 月 21 日不幸逝世，享年 86 岁。

杨岚先生是中国动物学会鸟类学分会第三、四、五、六届理事会理事，一生扎根西南地区，致力于鸟类研究工作整整 60 年，为我国西南地区鸟类研究，特别是云南地区的鸟类区系、分类工作做出了突出贡献，先后发现鸟类新亚种 4 个和中国鸟类科的新记录 1 个，其主持编写的《云南鸟类志上、下卷》两部专著不但是记录云南鸟类物种最多、最全面和最系统的文献，而且描记了我国 64% 的鸟类物种。对我国鸟类学的繁荣和发展起了重要的推动作用。1993 年退休之后，还坚持在鸟类学研究的一线工作，主编完成《云南鸟类志下卷》、《本草纲目禽部鸟类今释》两部专著，并参加了《中国动物志鸟纲》等专著的编写工作，甚至在去世前 10 天还在探讨修订《中国鸟类系统检索表》，真是将一生都奉献给了鸟类研究。杨岚先生的去世是中国鸟类学界的重大损失。

中国鸟类学界全体同仁将化悲痛为力量，继承和发扬杨岚研究员求实认真、严谨治学

的学风，推动中国鸟类学研究更好地发展。

（中国动物学会鸟类学分会）

第 23 届国际动物学大会（第一轮通知）

1. 会议主题

人类纪中的动物学 —— 生物多样性的全方位整合保护

2. 会议内容

本届会议将围绕气候变化、城市生态、生物多样性保护、人类纪对生物多样性的威胁、水资源短缺与污染对人类和动物的影响等议题开展学术研讨和交流。

3. 会议地点

南非开普敦（世纪城会议中心）。

4. 时间和日程安排

2020 年 7 月 19—22 日（19 日报到，20—24 日会议，25 日闭幕式）。会议详细日程安排请关注会议网站（<https://ic2020.co.za/welcome/>）。

5. 会议主办、承办单位

主办单位：国际动物学会（ISZS）；承办单位：南非比勒陀利亚大学（University of Pretoria, South Africa）；会议协办及支持单位：

	普通参会人员	学生
2020年1月16日至5月31日	12,000南非兰特	8,500南非兰特
2020年6月1日后、现场注册费用	14,000南非兰特	10,500南非兰特

南非动物学会 (ZSSA)、中国科学院、国际生物科学联合会 (IUBS)、中国科学院动物研究所、中国科学技术协会等。

6. 会议注册和缴费

在线注册: <https://icz2020.co.za/registration/>

注册费 (汇率: 1 南非兰特约等于 0.48 元人民币)

* 以上费用均不包含 7 月 23 日的会议晚宴, 参与晚宴需另行付费。

7. 其他信息

签证申请

请至当地使馆了解签证办理信息, 也可查看: <http://www.dha.gov.za/index.php/immigration-services/apply-for-a-south-african-visa>

关于开普敦

开普敦是南非的第二大城市, 也是南非的经济和法律中心。开普敦风景壮丽, 气候宜人, 有深厚的学术和历史底蕴。如需更多信息, 可浏览: <http://www.capetown.travel/>

(中国动物学会鸟类学分会)

国际分子进化生物学年会

国际分子进化生物学年会将于 2020 年 6 月 28—7 月 2 日在加拿大魁北克举办。注册信息, 大会报告与专题报告信息参见网址 <http://smbe2020.org>。

(北京: 屈延华)

第七届国际欧亚鸟类学大会

第七届国际欧亚鸟类学大会 (7th

International Eurasian Ornithology Congress) 将于 2020 年 4 月 21—25 日在土耳其伊兹密尔 (Izmir, Turkey) 召开。大会主题 (Congress topics) 包括: Behavior, Bird strikes and aircraft safety, Climate Change, Collision with obstacles, Conservation, Ecology. Evolution, Migration, Parasitology, Phylogeography and Phylogeny, Wildlife management 等。大会官方语言为英语, 早期注册截至 2020 年 3 月 9 日。

注册信息和会议内容请见网址 <https://ornithologylab.com/ieoc2020izmir>

(中国动物学会鸟类学分会)

东亚-澳大拉西亚迁飞区鸻鹬类学术会议

首届东亚-澳大拉西亚迁飞区鸻鹬类学术会议 (East Asian-Australasian Flyway Shorebird science meeting) 将于 2020 年 5 月 5—8 日在韩国舒川郡 (Seocheon-gun, Republic of Korea) 举行。会议语言为英语, 注册信息、大会报告与专题报告信息请参见网址 <http://eaafssm.com/>

(中国动物学会鸟类学分会)

北美鸟类学大会

第 7 届北美鸟类学大会 (North American Ornithological Congress) 将于 2020 年 8 月 10—15 日在波多黎各圣胡安 (San Juan, Puerto Rico) 举行。注册信息, 大会报告与专题报告信息参见网址 <https://naocbirds.org/>

(中国动物学会鸟类学分会)

英国鸟类学家联盟 (BOU) 2020 年秋季学术年会

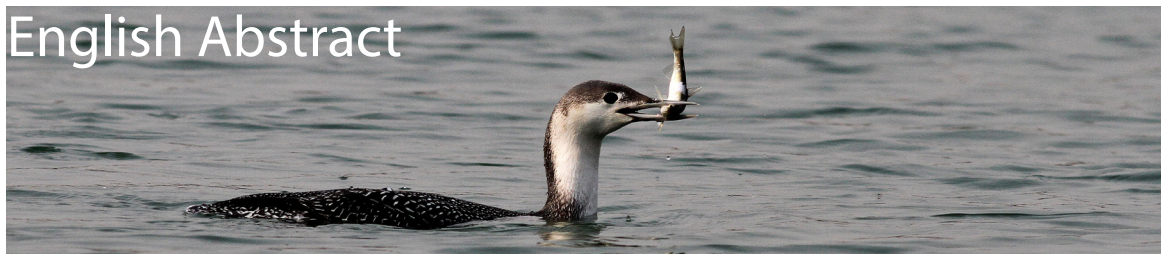
英国鸟类学家联盟 (British Ornithologists' Union, BOU) 2020 年秋季学术年会将于 11 月 24 日在英国彼得堡 (Peterborough, UK) 举行。

会议主题是“气候变化与鸟类：危机解决方案” (Climate change and birds: solutions to the crisis)。注册信息，大会报告与专题报告信息参见网址 <https://www.bou.org.uk/conference/climate-change-and-birds-solutions-to-the-crisis/>

(中国动物学会鸟类学分会)

封面：雉鸡 (*Phasianus colchicus*)，摄影：王雪峰

English Abstract



Notes of Meetings

“The Eighteenth Member Congress of China Zoological Society and the Twenty-fourth Symposium” hold in Shaanxi Xi’an

“The Eighteenth Member Congress of China Zoological Society and the Twenty-fourth Symposium” was held in Xi’an Shaanxi Province, from August 23-25, 2019. The conference is sponsored by China Zoology Society and hosted by Shaanxi Zoological Society, Shaanxi Normal University, Northwest University and some other units. The meeting is also co-organised by Institute of Zoology, Chinese Academy of Sciences. More than 1,000 domain experts and scholars from home and abroad congregated ceremoniously in the ancient city to discuss new discoveries and problems, and to share new methods and achievements in the field of zoology around “The New age of Zoology: viewpoint of interdisciplinary leads science new ground”. A total of 10 invited conference reports, 6 conference youth reports and 18 symposiums were arranged. A part of the academic reports fully demonstrated the latest research achievements of ornithology in China. The symposium of “Research and Protection of Migratory Birds”, chaired by Professor Ma Zhijun from Fudan University and Professor Cao Lei from Research Center for Eco-environmental Sciences, Chinese Academic of Sciences included 13 academic reports on cranes, geese and ducks, which focused on the latest progress on research and conservation for migration birds in China. The conference youth report by Professor Zhou Qi from Zhejiang University, entitled “Sex chromosome evolution in birds and bird-like mammals” won a good response. In addition, there are 15 academic reports on other aspects of ornithology, which related to bird behavior, diversity and protection, molecular mechanism of evolution and adaptation, co-evolution and physiology and ecology.

(Yu Xiaoping and Liu Danni, Shaanxi)

Symposium of cranes and habitat conservation in China and 2019 annual working meeting of United Crane Conservation Committee of China Wildlife Conservation Association was held in Chizhou, Anhui Province

From November 29 to December 2, 2019, Symposium of cranes and habitat conservation in China and annual working meeting of United Crane Conservation Committee of China Wildlife

Conservation Association was successfully held in Chizhou, Anhui Province. Zhang Xiwen, the secretary-general of the China wildlife conservation association; Fang Nengbin, the vice mayor of the Chizhou people's government, Guo Lixin, the deputy secretary general of the China wildlife protection association, Bao Xudong, the deputy secretary-general of Chizhou municipal people's government, the related departments of National bureau of forestry and grass, Anhui provincial forestry bureau, the international crane foundation, more than 200 representatives from universities and research institutes engaged in crane research, as well as stork-related protection areas from 17 provinces and cities attended the meeting.

Zhang Xiwen, chief supervisor, said that China is a country rich in crane resources in the opening ceremony. There are 15 kinds of cranes in the world, while there were 9 in China making that China has the largest number of cranes in the world, and is the country with the largest number of cranes in the world. United Crane Conservation Committee of China Wildlife Conservation Association serves as the scientific and technological support for crane protection, and it has played an important role in leading the technological progress of crane protection and scientific communication, as well as the simultaneous investigation of cranes, and coordinating the joint protection of cranes' wintering grounds, resting grounds and breeding grounds.

