2016

# 2016 International Symposium on Galliformes (Beijing, China: October 21-23, 2016): Programme and Abstracts

World Pheasant Association

China Ornithological Society

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会标

# Proceeding


Photo by: Jiang FENG

**October 21−23, 2016　　Beijing**

**2016 年 10 月 21−23 日　　北京**

# 2016 International Symposium on Galliformes

# 2016 北京国际雉类学术研讨会

Hosts: World Pheasant Association,
主办单位： 世界雉类协会
China Ornithological Society
中国动物学会鸟类学分会

Organizer: Beijing Forestry University
承办单位： 北京林业大学

Supporter: Department of Wildlife Conservation and
Nature Reserve Management, the
State Forestry Administration, China
支持单位： 国家林业局野生动植物保护与自然保护区管理司

| **Sponsors:** | **协办单位：** |
|---|---|
| China Wildlife Conservation Association | 中国野生动物保护协会 |
| Forestry Department of Shanxi Province | 山西省林业厅 |
| Beijing Zoo | 北京动物园 |
| Beijing Zoological Society | 北京动物学会 |
| BWRRC | 北京市野生动物救护中心 |
| Taiyuan Zoo | 太原动物园 |
| Chengdu Zoo | 成都动物园 |
| Pangquangou National Nature Reserve | 山西庞泉沟国家级自然保护区 |
| Fengtongzhai National Nature Reserve | 四川蜂桶寨国家级自然保护区 |
| *Avian Research* | Avian Research 编辑部 |
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| Hainan Normal University | 海南师范大学省部共建实验室 |
| BSEE, Beijing Normal University | 北京师范大学生物多样性与生态工程教育部重点实验室 |
| Nature Image of China | 自然影像中国 |

# Programme of
# 2016 International Galliformes Symposium

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| **21 October 2016, Friday** | | | |
| **Time** | | **Organizer** | **Location** |
| 13:00-19:00 | **Registration** | Jianqiang LI<br>Huan ZHANG | Xueyan Lecture Hall, Xueyan Building B1,<br>Beijing Forestry University |
| 15:00-17:00 | **Round Table Discussion I:** Management of Nature Reserves | Jiliang XU<br>Changqing DING | Room 1102, Main Building, Beijing Forestry University |
| 19:00 | Reception Dinner<br>(Buffet with beer and drinks) | | No.3 Dining Hall, Beijing Forestry University |
| **22 October 2016, Saturday** | | | |
| **Time** | | **Speaker** | **Title** |
| 9:00-9:50 | **Opening Ceremony**<br>**Chair:**<br>Zhengwang ZHANG | Keith Chalmers-Watson, Chairman of The World Pheasant Association<br>Ping DING, President of China Ornithological Society<br>Xiong LI, Vice-President of Beijing Forestry Univeristy<br>Xiwu ZHANG, Director of Wildlife Conservation and Nature Reserve Management, SFA<br>Distinguished Guests. | |
| 9:50-10:20 | Group photo & Coffee break | | |