At the 2019 annual meeting, Qian Fawen introduced the work achievements of CWCA-UCCC in 2019 and the work plan in 2020. In 2019, the association had carried out work in the areas of achievement exchange and technical training, promoting the synchronous investigation of national crane resources, scientific research and popularization of science, international exchange and cooperation, and improvement of organizational construction, hosted the 2nd session of the simultaneous survey and training on migratory cranes and waterbirds from hulun buir to bohai bay, co-organized the 7th black-necked crane network annual meeting and wetland monitoring and management seminar of international importance, and China rongcheng whooper swan conservation international academic exchange conference, and introduced the content and purpose of crane association at the international symposium on crane conservation in six east Asian countries. In 2020, the association will continue to carry out its work in the areas of science popularization, scientific and technological exchanges, and synchronized surveys on crane protection, especially in the event of the Chinese year of the crane. The association also set up a new "crane culture and ecology photography working group", and added 15 member units and 6 new members.

There were 6 conference reports and 16 special reports. Professor Zhou Lizhi, Anhui University; Professor Zou Hongfei, Northeast Forestry University; Jiang Hongxing, associate researcher of the national bird banding center of China, conservation center; Kong Dejun, associate professor, Kunming University; Professor Tian Xiuhua of Northeast Forestry University, Ms. Zhang Yanan,

yancheng reserve, Jiangsu Province reported on the ecological protection of cranes, habitat management and protection, and migration routes respectively. The report fully shows the latest progress of crane research and conservation in China in recent years from the aspects of crane population status, habitat utilization, migration, overwintering, ex-situ protection and rescue management.

Zhang Zhengwang, chairman of the crane federation and a professor at Beijing Normal University, presided over the closing ceremony. The meeting honored the winners of the national advanced crane protection member units, the winners of the excellent conference wall newspaper and the winners of the 2019 China crane photography competition. The meeting decided to continue to carry out the 2019-2020 national crane resources synchronized survey, and conducted relevant technical training; the next annual meeting of the crane association will be held in 2020 at the Heilongjiang longanqiao national wetland park. Delegates also watched the first Chinese special film about the natural history of China's nine crane species, "the sky is the crane's hometown", and visited the shengjinhu national nature reserve in Anhui Province.

The meeting was co-sponsored by United Crane Conservation Committee of China Wildlife Conservation Association and the people's government of Chizhou City, Anhui Province. Anhui key laboratory of wetland conservation and restoration, Anhui University, undertook, Anhui chizhou forestry bureau, Anhui shengjinhu national nature reserve management office, Anhui zoological society, Anhui wildlife protection association, natural image China, Anhui gravitational wave science and education equipment co., LTD., Anhui tianlitai technology co., LTD., hunan global trust technology co., LTD assisted this meeting.

(United Crane Conservation Committee of China Wildlife Conservation Association)

Research Reports

Individual diet differences in a molluscivore shorebird are associated with the size of body instruments for internal processing rather than for feeding

Especially in birds, it is widely found that the size of individual prey items follows the size of the instruments for prey capture, handling and processing, i.e. bill size. In fact, this is the natural history basis of major discoveries on adaptative evolution in the face of changing food resources. In some birds, e.g. the molluscivore shorebirds ingesting hard-shelled prey, most of the prey processing process takes place within the digestive tract. This study of a salvaged sample of actively feeding great knots *Calidris tenuirostris* accidentally drowned in fishing nets in northern China, is the first documentation of diet selection at the level of the individual in previously well-studied molluscivore shorebirds.

At the individual level, diet composition of Great Knots was not associated with the length of the bill, but with the mass of the muscular gizzard. Generally, gizzard mass was negatively correlated with the numerical percentages of the small-sized classes *U. thomasi*, whilst positively correlated with the large-sized classes *U. thomasi*. The larger gizzard mass, the higher the proportion and the large-sized classes *U. thomasi* of hard-shell *U. thomasi* in the diet. The dry mass of shell fragments in each gizzard did not significantly correlate with bill length, but exhibited a positive correlation with gizzard mass. Bill length was not correlated with average break force of the prey, but gizzard mass was.

Gizzard mass, which unlike bill length is a phenotypically flexible trait, enables Great Knots to adjust to changing food resources as an individual, i.e. instantly responding to the food on offer. For migratory species like Great Knots which rely on seasonal sequences of distant feeding areas offering a variety of prey characteristics, the capacity to individually adjust appears a key adaptation.

(Zhang Shoudong and Ma Zhijun, Shanghai)

Managed marshes can be good alternatives to natural marshes as breeding habitats for birds

Loss of natural tidal marshes has caused rapid population declines for many bird species, raising the question about whether managed marshes can be used for bird conservation. Although many studies have indicated that managed marshes can provide a complementary habitat for birds, it is unclear how the breeding habitats provided by managed marshes compare with those pro-

vided by natural marshes. We compared habitat conditions (vegetation and food) and breeding performance of a common reed specialist, the Oriental reed warbler (*Acrocephalus orientalis*), in natural and managed artificial reed marshes at Chongming Dongtan, an estuarine wetland in China. We found that vegetation was denser and warbler food resources were greater in managed than in natural marshes. The density of breeding territories, nest density, clutch size, egg size, and fledgling number per nest were greater in managed than in natural marshes. Breeding failure was reduced in managed marshes because of a reduced risk of nest predation. However, the high nest position on the reeds in the managed marshes increased the risk of nest destruction by strong wind. The better breeding performance in managed than in natural marshes could be attributed to the following factors: the high and stable water level in the managed marshes increased reed growth and arthropod reproduction and decreased access by terrestrial predators; dense vegetation helped conceal nests from predators; and human activities in the managed marshes deterred nest predators. The results suggest that managed marshes can provide quality breeding habitat for the Oriental reed warbler and probably for other marsh birds and can therefore help compensate for the loss of natural marshes. The preference of the Oriental reed warbler for managed marshes largely depends on the suitable habitat conditions. The current study highlights the importance of maintaining a relatively high and stable water level.

(Ma Zhijun, Shanghai)

Rapid phenotypic evolution with shallow genomic differentiation during early stages of high elevation adaptation in Eurasian Tree Sparrows

Organism-environment interaction represents a biological phenomenon that integrates ultimate and proximate causation on a global scale. Known as the “third polar region”, the Qinghai-Tibet Plateau represents one of the harshest highland environments in the world, yet a number of organisms thrive there. Previous studies in birds, animals and humans have focused on well differentiated populations in later stages of phenotypic divergence. The adaptive processes during the initial phase of highland adaptation remain poorly understood. We studied a human commensal, the Eurasian Tree Sparrow, which has followed human agriculture to the Qinghai-Tibet Plateau. Despite strong phenotypic differentiation at multiple levels, in particular muscle related phenotypes, highland and lowland populations show shallow genomic divergence, and the colonization event occurred within the past few thousand years. In a one-month acclimation experiment investigating phenotypic plasticity, we exposed adult lowland tree sparrows to a hypoxic environment and did not observe muscle changes. Through population genetic analyses, we identified a signature of polygenic adaptation, whereby shifts in allele frequencies are spread across multiple loci, many of which are associated with muscle related processes. Our results reveal a case of positive selection in which polygenic adaptation appears to drive rapid phenotypic evolution, shedding

light on early stages of adaptive evolution to a novel environment. The article is available online in *National Science Review* (<https://academic.oup.com/nsr/advance-article/doi/10.1093/nsr/nw-z138/5567447?guestAccessKey=908825cb-b298-4e7b-8526-99bbf40e9e0c>).

(Qu Yanhua, Beijing)

Effects of capture and captivity on plasma corticosterone and metabolite levels in breeding Eurasian Tree Sparrows

Bringing free-living animals into captivity subjects them to the stress of both capture and captivity, leading to the alteration of normal physiological processes and behaviors through activation of the hypothalamic–pituitary–adrenal axis. In free-living birds, although elevated plasma corticosterone (CORT) is an important adaptation regulating physiological and behavioral responses during the process of capture and captivity stress, little information is currently available on the effects of such stress on plasma metabolite levels. In the present study, we examined the effects of immediate capture and 24-h captivity on body mass, body condition, plasma CORT and metabolite levels including glucose (Glu), triglyceride (TG), total cholesterol (TC), uric acid (UA), in breeding Eurasian Tree Sparrows (*Passer montanus*). The results showed that CORT and Glu levels were significantly increased after the stress of capture, whereas TC and UA levels decreased. After 24-h in captivity, body mass and body condition of the sparrows were notably declined, but CORT, Glu, and UA levels were significantly increased. Furthermore, male sparrows had lower TG levels after both capture and captivity than those of females. In addition, we investigated the relationship between CORT and metabolites and found that the correlation between plasma CORT and metabolites levels varied between sexes. Our results revealed that the metabolic status of Eurasian Tree Sparrows could be dramatically altered by capture and captivity. Monitoring the dynamic effects of both capture and captivity on plasma CORT, metabolite levels in a free-living bird contributes to a better understanding of the stress-induced pathways involved in sex-dependent energy mobilization. This study was published in *Avian Research* (2019, 10: 16).

(Li Mo, Zhu Weiwei, Wang Yang, Sun Yanfeng, Li Juyong, Liu Xuelu, Wu Yuefeng and
Li Dongming, Hebei; Gao Xuebin, Shaanxi)

Limits to load-lifting performance in a passerine bird: the effects of intraspecific variation in morphological and kinematic parameters

Although more massive flight muscles along with larger wings, higher wingbeat frequencies, and greater stroke amplitudes enhance force and power production in flapping flight, the extent to which these parameters may be constrained by other morphological features relevant to flight

physiology and biomechanics remains unclear. To explore intraspecific correlates of flight performance, we assembled a large dataset that included twenty morphological and kinematic variables for a non-migratory passerine, the Eurasian Tree Sparrow (*Passer montanus*). We hypothesized that greater vertical load-lifting capacity would correlate with higher greater wingbeat frequency, and relatively more massive flight muscles, along with bigger hearts and lungs to enhance metabolic capacity and energy supply, but also with relatively smaller digestive organs that might correspond a reduction in body mass. We found that heavier flight muscles and larger wings, heavier stomach, but also shorter bills were the most important correlates of maximum load-lifting. Surprisingly, wingbeat frequency, wing stroke amplitude and masses of the heart, lungs and digestive organs (except for the stomach) were non-significant predictor variables relative to lifting capacity. The best-fit structural equation model (SEM) indicated that load-lifting capacity was positively correlated with flight muscle mass, wing area and stomach mass, but was negatively correlated with bill length. Characterization of individual variability in flight performance in a free-ranging passerine indicates the subtlety of interaction effects among morphological features, some of which differ from those that have been identified interspecifically for maximum flight performance in birds. This study was published in *PeerJ* (2019; 7: e8048).

(Wang Yang, Yin Yuan, Ge Shiyong, Li Mo, Zhang Qian, Li Juyong, Wu Yuefeng and
Li Dongming, Hebei; Robert Dudley, US)

A case report of bill color aberration in a free-living Eurasian Tree Sparrow (*Passer montanus*): Morphological and physiological description

Color aberration in birds is a common biological phenomenon relative to other vertebrates. To date, a large number of avian species with abnormally colored individuals have been documented. Although evidence has shown that color aberration may co-vary with morphological and physiological traits, little information is available on the variations of morphological and physiological traits of free-living aberrantly colored birds. Here we report a case of a free-living female Eurasian Tree Sparrow (*Passer montanus*) with bleached bill but normally pigmented plumage. We further compared the differences in 5 morphological indices including body mass, body condition index (BCI), length of the bill, tarsus, and wing, and 14 physiological indices including core temperature, hematocrit (Hct), baseline plasma glucose (GLU), total protein (TP), uric acid (UA), total cholesterol (TC), triglycerides (TG), free fatty acid (FFA), beta-hydroxybutyrate (b-HB), high-density lipoprotein cholesterol (HDL-C), low-density lipoprotein cholesterol (LDL-C), lactate dehydrogenase (LDH), alkaline phosphatase (ALP), and creatinine (CREA) between the aberrant individual and other normal birds. Our results showed that the aberrant sparrow has significantly shorter tarsi, longer wings, and higher core temperature, lower levels of plasma TP, UA, LDL-C, ALP, and CREA than normal sparrows, while no significant differences were noted in other morphological and

physiological indices between the 2 phenotypes. Our results indicate that bill-color aberration in the Eurasian Tree Sparrow may be associated with a few morphological and physiological alterations, especially in terms of thermoregulation and protein metabolism. However, these alterations do not result in dramatic changes in body condition, other plasma metabolites, or enzyme activities. This study was published in *Wilson Journal of Ornithology* (2019, 131: 553-560).

(Li Mo, Zhang Qian, Gao Xiaohan, Sun Yanfeng, Cao Jiaxin, Li He, Wu Yuefeng and Li Dongming, Hebei)

Predicting the vulnerability of birds to trophic threat posed by phenological mismatch based on nutritional and physiological status of nestlings

Climate change induced phenological mismatches between nestlings and their optimal food resources have been found to negatively influence the survival of many bird species. Discriminating which species is vulnerable to such threat is difficult only based on the diet observation, and therefore it is necessary to establish a more reliable method to predict the vulnerability of bird species. In the case of Asian short-toed lark (*Calandrella cheleensis*), we predicted such vulnerability by evaluating whether nestlings can absorb equal level of nutrients from different diets and maintain equal physiological status. We compared the diet, plasma nutrients, plasma insulin-like growth factor-1 (IGF-1), body mass and survival rate of nestlings hatched under different optimal food (grasshopper nymph) abundance conditions in two breeding seasons. Plasma glucides, amino acids, tricarboxylic acid (TCA) cycle metabolites, some fatty acids, IGF-1, body mass and survival rate of the nestlings hatched under medium or low nymph abundance conditions were significantly lower than those of nestlings hatched under high nymph abundance condition. The relative abundance of plasma amino acids, glucides, TCA cycle metabolites and fatty acids were significantly, and positively, correlated with IGF-1 levels, which, in turn, was positively correlated with nestling body mass. These results indicate that the diet with low optimal food proportion was nutritionally inferior to the diet with high optimal food proportion and inhibited the growth of nestlings. Species like Asian short-toed lark is vulnerable to the trophic threat induced by phenological mismatch because the alternative food is insufficient to satisfy the nutritional requirement of nestlings.

(Zhang Shuping, Beijing; Liang Wei, Hainan)

Differently sized cuckoos pose different threats to hosts

Hole-nesting tits *Parus* spp. have been classified as “unsuitable” hosts for cuckoo parasitism because cuckoos cannot enter a cavity if the entrance is too small. However, Chinese tits could reject

alien eggs and egg ejection rate increased with the local diversity of parasitic cuckoo species. Antiparasitic behavior among Chinese tits may have evolved due to greater size variation among sympatric cuckoo species. This raises the question of whether differently sized parasitic cuckoos pose different threats to Chinese tits. A green-backed tit *Parus monticolus* population that is sympatric with Asian emerald cuckoo *Chrysococcyx maculatus* (eme-cuckoo, small-sized parasite) and common cuckoo *Cuculus canorus* (com-cuckoo, large-sized parasite), and a cinereous tit *P. cinereus* population that is only sympatric with com-cuckoo were chosen as study organisms. We observed behavioral response and recorded alarm calls of the 2 tit species to eme-cuckoo, com-cuckoo, chipmunk *Tamias sibiricus* (a nest predator) and dove *Streptopelia orientalis* (a harmless control), and subsequently played back alarm calls to conspecific incubating females.

In dummy experiments, both tit species performed intense response behavior to chipmunk, but rarely responded strongly to the 3 avian species. In playback experiments, both tit species responded strongly to conspecific chipmunk alarm calls, but rarely responded to dove alarm calls. The intensity of response of incubating female green-backed tits to eme-cuckoo and com-cuckoo alarm calls were similar to that of chipmunk alarm calls, while the intensity to eme-cuckoo alarm calls was higher than the intensity to dove alarm calls which was similar to that of com-cuckoo alarm calls. In contrast, few female cinereous tits responded to eme-cuckoo and com-cuckoo alarm calls. These findings indicated that the threat level of eme-cuckoo was slightly greater than that of com-cuckoo for sympatric green-backed tits, but not for allopatric cinereous tits.

(Yu Jiangping, E Mingju and Wang Haitao, Jilin; Liang Wei, Hainan; Anders Pape Møller, France)

Comparative analysis of hissing calls in five tit species

Nest predation often leads to breeding failure and is an important component of natural selection that affects the evolution of nest defense behavior in birds. Many tit species give a hissing call as nest defense, but there are few studies of interspecific variation in hissing calls, and whether these are related to nest predation and nesting success. In this study, we compared the hissing calls of five tit species including cinereous tits (*Parus cinereus*), marsh tits (*Poecile palustris*), varied tits (*Sittiparus varius*), willow tits (*Poecile montanus*), and coal tits (*Periparus ater*) in Saihanba National Forest Park in Hebei and Xianrendong National Nature Reserve in Liaoning. In Saihanba of Hebei, the proportion of cinereous, willow, and coal tit individuals giving a hissing call differed significantly but the rate of nest predation was similar. It was also true for the three tit species (cinereous, varied, and marsh tits) in Xianrendong of Liaoning. Cinereous and varied tits showed no differences in clutch size, date of the first egg, nest predation and nesting success between individuals that gave and those that did not give a hissing call. These results indicate that for tit species that breed in nest boxes distributed within the same area, there is interspecific vari-

ation in hissing calls but this variation is not significantly correlated with nest predation risk.

(Zhang Li, Zhang Lei and Wan Dongmei, Liaoning; Liu Jianping and Liang Wei, Hainan; Anders Pape Møller, Paris)

The corresponding relationship between the change of wintering area of common crane (*Grus grus*) and global climate change

In recent years, some waterfowl have moved northward in winter. Taking the common crane (*Grus grus*) as an example, which migrated to China in the past, mainly lived in the south of the Yangtze River, such as Yunnan, Guizhou, Jiangxi and other provinces. However, in recent years, it has been found that there are a large number of common crane populations staying or overwintering around the Tarim Basin of Xinjiang, mainly in Baicheng County, Wushi County, Moyu County, Minfeng County, Pishan County and other regions.

In 2016, for the first time, thousands of common crane populations were found to overwinter in the Southern Xinjiang, for which continuous tracking observation was conducted to explore the impact of climate change. From October to December 2019, survey around the Southern Xinjiang, preliminary statistics show that there are tens of thousands of common cranes. This may be the northernmost overwintering area in Central Asia, which is far away from the original overwintering area. The straight line is 1,800-2,100 km away from the original overwintering area, and the latitude increases by 8-12 degrees. A similar situation has occurred in Europe, where the distance between breeding grounds and wintering grounds has been shortened. This is closely related to global climate change, as well as food, such as changes in planting species and mechanization of harvesting methods.

(Ma Ming, Xinjiang Institute of ecology and geography)

Effects of Testosterone on Reproduction in the Varied Tit (*Sittiparus varius*)

Steroid hormone testosterone (T) is one of the most important sex hormones in bird reproduction, which is closely related to breeding behavior, such as promoting the expression of spermatogenesis-related proteins, follicular development and maturation, and stimulating ovulation. Varied Tit (*Sittiparus varius*) is a small social monogamous bird species with biparental care behavior and high extra-pair paternity ratio bird. During March to July 2019, we measured the T levels of Varied Tit during the breeding period. Results showed that female and male T levels peaked at the start of the breeding season, and did not change across stages of the nest cycle. T level of male parents showed a significant positive correlation with clutch size. However, there was no correla-

tion between T levels and physical parameters, or female T concentrations and reproduction parameters. In general, T had up-regulated effects on the clutch size of male Varied Tit, and males with higher T levels had higher clutch size. However, the effects of T levels on female reproduction need further investigation.

(Wang Juan and Wan Dongmei, Shenyang)

Genome-wide analysis of the buff-throated partridge (*Tetraophasis szechenyii*)

The buff-throated partridge (*Tetraophasis szechenyii*, Phasianidae, Galliformes), which is endemic to China, is distributed in Sichuan, Yunnan, Gansu, and Qinghai provinces and the Tibetan Autonomous Region. The alpine shrubberies, coniferous forests, and tundra above the treeline at 3,350-4,600 m above the sea level are the habitats of the buff-throated partridge from the eastern Tibetan Plateau to central China. The buff-throated partridge is a hypoxia-tolerant bird living in an extremely inhospitable high altitude environment, which has high ultraviolet (UV) radiation as well as a low oxygen supply when compared with low altitude areas. To further understand the molecular genetic mechanisms of the high-altitude adaptation of the buff-throated partridges, we de novo assembled the complete genome of the buff-throated partridge.