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|---|---|---|---|
| 10:20-12:20 | **Plenary 1-3**<br>**Chairs:**<br>Yuehua SUN<br>Jacob HÖGLUND | Rebecca KIMBALL | P1. Evolutionary relationships among galliforms using 1000's of unlinked loci |
| | | Siegfried KLAUS | P2. Ecology, behaviour and conservation problems in Siberian grouse *Falcipennis falcipennis* (Hartlaub 1855) |
| | | Yang LIU | P3. Taxonomy, genetics and evolution in a highly subspecies-rich pheasant *Phasianus colchicus* |
| 12:20-13:30 | Lunch (No.1 Dining Hall, BFU ) | | |
| 13:30-13:50 | **Oral Presentation Session I:**<br>**Chairs:**<br>Jiliang XU<br>Geffery DAVISON | Nan WANG | O1. Survey of the Blyth's Tragopan *Tragopan blythii* in western Myanmar |
| 13:50-14:10 | | Pengfei SHAN | O2. Activity rhythm of Green Peafowl (*Pavo muticus*) in Konglonghe Nature Reserve based on camera-trap data |
| 14:10-14:30 | | Yiqiang FU | O3. Studies on Unusual Incubation Behavior and Embryonic Tolerance of Hypothermia by the Sichuan Partridge (*Arborophila rufipectus*) |
| 14:30-14:50 | | Ge GAO | O4. The Breeding Behavior and Nest Selection of Sclater's Monal (*Lophophorus sclateri*) at Mt. Gaoligong in Yunnan |
| 14:50-15:10 | | Yu XU | O5. Selection and overlap of dust bathing habitat among three sympatric montane Galliform species |
| 15:10-15:30 | | Yingqiang LOU | O6. Male vigilance and presence are important for foraging by female Chinese Grouse in the pre-incubation period |
| 15:30-16:00 | Coffee break | | |
| 16:00-16:20 | **Oral Presentation Session II**<br>**Chairs:**<br>Wei LIANG,<br>Rahul KAUL | Hongyan YAO | O7. Habitat association and availability of Snow Partridge *Lerwa lerwa* on the Qinghai–Tibet plateau |
| 16:20-16:40 | | Peng CUI | O8. Progress of the national bird monitoring program in China and results review of Galliformes |

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| 16:40-17:00 |  | Lu DONG | O9. Reconstructing the phylogeographic patterns of *Chrysolophus* pheasants by multilocus DNA sequence data |
| 17:00-17:20 |  | Bisong YUE | O10. Microsatellites in Genome and Application in Genetic Diversity Study of Sichuan Hill Partridge *Arborophila rufipectus* in Laojunshan Reserve |
| 17:20-17:40 |  | Shu-Sheng ZHANG | O11. The Conflict between Conservation and Development: the case of the Cabot's tragopan in Wuyanling National Nature Reserve |
| 17:40-18:00 |  | Laxman Poudyal | O12. The status assessment and conservation of Nepal's galliforms |
| 18:00-18:20 |  | John CORDER | O13. Recent developments in the reintroduction of pheasant species |
| 18:30-20:00 | Dinner (No.3 Dining Hall, BFU) |  |  |
| 20:00-21:00 | **Round Table Discussion II** | Room 1102,<br>Main Building, BFU | Survey of Blyth's Tragopan and census on Galliformes |
|  | **Round Table Discussion III** | Room 1105,<br>Main Building, BFU | *Ex-situ* conservation of Galliformes in Zoos |

## 23 October 2016, Sunday

| **Time** |  | **Speaker** | **Title** |
|---|---|---|---|
| 8:30-10:00 | **Plenary 4-5**<br>**Chairs:**<br>Changqing DING<br>Brigadier Mukhtar Ahmed | Jacob HOGLUND | P4.Genomics studies on the grouse |
|  |  | Simon BRUSLUND<br>John CORDER | P5A. The European Association of Zoos and Aquaria (EAZA) structure and management programmes for Galliformes;<br>P5B. WPA & Conservation Breeding of Pheasant Species in Europe |

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| 10:00-10:30 | Coffee break | | |
| 10:30-10:50 | **Oral Presentation Session III**<br>**Chairs:**<br>Yanyun ZHANG<br>Huw LLOYD | Heidi KALLIONIEMI | O14.Bird quality, origin and predation level affect survival and reproduction of translocated common pheasants *Phasianus colchicus* |
| 10:50-11:10 | | Muhammad Naeem AWAN | O15.Recent investigations on distribution and threats of Western Tragopan *Tragopan melanocephalus* in Pakistan: Challenges for conservation |
| 11:10-11:30 | | Dang Gia TUNG | O16.Conservation breeding programme for the Edwards' Pheasant *Lophura edwardsi*, Vietnam |
| 11:30-11:50 | | Adrish PODDAR | O17.Are Blyth's tragopans (*Tragopan blythii*) secure in community conserved landscapes of Nagaland? |
| 11:50-12:10 | | Mukesh THAKUR | O18.Genetic evolution Cheer Pheasant and Western Tragopan |
| 12:10-12:30 | | Sean WALLS | O19. How to track Galliformes |
| | | | |
| 12:30-13:30 | Lunch (No.1 Dining Hall, BFU ) | | |
| 13:30-14:10 | **Plenary 6-7**<br>**Chairs:**<br>Yong WANG<br>Rebecca KIMBALL | Xiangjiang ZHAN | P6.Avian genomes and population genetics |
| 14:10-14:50 | | Edward BRAUN | P7.Insights into the evolution of pheasants from whole genome sequencing |
| 14:50-15:30 | **Poster Session** | **Organizer:** Lu DONG, Jianqiang LI | |

| 15:30-16:00 | Coffee break | | |
|---|---|---|---|
| 16:00-16:40 | **Plenary 8-9**<br>**Chairs:**<br>Yang LIU<br>John CORDER | Zhiming HONG | P8.Species delimitation in the Chinese bamboo partridge *Bambusicola thoracica* |
| 16:40-17:20 | | Rahul KAUL | P9.Conservation of Galliformes of India: a journey |
| 17:20-18:00 | **Closing Ceremony** | Chairs: Ping DING, Keith Chalmers-Watson<br>Summary: Geofrrey DAVISON | |
| 19:00 | **Banquet** | Shangyuan Restaurant, XIJIAO HOTEL (the 2nd Floor of NO. 5 Building) | |

# 2016 北京国际雉类研讨会

## 会议日程

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|---|---|---|---|
| **10 月 21 日，星期五** | | | |
| **时间** | | **主持人** | **地点** |
| 13:00-19:00 | **会议注册** | 李建强，张欢 | 北京林业大学，学研大厦，地下一层报告厅 |
| 15:00 | **圆桌讨论会 I:** 自然保护区管理 | 徐基良，丁长青 | 北京林业大学，主楼 1102 会议室 |
| 19:00 | **招待晚宴**（自助餐，提供啤酒和饮料） | | 北京林业大学，学三食堂 |
| **10 月 22 日，星期六** | | | |
| **时间** | | **报告人** | **题目** |
| 9:00-9:50 | **开幕式**<br>**主持人：** 张正旺 | Keith Chalmers Watson, 世界雉类协会主席<br>丁平，中国动物学会鸟类学分会理事长<br>李雄，北京林业大学副校长<br>张希武，国家林业局野生动植物保护与自然保护区管理司司长<br>其他嘉宾致辞 | |
| 9:50-10:20 | 合影、茶歇 | | |
| 10:20-12:20 | **大会报告 1～3**<br>**主持人：** 孙悦华，Jacob HÖGLUND | Rebecca KIMBALL | P1. 鸡形目鸟类的进化关系 |
| | | Siegfried KLAUS | P2. 镰翅鸡 *Falcipennis falcipennis* 的生态、行为和保护问题 |
| | | 刘阳 | P3. 亚种高度分化的雉鸡 *Phasianus colchicus* 的分类、遗传和进化 |