Comparative genomics revealed that positively selected hypoxia-related genes in the buff-throated partridge were distributed in the HIF-1 signaling pathway (map04066), response to hypoxia (GO:0001666), response to oxygen-containing compound (GO:1901700), ATP binding (GO:0005524), and angiogenesis (GO:0001525). Of these positively selected hypoxia-related genes, one positively selected gene (*LONP1*) had one buff-throated partridge-specific missense mutation which was classified as deleterious by PolyPhen-2.

Moreover, positively selected genes in the buff-throated partridge were enriched in cellular response to DNA damage stimulus (corrected *P* value: 0.028006) and DNA repair (corrected *P* value: 0.044549), which was related to the increased exposure of the buff-throated partridge to UV radiation. Compared with other avian genomes, the buff-throated partridge showed expansion in genes associated with steroid hormone receptor activity and contractions in genes related to immune and olfactory perception. Furthermore, comparisons between the buff-throated partridge genome and red junglefowl genome revealed a conserved genome structure and provided strong evidence of the sibling relationship between *Tetraophasis* and *Lophophorus*. Our data and analysis contributed to the study of Phasianidae evolutionary history and provided new insights into the potential adaptation mechanisms to the high altitude employed by the buff-throated partridge.

(Zhou Chuang, Meng Yang and Yue Bisong, Sichuan)

Size matters: wintering ducks stay longer and use fewer habitats on largest Chinese lakes

Evidence suggests that wintering waterbirds have become conspicuously more concentrated at two largest lakes of the Yangtze River Floodplain, East Dong Ting Lake (Hunan Province, 29°20'N, 113°E) and Poyang Lake (Jiangxi Province, 29°N, 116°20'E), relative to other lakes, despite the establishment of reserves elsewhere. While this relationship is likely due to greater extent of undisturbed habitats in larger lakes, we understand little of the drivers affecting individual behaviours behind this tendency. We tracked wintering movements of three duck species (Eurasian Wigeon *Mareca penelope*, Falcated Duck *M. falcata* and Northern Pintail *Anas acuta*) using GPS transmitters, examining differences between the two largest lakes and other smaller lakes in ducks' habitat use, duration of stay at each lake and the daily distances moved by the tagged birds while at these sites. The Eurasian Wigeon and Falcated Duck stayed five times longer and almost exclusively used natural habitat types at the two large lakes (91-95% of positions) compared to length of stay time at smaller lakes, where they spent 28-33 days on average (excluding the capture site) and exploited many more different habitats (including c. 50% outside lakes). Our study is the first to show that shorter length of stay and more varied habitat use by ducks at small lakes may contribute to explaining the apparent regional concentration of numbers present of these and other species at the largest lakes in recent years. This compares with their declining abundance at smaller lakes, where habitat loss and degradation has been more manifest than on the larger lakes.

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(Meng Fanjuan and Cao Lei, Beijing)

Consistent habitat preference underpins the geographically divergent autumn migration of individual Mongolian Common Shelducks

While many avian populations follow narrow, well-defined "migratory corridors," individuals from other populations undertake highly divergent individual migration routes, using widely dispersed stopover sites en route between breeding and wintering areas, although the reasons for these differences are rarely investigated. We combined individual GPS-tracked migration data

from Mongolian-breeding common shelduck *Tadorna tadorna* and remote sensing datasets, to investigate habitat selection at inland stopover sites used by these birds during dispersed autumn migration, to explain their divergent migration patterns. We used generalized linear mixed models to investigate population-level resource selection, and generalized linear models to investigate stopover-site-level resource selection. The population-level model showed that water recurrence had the strongest positive effect on determining birds' occupancy at staging sites, while cultivated land and grassland land cover type had strongest negative effects; effects of other land cover types were negative but weaker, particularly effects of water seasonality and presence of a human footprint, which were positive but weak or non-significant, respectively. Although stopover-site-level models showed variable resource selection patterns, the variance partitioning and cross-prediction AUC scores corroborated high inter-individual consistency in habitat selection at inland stopover sites during the dispersed autumn migration. These results suggest that the geographically widespread distribution (and generally rarity) of suitable habitats explained the spatially divergent autumn migrations of Mongolian breeding common shelduck, rather than the species showing flexible autumn staging habitat occupancy.

The study was supported by the National Key Research and Development Program of China (Grant No. 2017YFC0505800), the National Natural Science Foundation of China (Grant Nos. 31661143027, 31670424, and 31870369), the Chinese Academy of Sciences Key Strategic Program, Water Ecological Security Assessment, the Major Research Strategy for Middle and Lower Yangtze River (Grant No. ZDRW-ZS-2017-3-3), and the China Biodiversity Observation Networks (Sino BON). This work was published in *Current Zoology*, zoz056, <https://doi.org/10.1093/cz/zoz056>.

(Meng Fanjuan and Cao Lei, Beijing)

Human infrastructure development drives decline in suitable habitat for Reeves's pheasant in the Dabie Mountains in the last 20 years

In China, human infrastructure development has increased particularly rapidly in the past 20 years. Unfortunately, these areas have coincided with an important distribution area of the IUCN Red Listed Vulnerable Reeves's pheasant (*Syrnaticus reevesii*). As a nationally protected animal, it is a flagship species in some of the mountainous massifs of central China and is important in maintaining some natural forest reserves. If uncontrolled, development will threaten survival of this rare wild animal. Understanding the spatio-temporal response of Reeves's pheasant to habitat changes will be useful for providing information and improving habitat quality when making decisions on the use and management of land-use resources.

In order to elucidate the impacts of human infrastructure development on changing the potential habitat of Reeves's pheasant between 2001-2002 and 2018-2019, we compared three different distribution models: a model with topographic and land cover variables, a model with topographic and human infrastructure development, and a model with all variables. Then we estimated the relative strength of land use/land cover (LULC) factors contributing to these changes by integrating Geo-Information technology and CA-Markov analysis. Finally, we evaluated habitat fragmentation between the two periods.

We found that the distribution of suitable habitat decreased between 2001-2002 and 2018-2019. Moreover, the directional distribution became more elongated and the mean center moved to southeast, which is closer to the highest peak in the Dabie Mountains. During 2000-2015, cultivated land and grassland area declined, while artificial surface area increased. Detailed examination of the LULC changes suggested that desertification had also occurred. Importantly, functional categorization revealed that all the different habitat area types predicted for Reeves's pheasant had decreased from 2001 to 2019. With the likely movement of the pheasant to higher elevations, human infrastructure development and environmental goals must both be considered to ensure the survival of this charismatic species.

(Tian Shan and Xu Jiliang, Beijing; Wang Yong, USA)

Prediction of suitable distribution area of Eurasian Spoonbill (*Platalea leucorodia*) in Northeast China based on MaxEnt Model

The habitat suitability of Eurasian Spoonbill in Northeast China was studied by using MaxEnt model and GIS spatial technology. By analyzing how environmental factors affect the breeding habitat suitability of Eurasian Spoonbill and the importance of these predictive factors, the suitable habitat of Eurasian Spoonbill in northeast China is evaluated and its potential breeding habitat is predicted. It is considered that the preferred habitat of Eurasian Spoonbill is close to water source, covered with vegetation, low altitude, and has a certain choice to climate change. However, human disturbance, distance from the river and land cover have little influence on the distribution of Eurasian Spoonbill.

(Li Min, Qian Fawen)

Study on the Migration Routes and Important Stopover Sites of the Wintering Whooper Swan (*Cygnus cygnus*) in Rongcheng, Shandong Province

Satellite tracking technique was used to track the Whooper Swans in Rongcheng National Nature

Reserve in Shandong Province. Five migration routes were found through the tracking, and the tracked Whooper Swans were migrating through Tianjin, Liaoning, Hebei, Jilin, Shanxi and Inner Mongolia. Its summering areas distributed in Inner Mongolia, Mongolia and Russia. There are many stopover sites on the migration routes, and the most important stopover sites are Baishi Reservoir in Liaoning, Laoha River and Xira Moron River in Inner Mongolia. It was also found that the migration duration and distance of Whooper Swans in spring were longer than that in autumn. This study reveals the migration routes and migration rules of Whooper Swans wintering in Rongcheng, which has important scientific value for the the protection and management of Whooper Swans and their habitats.

(Wu Aiming and Qian Fawen, Beijing)

Sex-biased dispersal pattern may be correlated with the study scale in the Black-throated Tit (*Aegithalos concinnus*)

Animal dispersal patterns have been research hot spots in behavioural ecology and evolutionary ecology, but measuring dispersal is challenging and often requires the use of complementary approaches. We investigated local-scale sex-biased dispersal pattern in the Black-throated Tit (*Aegithalos concinnus*), in the Dongzhai National Nature Reserve of Henan province. Spatial genetic autocorrelation analyses suggested that significant fine scale genetic structure existed in males but not in females. Mark-recapture analyses of individuals ringed also showed that female offspring were more dispersive than male offspring, supporting genetic evidence of local female-biased dispersal. These results were contrary to a previous finding of male-biased long-distance dispersal in this species that was based on analyses of gene flow across the species' range in China. As we have found two males dispersed exceptionally long distance (ca. 4.8 km) during the study, the results imply that the species may potentially have a scale-dependent dispersal strategy, with females frequently dispersing further than males at the local level, but a proportion of males occasionally disperse long distances, contributing more to gene flow at a larger geographic scale. Long-distance dispersal by male black-throated tits may be induced by competition for resources or by unfavourable environmental conditions, warranting further investigation, but our findings increase evidence that geographic scale is an important factor to be considered when investigating animal dispersal patterns. The details of the study can be found at Li et al. (2013) Sex-biased dispersal patterns of a social passerine: complementary approaches and evidence for a role of spatial scale. *Biological Journal of the Linnean Society*, 128(3): 592–602.

(Li Jianqiang and Zhang Zhengwang, Beijing)

Ph.D Thesis

Effects of food changes in Yalu Jiang coastal wetland on migratory shorebirds

Coastal wetlands in the Yellow Sea Region are important stopover habitats for migration shorebirds along the East Asian-Australasian Flyway (EAAF). Human activities have caused the rapid loss and degradation of these coastal wetlands. This is a main reason for the rapid decline of shorebird populations along the EAAF. Most previous studies focused on how the loss of stopover habitats has affected shorebirds. The impact of changes in food conditions on shorebirds in the Yellow Sea Region has seldom been studied. The Yalu Jiang coastal wetland, being one of the most important stopover sites in the Yellow Sea, provides key food resources for large numbers of Bar-tailed Godwits *Limosa lapponica* and Great Knots *Calidris tenuirostris* to fuel up during migration. Focusing on the Yalu Jiang coastal wetland and two shorebirds species (Bar-tailed Godwit and Great Knot), this study described shorebirds' responses to food decline in stopover habitats, in terms of population dynamics, the food-niche differentiation, and the physiological and behavioral features. A variety of techniques were employed: macrobenthos survey, shorebirds population survey, fecal and regurgitate analysis, foraging behavior analysis and morphometry. Moreover, this study analyzed the effectiveness of food supplementation on conserving migratory shorebirds. The main results of this study are listed as follows:

1) The monitoring of the macrobenthos food for these shorebirds, from 2011 to 2016, exhibited declines of over 99% in individual densities of the bivalve *Potamocorbula laevis*, the main prey for both the Bar-tailed Godwits and Great Knots. Surprisingly, the population survey indicated that the numbers of the subspecies of Bar-tailed Godwit *L. l. baueri* and Great Knots using the Yalu Jiang coastal wetland remained stable, except for the subspecies of Bar-tailed Godwit *L. l. menzbieri*, which exhibited a 91% decline in peak numbers during the study.

2) The study found that to cope with the dramatic decline of high-quality food *P. laevis* in the Yalu Jiang coastal wetland, the food composition of Great Knots and Bar-tailed Godwits have changed, by widening their diet niche and choosing more types of food. The diet niches breadth index of Great Knot increased from 0.001 in 2011 to 0.093 in 2018, Bar-tailed Godwits increased from 0.053 in 2011 to 0.15 in 2018. The diet niche overlap between male and female of Bar-tailed Godwit did not significantly decrease with the reduction of high-quality food, but the diet niche overlap between Bar-tailed Godwit and Great Knot did. In the years with shortage of high-quality food (2016-2018), the diet niches overlap index between Great Knot and Bar-tailed Godwit decreased from 0.63 to 0.07, from early to late staging season. Although 25% of Great Knots and 52% of Bar-tailed Godwits have abandoned the Yalu Jiang coastal wetland, the intake rates of the highly faithful individuals of these two species still decreased dramatically.

3) The staple prey of Great Knots shifted from the relatively soft-shelled bivalve *P. laevis* in 2011-2012 to harder-shelled molluscs, such as the gastropod *U. thomasi*, in 2016-2017. The crushing of the molluscs in the gizzard would require a 3-11-fold increase in break force. This was partially resolved by a 15% increase in gizzard mass which would yield a 32% increase in shell processing capacity. The consumption of harder-shelled molluscs was also accompanied by reliance on regurgitates to excrete unbreakable parts of prey, rather than the usual intestinal voidance of shell fragments as faeces. Despite the changes in digestive morphology and strategy, there was still an 85% reduction in intake rate in 2016-2017 compared with 2011-2012.

4) At the individual level, diet composition of Great Knots was not associated with the length of the bill, but with the mass of the muscular gizzard. Generally, gizzard mass was negatively correlated with the numerical percentages of the small-sized classes *U. thomasi*, whilst positively correlated with the large-sized classes *U. thomasi*. The larger gizzard mass, the higher the proportion and the large-sized classes *U. thomasi* of hard-shell *U. thomasi* in the diet. The dry mass of shell fragments in each gizzard did not significantly correlate with bill length, but exhibited a positive correlation with gizzard mass. Bill length was not correlated with average break force of the prey, but gizzard mass was.

5) To investigate the methodology and the effectiveness of food supplementation in the case of food shortage, a food supplementation experiment was carried out. More than 40% of Great Knots at the Yalu Jiang coastal wetland was concentrated in the supplementation area. Great Knots mainly fed on *P. laevis* in the supplementation area, while those in the control area mainly fed on *U. thomasi*. The intake rate of Great Knots in the supplementation area was 4.2 times higher (1.17 mg AFDM/s) than that in the control area (0.28 mg AFDM/s). The prey reject ratio of Great Knots in the control area was 2.2 times higher than that in the supplementation area, and the average processing time was 5.5 times longer than that in the supplementation area.

Based on the above findings, the study found that: (1) Food decline at staging sites could be an overlooked but important factor causing population decline of shorebirds along the Flyway. In shorebird conservation, maintaining the quality of staging sites is as important as protecting staging from disappearing via land claims. (2) In years with high quality food, Great Knots and Bar-tailed Godwits could both consume these foods. However, in years when these high-quality foods were scarce, Great Knots and Bar-tailed Godwits reduce the interspecific competition by increasing their diet niche breadth and reducing the diet niche overlap. (3) Although migratory shorebirds have adapted in their physiology, morphology, foraging behavior, and local activity, these adjustments are not adequate in buffering the adverse effects of food decline on energy accumulation rates, and shorebird populations along EAAF would continue to decline. (4) Although artificial supplementation increased the energy accumulation rate of shorebirds significantly, it

was only a short-term relief and could not solve the issue of prolonged food shortage. This study calls for immediate action to study the reasons for food decline and to restore the food base for these beleaguered migrant shorebirds at Yalu Jiang.

This study highlights the multiple impacts of foods decline of the key staging site on shorebird population numbers, as well as the physiological, ecological and behavioral responses of shorebirds. The results are important in understanding the adaptation of organisms to environmental changes and the constraints of adaptation.

(Zhang Shoudong, PhD student, Prof. Ma Zhijun, Supervisor, Fudan University)

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

With the increase of population and the global warming, the ecosystem has suffered serious damages, leading to the growing threats for the global biodiversity. Studying the spatial distributions of organisms is critical to identify biodiversity hotspots, which contributes to the designation of priority areas for conservation when making a biodiversity conservation plan. By revealing the mechanisms underlying the build-up and maintenance of the diversity patterns, we can understand how the diversity patterns interact with climate, and predict the impact of climate change on biodiversity in the future. The Sino-Himalayan Mountains (SHM) region, which harbors 10% of vertebrates and 8% of plants on earth, is one of the most important diversity hotspots. Previous studies made attempts to reveal the mechanisms underlying the diversity patterns in this region. However, the ecological factors and evolutionary processes that drive and maintain the high biodiversity remain unclear. In this study, two groups of birds with different ages were chosen as subjects: (1) pheasants as an old group which originated at the late Eocene–early Oligocene, and (2) babblers as a young group which originated at the late Oligocene–early Miocene. We integrated ecological factors, evolutionary processes and functional diversity to fully understand their roles in the build-up and maintaining of the extraordinary diversity in the SHM. This thesis contains four topics as follows. (1) Phylogeny and taxonomic revision of the world’s babblers. (2) The role of evolutionary time, diversification rates and dispersals in determining the global diversity of babblers. (3) The role of ecological and evolutionary processes in build-up diversity hotspots of pheasants in the SHM. (4) The role of functional traits divergence in co-existence of babblers.

The babblers have a chequered taxonomic history, and the group was long regarded as a “scrap basket” for genera that did not fit well into other families. In this study, we use a multi-locus dataset combining published and newly generated sequences to reconstruct a time-calibrated phylogeny and taxonomic revision for 89% of the world’s babblers species. By calibration using a fossil and a biogeographic event, our phylogeny implies that babblers originated in the late Oligocene–

early Miocene, at approximately 22 Ma (26.4-18.6 Ma). Our phylogeny supports seven primary clades with non-monophyly for some genera. Our phylogeny suggests that babblers could be recognized as seven families including Sylviidae, Zosteropidae, Paradoxornithidae, Timaliidae, Pellorneidae, Alcippeidae and Leiothrichidae. We used a cut-off limit of 10 Ma for recognizing genera, while also taking morphological and ecological similarity into account, which supports 64 genera of babblers. The taxonomic revision proposed a new family (Alcippeidae) and a new genus (*Parayuhina*). The near-complete phylogeny provides a backbone for further studies on biogeography, species richness patterns and co-existence of babblers.

The species richness of babblers varies widely across the earth's surface with the highest diversity in the SHM. The megadiversity of babblers in the SHM could be the direct result of accelerated diversification rate, multiple dispersals and longer evolutionary time to accumulate species. In this section, we evaluate the role of diversification rate, dispersals and evolutionary time on shaping global species richness patterns of babblers based on a near-complete phylogeny. Firstly, we reconstructed the ancestral ranges of babblers and inferred their origin and dispersal routes based on 13 geographic regions. We estimated the first colonization time and the number of immigration events in each region. Secondly, we estimated diversification dynamics through time and among seven geographic regions. In addition, pairwise comparisons of speciation, extinction and dispersal rates between SHM and non-SHM (or continental vs. insular regions) were conducted using GeoSSE models. Lastly, we used the ordinary linear model to compare the relative predictive power of evolutionary time, speciation rate and the number of immigration events upon the species diversity of babblers. We found that babblers originated in the SHM in the early Miocene and from here they colonized other regions, suggesting a longer time for diversification and accumulation of species in the SHM. The diversification rate analysis marked a rate increase at 2.5 Ma associated with the radiation of *Zosterops* in oceanic islands, which coincides with the period of repeated sea level fluctuations in the late Pliocene–Pleistocene. Multiple regression analyses showed the global diversity of babblers can be well explained by the timing of the first colonization within major regions, while the effects of speciation rate and repeated colonizations have been relatively weak. Our results suggest that the global diversity patterns in these birds have mainly been caused by the “time-for-speciation effect”. Our findings also support tropical and subtropical mountains (e.g., SHM) as an origin centre and oceanic islands as the evolutionary cradle for babblers, which provide new insights into the generation of global diversity hotspots.

The SHM have higher species richness than adjacent lowland regions, making them a global biodiversity hotspot. Various mechanisms, including ecological constraints, energetic constraints, diversification rate variation, “time-for-speciation effect” and multiple colonizations, have been posited to explain this pattern. We used pheasants (Aves: Phasianidae) as a model group to test these hypotheses and to understand the ecological and evolutionary processes that have con-

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

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

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

(Cai Tianlong, PhD student, Prof. Lei Fumin, Supervisor, Institute of Zoology)

Evolutionary history of Paridae birds and their adaptation to environmental challenges on the Qinghai-Tibet Plateau

Natural selection is the driving force behind adaptive evolution. Strong selection pressure imposed by environmental challenges forces life to adaptively change their physiology, phenotype or/and genetics, which leave genetic footprints in their genomes. The Qinghai-Tibet Plateau (QTP) is an excellent area in which to investigate adaptation, because its uplift caused dramatic changes in environments of this region, including cooler climate, reduced availability oxygen and opening of habitat. These environmental changes have significantly influenced the distribution and survival of local organisms. The well-studied passerine family, the tits (Aves: Paridae), originated in the Sino-Himalayan mountain region, is an ideal system to investigate adaptive mechanisms related to adaptation to high-elevation environments due to their broad and elevational distribution. In this context, the current study obtained whole-genome sequence data of 87 samples from 19 parid species with ranges spanning the family's elevational range, and transcriptomic data of

embryonic beaks from *Pseudopodoces humilis* and *Parus major*. We integrated phylogenetic, population genetics, morphology, evolutionary development, comparative genomics and transcriptomic to discuss the evolutionary history of parids, the high-elevation hypoxic adaptation, and the open-habitat adaptation. We finally generated some interesting results as follows.

(1) Maximum-likelihood trees and species tree based on SNPs data displayed exactly same topology that generally coincides with previous taxonomy, except for the placement of *Ps. humilis*. This study resolved the controversial classification status of ground tits, and determined the closest relationship between *Ps. humilis* and *Machlolophus*. Additionally, we confirmed that *Poecile palustris hypermelaenus* is not a sister species of *Poecile montanus* but a subspecies of *Poecile palustris*.

(2) Comparing the hording and non-hoarding clades, our F_{st} analysis found that most highly divergent regions were related to the detection and response to external or abiotic stimulus. Genes in these highly diverged regions were annotated to significantly correlate to the hippocampus or brain development and sensory perception of light or sound stimulus, further providing genetic evidence that differentiation between hording and non-hoarding clades is associated with food-coaching behavior and song.

(3) The dating for parids phylogeny showed that extant parids originated from the late Oligocene (ca. 24.8 Mya) but not the Miocene, congruenting with the uplift time (ca. 35-20 Mya) of the southern QTP. The subsequent diversification of parids occurred in the late Miocene (8.8-5.1 Mya) that matches with the last uplift time of the Hengduan Mountain of the QTP (ca. 10 Mya to present).

(4) The calculation of nucleotide diversity found the very low genetic diversity (0.073×10^{-3} - 1.77×10^{-3}) in parids compared to other bird species (10^{-3} - 10^{-2}). Moreover, the geographic distribution of genetic diversity displayed that parids in western high-elevation and mountains had strikingly lower genetic diversities than parids in East Asian lowlands.

(5) The inference of demographic history from PSMC showed significant population fluctuations in most species during the Pleistocene. In line with geographic patterns of genetic diversity and Quaternary glaciers, most species in western, high-elevation and montane regions experienced a dramatic population reduction during the Last Glacial Period, whereas the population expansion was observed in most species from East Asian lowlands. However, the population dynamics of a few species were found to be unaffected by the glaciation. Considering their reduced genetic diversity and residual ranges, we speculated that their population history might result from the range shift.

(6) Multiple F_{st} analyses were applied to discuss hypoxia adaptation at different levels: nucleotide substitution, gene and biological function mechanisms. The results showed that no convergent nucleotide substitution was found among high-elevation parids. Although the HBA gene cluster was highly diverged between high- and low-elevation parids, not all high-elevation parids had the elevation-related amino acid substitutions in HBA genes. Luckily, we found many candidate genes that associate with physiological responses to hypoxia involving in respiratory, circulatory, muscular and energy systems. Among these candidates, *PLB1*, involving in the lipid metabolic process of energy systems, had the largest number of fixed missense sites in most high-elevation parids.

(7) Morphological analyses indicated that long decurved beak of *Ps. humilis* is the most adaptive phenotype related to open habitat. A comparative transcriptomic analysis between *Ps. humilis* and *P. major* based on embryonic beaks at HH28/29 stages detected 17 genes to correlate with bone development and morphogenesis. RT-qPCR, *in situ* hybridization and functional assays in chicken embryos demonstrated that *FGF13* and *ITGB3* may affect beak development by modulating levels of osteoblasts and osteoclasts. Furthermore, genome-wide scanning based on F_{st} and PMT analyses identified 7 candidate genes to be associated with bone morphogenesis and remodeling. Subsequently neutral tests and functional prediction showed that only the highly conserved *COL27A1* suffered strong positive selection, and the R1493Q and P1501L in the domain of *COL27A1* could be damaging.

In conclusion, the uplift of the QTP not only influences the origin and diversification of parids, but also affects their distribution and genetic basis via caused environmental changes. These changes lead to the distinct population history in high-elevation parids from lowlanders, result in convergent adaptation to hypoxia at biological function level among high-elevation parids, and also force *Ps. humilis* to evolve a specialized beak morphology that is regulated by multiple genes at multi-levels. These findings suggest that the combined effect of evolutionary history and natural selection results in the low levels of genetic diversity in parids.

(Cheng Yalin, PhD student, Prof. Lei Fumin, Supervisor, Institute of Zoology)

Bird Banding Research

Autumn Bird Banding Training Class of 2019 were held in Fuyuan, Heilongjiang

“Autumn Bird Banding Training Class of 2019” were held in Fuyuan, Heilongjiang. The main topics of the training class included the knowledge of ornithology, bird classification and identification, wildlife rescue, birds banding database management, the application of satellite-tracking in migration researches and so on. About 40 banders from Heilongjiang, Inner Mongolia, Hubei, Shandong, Henan and Yunnan attended the training class.

(Chen Lixia and Wang Yihua, Beijing)

Bird Banding information of Dongzhai Reserve

A total of 5,581 birds, which belonged to 77 species, 23 families and six orders, were banded during more than ten banding activities in Dongzhai Reserve, 2019. Among them 5,435 birds, which belonged to 77 species, 23 families and six orders, were first captures. A total of 146 birds, which belongs to 17 species, 10 families and two orders, were recaptured.

Moreover, one yellow-throated bunting, three red-flanked blue-tailed robins, one hair-crested drongo, one yellow-rumped flycatcher and one chestnut-winged cuckoo was identified as homing individual. One yellow-throated bunting was recaptured and its band number was B120-0223.

One blue-throated flycatcher was captured and identified as new record of Dongzhai. A total of 88 striated yuhina were captured and identified as new record of Henna Province.

Dongzhai Banding Station was approved as one of the fifteen statewide migratory bird monitoring sites by NBBC in 2012. A summer monitoring from May 10th to 26th and a winter monitoring from November 10th to 26th was conducted according to the local situation. The spring-summer banding and winter banding were conducted by banding station in accordance to the schedule of statewide migratory bird monitoring.

(Xi Bo, Du Zhiyong and Zhang Junfeng, Henan)

The 2019 summary of bird banding in Xinqing, Heilongjiang

Xinqing Bird Banding Station, Heilongjiang banded a total of 30,164 individuals, which belonged to 65 species, 24 families and 7 orders. Among them, 553 birds were recaptured and 244 birds

returned to their birth places. Two species, Eurasian Woodcock *Scolopax rusticola* and Baillon's Crake *Porzana pusilla*, were banded for the first time. A Yellow-throated Bunting *Emberiza elegans* (The metal ring was KANKYOSHO2AK JAPAN93827) which banded in Punago, Zhuzhou city, Ishikawa prefecture, Japan on Oct. 31, 2018 was recaptured at Xinqing banding station on Apr. 17, 2019.

The dominant banding species of this year were common redpoll *Carduelis flammea* of 7,421 individuals, rustic bunting *Emberiza rustica* of 5,470 individuals, black-faced bunting *Emberiza spodocephala* of 4,208 individuals, Siberian Rubythroat *Calliope calliope* of 2,041 individuals, Brambling *Fringilla montifringilla* of 1,715 individuals and hawfinch *Coccothraustes coccothraustes* of 1,258 individuals.

Since the start of bird-banding in 2007, the Xinqing Bird Banding Station had recorded 223 species, 46 families, 18 orders and banded 453,872 individuals, 193 species, 41 families, 14 orders in this area.

(Hou Linxiang and Li Hongwei, Heilongjiang)

Autumn Bird Banding report of Qingfeng bird banding station in 2019

The work was conducted in Qingfeng bird banding station in autumn from 15 August to 15 November. A total of 8,993 birds, which belonged to 67 species, 19 families, 4 orders were banded and 34 birds of 10 species were come back home, 33 birds of 8 species were recaptured.

Compared the number of the autumn banded birds, Passeriformes are the most, and 8,941 birds of 61 species, 16 families were banded and the percentage is 99.4% ; 52 non-Passeriformes birds of 6 species, 3 families, 3 orders were banded and the percentage is 0.6%. In the birds Fringillidae were the most, then the Emberizidae, Turdidae, Sylviidae, Prunellidae, Zosteropidae, Muscicapidae, Motacillidae and Laniidae.

The total of the banded birds this autumn is the least compared to former years. The reason is that the number of the *acanthiflammea* is increased.

(Yang Yanlan, Heilongjiang)

Bird banding information of Shuanghe National Reserve, Heilongjiang

The bird banding and wildlife disease surveillance were conducted simultaneously in Shuanghe

National Reserve, Heilongjiang in 2019, with the support of reserve leaders.

The spring bird banding was conducted at the central station and began in April 11th. Four net sites and a total of six mist nets were established based on the habitat around the banding station, and the herbs and trees were removed within each net site. The banding stopped on May 10th due to the drought and other factors. A total of 23 species and more than 300 birds were banded.

In autumn, we got familiar with the local bird migration pattern, changed the net sites and increased the number of mist nets, which increased the banded bird numbers significantly. From September 20th to October 18th, a total of 23 species and 1,047 birds were banded with eight mist nets at the central station.

We found a non-invasive method for the bird disease surveillance sampling based on our field experience. Since the anal swabs were harmful to birds, we preferred to put different bird species into different cages after the banding, wait the birds to defecate, and collect their droppings and make records. A total of more than 150 bird scat samples were collected in 2019.

(Chen Peng, Heilongjiang)

For the Ailaoshan Migratory Bird Migration

As Ailaoshan rises and falls from north to south, the Golden Gate becomes the gateway for many migratory birds to cross the Ailaoshan Mts.

In late August 2019, the staff of the bird monitoring and banding station in Xinping, Ailaoshan, officially entered the station to carry out bird monitoring and banding work in autumn and winter. At the same time, Dr. Zhao Xuebing from Guangdong Institute of Biological Resources Applied Research carried out a “study on the effects of different wavelengths of light on nocturnal migratory birds” during the period of bird banding, relying on the Xinping Banding Station, and good results have been achieved and the desired objectives have been achieved. Up to now, 3,337 birds have been caught, and 3,299 of them have been banded, 38 birds have been re-caught *in situ*, 12 orders, 22 families and 129 species have been recorded, including 6 species of National Class II protected birds. Compared with the previous year, 14 new species have been recorded, and the ringed birds are the most numerous, the most species and the newest records in recent 5 years.

Ailaoshan Xinping Management and Protection Bureau will not forget its original intention, keep in mind its mission, escort migratory birds, increase the sense of security of migratory birds over Ailao shan, and at the same time make due contributions to the construction of ecological civiliza-

tion in our county.

(Pu Xiu, Yunnan)

News from China and Abroad

Avian Research granted by the Excellence Action Plan of China's STM Journals

In mid-November, 2019, the office of the Excellence Action Plan of China's STM Journals announced the journals that will be funded by the Plan. The journal *Avian Research* that is supported by the China Ornithological Society was listed among the "echelon journals" of the Plan.

In order to implement the government's important instructions on nurturing world first class STM journals, and push forward the high-quality development of Chinese journals, seven government sectors, including the China Association for Science and Technology, the Ministry of Finance and the Ministry of Education, jointly put into practice of the Plan. The Plan is comprised of five sub-categories, i.e., leading journals, key journals, echelon journals, high baseline new journals, and clustered pilot projects. In total, more than 860 journals in China bid for the Plan, 285 of which, including 180 English language journals, 100 Chinese language journals and 5 cluster pilot projects, were eventually chosen after qualification examination, quantitative assessment, on-site defense, and experts review. Among the 180 English journals is the *Avian Research* which is jointly sponsored by the China Ornithological Society and Beijing Forestry University, and will get a financial support of RMB 400,000 yuan each year, for a five-year term.

During the term of the Plan, *Avian Research* will target to further improving the professional and international level of publishing, enhancing the capability of scientific dissemination and service, and striving for a higher impact among the world ornithology journals. We hope the society members could continue to support the development of *Avian Research* and contribute more high-caliber submissions.

(Cheng Pengjun, Beijing)

An important breeding site of Baer's Pochard found in Minquan wetland, Henan Province

On September 7, 2019, a press conference jointly held by China Baer's Pochard Conservation Working Group and Shangqiu Municipal Government, released that, according to the survey and monitoring result of Beijing Forestry University and Minquan Ancient Yellow River National Wetland Park, Minquan wetland is an important habitat and breeding site of Baer's Pochard.

Baer's Pochard (*Aythya baeri*) is ranked in critically endangered species (CR) by IUCN in 2012, with a global population less than 1,000 individuals. In winter of 2018-19, 155 Baer's pochards were monitored in Minquan wetland, and the population was stable in the year. From 2018 to 2019, China Baer's Pochard Conservation Working Group and MinQuan Ancient Yellow River National Wetland Park cooperately carried out a special investigation during breeding period, and found fifteen nests of Baer's Pochard in May 2019. This is the first record of BP nest in Minquan wetland and confirming this place is an important breeding site of Baer's Pochard.

On the press conference, Prof. Ding Changqing, chair of China Baer's Pochard Conservation Working Group, released videos, photos and survey data of Baer's Pochard, including nests and eggs, incubation and ducklings raising. He also proposed the protection suggestions according to the main threats. Reasons for nest failure include picking up of eggs, nest abandoning and weasel predation.

In order to protect Baer's Pochard and other wild birds, with technical supports provided by China Baer's Pochard Conservation Working Group Minquan wetland park increased the frequency of monitoring and patrol, controlled the water level in breeding season, and enhanced the management of main habitat. In the future, we will further strengthen the publicity on the protection of Baer's Pochard, promote habitat improvement, and reduce threats during breeding period. China Baer's Pochard Conservation Working Group will continue the researches on breeding ecology, habitat selection and main threats, and help MinQuan Ancient Yellow River National Wetland Park to join in East Asian-Australasian Flyway Partnership Flyway Site Network (EAAFP - FSN) and Ramsar Site.

(Li Lu, Ma Fuguang and Ding Changqing, Beijing)

An improved automatic trap for capturing birds in nest boxes

Several traps have been designed for capturing birds in their nest boxes, and questions remain concerning the effectiveness, reliability and automatism of the traps. Here we developed an

automatic trap, designed to capture parent birds in artificial nest boxes. When a bird enters the nest box, the trap will be triggered by pulling on a twig treadle and the door will shut securely with a magnet. During 2014-2016, the trap was used to capture Varied tits (*Sittiparus varius*), Marsh tits (*Poecile palustris*) and Great tits (*Parus cinereus*) during the breeding seasons. We captured 177 birds, with a trigger rate of 92.2%, a capture rate of 100% and an average capture time of 22.5 ± 19.6 min. No known trap-related injuries or desertions occurred. This light weight, easily operated, and highly efficient trap improves the data collection and results during field work. This trap can be used in a wide variety of nest boxes to capture songbirds.

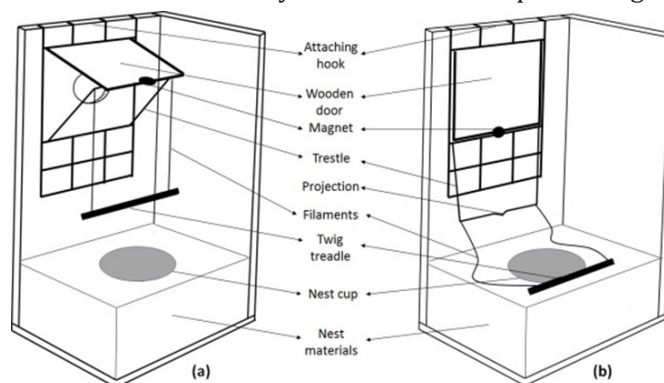


Fig View of the trap set within a nest box. (a) Details when the trap is activated, (b) Details when the trap is triggered

(Zhang Lei, Liaoning)

The Second Phase of the *Crane Migration Research on the Silk Road and Chinese Crane Culture Communication* was successfully completed

The project, *Crane Migration Research on the Silk Road and Chinese Crane Culture Communication*, which executed by the School of Ecology and Nature Conservation of Beijing Forestry University invited 17 ornithologists Nov-Dec 2019. The experts came from Russia, Mongolia, Kazakhstan and Nepal. With the migrating cranes, the journey started from Beijing, passed through Yellow River Delta, Yancheng, Yangtze Estuary and Hangzhou Bay. During this period, we visited 9 nature reserves, the China Silk Museum and signed the Memorandum of Understanding on Cooperation in Crane Conservation and Research. Four international symposiums were held at the Capital Normal University, Shanghai Natural History Museum and other places along the way. Finally, 5 foreign teams were built to take part in the 2019 Poyang Lake International Birdwatching Week, organized by the Jiangxi Provincial Government and the China Wildlife Conservation Association, undertaken by Jiangxi Provincial Department of Forestry and other organizations.

Foreign ornithologists who participated in the project experienced the achievements of wildlife conservation in China through field trips. This process has changed the wrong views which

attributed the decline of regional biodiversity to China thoroughly. In the meanwhile, the experts learned the excellent traditional ecological concepts of China, heard more Chinese voices and enjoyed many aspects of Chinese speeds. At the end, they expressed great expectations for the cooperation with Chinese experts.

(Pu Zhen and Guo Yumin, Beijing)

Tundra Swans (*Cygnus columbianus*) found wintering in Three Gorges Reservoir after impoundment

Tundra Swan (*Cygnus columbianus*) belongs to the Anatidae of Anateriformes. The IUCN classifies it as a Least Concern species (2019), and China classifies it as the Class II National Protected Species. According to Zheng Guangmei (2017), Tundra Swan is distributed in China except Chongqing, Hainan, Shaanxi, Qinghai, Xizang, Xianggang, and Aomen. Poyang Lake in Jiangxi Province is the largest wintering place for Tundra Swans in China, where the wintering Tundra Swans reach about 110 thousand according to the latest data.

We conducted a survey of terrestrial wildlife in the Three Gorges Reservoir, and wintering Tundra Swans were found on the Daning River (Figure 1) on December 11, 2019. Before the impoundment of the Three Gorges Reservoir, Tundra Swans were recorded in Changshou District, Chongqing City, but the time and quantity are unknown. Tundra Swan is a new record of birds in the Three Gorges Reservoir since the impoundment. The swans are a family group with two adults and one child.

(Li Xiuming, Liu Fuguo, Qian Fawen and Liu Xiaoyun, Beijing)

Rescued birds Released to Poyang Lake in International Bird Watching Week of Poyang Lake

On the morning of December 8, 2019, staff of wildlife rescue centers from Beijing, Tianjin, Heilongjiang, Jiangxi and Guangdong, released 237 rescued birds in the Dahuchi of Jiangxi Poyang lake National Nature Reserve, including Swan Goose (*Anser cygnoid*), Ruddy Shelduck (*Tadorna ferruginea*), Mallard (*Anas platyrhynchos*), Bean Goose (*Anser fabalis*), Bar-headed Goose (*Anser indicus*), Oriental Stork (*Ciconia boyciana*), White-naped Crane (*Grus vipio*), Greylag Goose (*Anser anser*), Common Moorhen (*Gallinula chloropus*), Tundra Swan (*Cygnus columbianus*), Eastern Spot-billed Duck (*Anas zonorhyncha*), belonging to 11 species of 4 families of 3 orders.

These birds being rescued or confiscated by law enforcement, after careful treatment and rearing,

have reached the standard for release to the wild. In order to help the rescued birds keep up with the migratory troops that have arrived at Poyang Lake to survive the winter, wildlife rescue centers send them directly to Poyang Lake for collective release.

Before the release, staff of the Jiangxi Wildlife Rescue Center and the National Bird Banding Center banded 33 of the birds and fit with satellite trackers including 10 Eastern Spot-billed Ducks, 1 Ruddy Shelduck, 3 Mallards, 4 Swan Geese, 3 Bean Geese, 4 Oriental Storks, 4 White-naped Cranes.

(Pan Kaijun and Qian Fawen, Beijing)

The expert studying bird louse work in China

Dr Daniel R. Gustafsson, originally from Sweden, is an expert in the taxonomy, morphology, and evolution of parasitic chewing lice (Phthiraptera) on birds. Since 2017 he is working at the GIABR through the Guangdong Academy of Sciences Special Talent Program, surveying the chewing louse fauna of China. Dr. Gustafsson loves parasites, China, his work, and his profession, which combines both field work in South China, lab work at the GIABR, and helping his colleagues and graduate students to revise their English manuscripts. During 2019, a total of 17 SCI papers were published by Dr. Gustafsson, 12 of which he is first author on. In total, these papers saw the description of 2 new genera, 42 new species, and the redescription of 18 previously named species. In 2019, his research was supported by the “Pearl River Talent Program in Guangdong Province – Young Top Talents”.

Not much is known about the bird louse fauna of China, and it is estimated that less than 5% of the fauna in China is actually known. Over half of the known species records for China have been published by Dr. Gustafsson and his co-workers in the last 10 years. Much of the unknown fauna likely represent new species for science, especially in South and West China and in the Himalayas.

We are very interested in finding collaborators who can provide us with chewing louse samples from all birds in China, particularly from larger-bodied birds and water birds. We are open to traveling to show you how to collect chewing lice, and we are happy to publish new records or new species together with you and provide financial compensation. Contact us at tel: 18675885773, Email Address: zoufs@giabr.gd.cn (Professor Fasheng Zou) or kotatsu@fripost.org (Dr Daniel Gustafsson, English only).

(Zou Fasheng, Guangdong)

The introduction of collaborative research between China and USA

Dimensions US-China: Collaborative Research: Replaying the Tape of Lice – Functional Genomics and Experimental Endosymbiont Replacements was supported by the National Natural Science Foundation of China and the National Science Foundation of the USA. The project starts in 2020, and researchers at the Guangdong Institute of Applied Biological Resources will initiate a new collaborative project on the co-evolution of birds, their parasitic lice, and the gut bacteria of lice that make this relationship possible. This project is co-funded by the National Natural Science Foundation of China and the National Science Foundation of the USA, and our partners in the US are Professors Sarah Bush, Dale Clayton, and Colin Dale at the University of Utah, and Dr Kevin Johnson at the Illinois Natural History Survey. The project concerns the genomic evolution of symbiotic bacteria in the guts of chewing lice parasitic on pigeons and song birds, as well as their routes of infection and the co-evolution of three layers of biodiversity: bird, louse, and bacteria.

By comparing different lineages of gut bacteria with reduced genomes, we hope to gain fundamental insights into the genomic mechanisms that enable parasitism in nutrient-poor environments, such as feathers.

Within this project, we hope to hire two post-doctors and one PhD student, as well as some master students. For more information on these positions, and the project in general, please contact us, tel: 18675885773, Email Address: zoufs@giabr.gd.cn/kotatsu@fripost.org.

(Zou Fasheng, Guangdong)

Great Bustard Rediscovery in Huaihe River Basin, Anhui Province

On March 1, 2020, Great Bustards (*Otis tarda*) was found in Zhangwei village (116°52'21.01"E, 33°01'22.31"N), Huaiyuan County, Bengbu, Anhui Province, a site near Cihe River in the Huaihe River floodplain. From March 1 to 4, the distribution sites of the Great Bustard were investigated by field observation and visiting villagers. The results showed that the Great Bustard stayed for about one month in this area, and its habitat was located in the open beach, wheat land, fallow land, etc. near the river. During the investigation, the Great Bustard was found three times and photographed. Every time only one individual was found. Five feathers also were found in the foraging habitat. It may be an important reason for the birds to reappear in their traditional habitat that the travel restriction for the prevention and control of Novel Coronavirus-infected Pneumonia (NCP) greatly reduces human activities.

(Zhang Jianping and Zhou Lizhi, Anhui)

Publication

Two Chinese Books on Raptors published

On the basis of undertaking four NSFC projects on raptor research, Prof. Ma Ming of Xinjiang Institute of Ecology edited and published two new books, such as Black Vulture's Story and Saker Falcon's Story, both of which are series books by the China Forestry Publishing House, in the end of 2019. For the past two decades, Prof. Ma Ming's Research Group has focused on the field population ecological investigation of raptors, and has successively obtained NSFC support projects for saker falcons (*Falco cherrug*), golden eagles, Himalayan vultures and black vultures (*Aegypius monachus*). The members of the research team crossed the Tianshan, Altay and Kunlun Mountains, across the Taklimakan Desert, the Qinghai Tibet Plateau and the Qiangtang area, with deserts, mountains and rivers all over the West of China. These two books are the first single line books in China. Ma Ming was the first to use UAV to find the nest of big raptor, the first to use infrared camera to monitor the breeding behavior of raptor, and the first to use satellite tracker to study on the migration of raptor in China. Over the past twenty years, raptor research and monitoring has accumulated millions of pictures, and two books with more than 400 photographs, including automatic shooting of infrared cameras. The new edition concentrates the essence.

(China Raptor Team, Xinjiang)

"Atlas of birds in Liupanshan" published

The Atlas of birds in Liupanshan edited by Wang Shuanggui, Song Sen and Yuan Hailong has been published by Sunshine Press of Ningxia Yellow River Publishing Media Company in November 2019. A total of 200 species belonging to 46 families and 17 orders of wild birds were recorded in Liupanshan National Nature Reserve, among which 16 species are newly recorded in Ningxia, and they are Brown-breasted Bulbul *Pycnonotus xanthorrhous*, Light-vented Bulbul *Pycnonotus sinensis*, Barred Laughingthrush *Garrulax lunulatus*, Grey-winged Blackbird *Turdus boulboul*, Buff-throated Warbler *Phylloscopus subaffinis*, Buff-barred Warbler *Phylloscopus pulcher*, Ashy-throat Warbler *Phylloscopus maculipennis*, Eastern Crowned Warbler *Phylloscopus coronatus*, Bianchi's Warbler *Seicercus valentini*, Hwamei *Garrulax canorus*, Eurasian Nuthatch *Sitta europaea*, Slaty-nacked Flycatcher *Ficedula sordida*, Rufous-breasted Accentor *Prunella strophiata*, Long-tailed Rosefinch *Carpodacus sibiricus*, Slaty Bunting *Emberiza siemsseni* and Large Hawk-Cuckoo *Hierococcyx sparveroides*. The book gives a detailed description of the morphological characteristics, habits, resident type and conservation status of each bird species. This book provides basic information for researchers, bird lovers and management and protection personnel who study and protect birds in Liupanshan in the future, which not only has important reference value for researchers to

understanding the current situation of birds in Liupanshan and the status of birds in Ningxia Hui Autonomous Region, but also has the value for the science popularization.

(Song Sen, Gansu)

Announcement

SMBE 2020

SMBE 2020 is taking place in Québec city, QC, Canada on June 28th-July 2nd 2020 at the Québec Convention Center. Full details on the symposia programme and confirmed keynote speakers and information on the registration fees can be viewed in <http://smbe2020.org>.

(Qu Yanhua, Beijing)

International Eurasian Ornithology Congress

The 7th International Eurasian Ornithology Congress will be held in April 2020 at Ege University, Izmir, Turkey. The Congress topics are: Behavior, Bird strikes and aircraft safety, Climate Change, Collision with obstacles, Conservation, Ecology, Evolution, Migration, Parasitology, Phylogeography and Phylogeny, Wildlife management and Others. The Early Registration Deadline is 09 March 2020. Please find the details at: <https://ornithologylab.com/ieoc2020izmir>.

(China Ornithological Society)

East Asian-Australasian Flyway Shorebird science meeting

The first East Asian-Australasian Flyway Shorebird science meeting will be held on 5-8 May, 2020 in Seocheon-gun, Republic of Korea. Please find the details at: <http://eaafssm.com/>.

(China Ornithological Society)

North American Ornithological Congress

The 7th North American Ornithological Congress will be held on 10-15 August 2020 in San Juan, Puerto Rico. Please find the details at: <https://naocbirds.org/>.

(China Ornithological Society)

Climate change and birds: solutions to the crisis | BOUsci20

The 2020 Annual Conference of British Ornithologists' Union will be held on November 24, 2020 in Peterborough, UK. The topic is Climate change and birds: solutions to the crisis. Please find the details at: <https://www.bou.org.uk/conference/climate-change-and-birds-solutions-to-the-crisis/>.

(China Ornithological Society)