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| 12:20-13:30 | 午餐（北京林业大学，学一食堂） | | |
| 13:30-13:50 | **口头报告 I**<br>**主持人：**徐基良，Geffery DAVISON | 王楠 | O1. 缅甸西部的灰腹角雉 *Tragopan blythii* 调查 |
| 13:50-14:10 | | 单鹏飞 | O2. 利用红外相机技术分析恐龙河保护区绿孔雀(*Pavo muticus*)活动节律 |
| 14:10-14:30 | | 付义强 | O3. 四川山鹧鸪(*Arborophila rufipectus*)奇特孵卵行为及其胚胎耐受低温研究 |
| 14:30-14:50 | | 高歌 | O4. 云南高黎贡山白尾梢虹雉(*Lophophorus sclateri*)繁殖特征和巢址选择 |
| 14:50-15:10 | | 徐雨 | O5. 三种同域高山鸡形目鸟类（血雉、雉鹑、白马鸡）沙浴生境的选择与重叠分析 |
| 15:10-15:30 | | 楼瑛强 | O6. 雄鸟警戒对斑尾榛鸡雌鸟孵化前期的重要性 |
| 15:30-16:00 | 茶歇 | | |
| 16:00-16:20 | **口头报告 II**<br>**主持人：**梁伟，Rahul KAUL | 姚红艳 | O7. 基于生态位模型的青藏高原雪鹑栖息地选择和预测 |
| 16:20-16:40 | | 崔鹏 | O8. 中国鸟类观测网络进展与鸡形目鸟类结果回顾 |
| 16:40-17:00 | | 董路 | O9. 基于多位点 DNA 测序数据的锦鸡属（*Chrysolophus*）谱系地理重建 |
| 17:00-17:20 | | 岳碧松 | O10. 微卫星在老君山保护区四川山鹧鸪（*Arborophila rufipectus*）基因组和遗传多样性研究中的应用 |
| 17:20-17:40 | | 章书声 | O11. 乌岩岭国家级自然保护区黄腹角雉保护的矛盾与发展 |
| 17:40-18:00 | | Laxman Prasad Poudyal | O12. 尼泊尔雉类的保护与现状评估 |
| 18:00-18:20 | | John CORDER | O13. 雉类再引入项目进展 |
| 18:30-20:00 | 晚餐 (北京林业大学，第三食堂) | | |

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|---|---|---|---|
| 20:00-21:00 | **圆桌讨论会 II** | 北京林业大学，<br>主楼 1102 会议室 | 灰腹角雉及其他鸡形目鸟类数量调查与监测 |
| | **圆桌讨论会 III** | 北京林业大学，<br>主楼 1105 会议室 | 动物园易地保护的鸡形目鸟类 |

**10 月 23 日，星期日**

| **时间** | | **报告人** | **题目** |
|---|---|---|---|
| 8:30-10:00 | **大会报告 4～5**<br>**主持人：**丁长青，<br>Brigadier Mukhtar Ahmed | Jacob HÖGLUND | P4. 松鸡的基因组学研究 |
| | | Simon BRUSLUND<br>John CORDER | P5A. 欧洲动物园和水族馆协会(EAZA)及其鸡形目鸟类管理项目；<br>P5B. 世界雉类协会（WPA）的欧洲雉类饲养繁殖项目 |
| 10:00-10:30 | 茶歇 | | |
| 10:30-10:50 | **口头报告 III**<br>**主持人：**张雁云，Huw LLOYD | Heidi KALLIONIEMI | O14. 鸟类质量、来源和反捕食能力对雉鸡（*Phasianus colchicus*）迁地重建种群存活与繁殖的影响 |
| 10:50-11:10 | | Muhammad Naeem AWAN | O15. 巴基斯坦黑头角雉（*Tragopan melanocephalus*）分布与受胁因素调查：保护的挑战 |
| 11:10-11:30 | | Dang Gia TUNG | O16. 越南爱氏鹇（*Lophura edwardsi*）的保育繁殖项目 |
| 11:30-11:50 | | Adrish PODDAR | O17.Are 灰腹角雉(*Tragopan blythii*)在 Nagaland 景观保护群落中是否安全? |
| 11:50-12:10 | | Mukesh THAKUR | O18. 印度彩雉（*Catreus wallichii*）黑头角雉（*Tragopan melanocephalus*）易地保护繁育项目的遗传学评估 |
| 12:10-12:30 | | Sean WALLS | O19. 如何遥测鸡形目鸟类 |
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|---|---|---|---|
| 12:40-13:30 | 午餐（北京林业大学，学一食堂） | | |
| 13:30-14:10 | **大会报告 6～7**<br>**主持人：**王勇，Rebecca KIMBALL | 詹祥江 | P6. 野生鸟类基因组和种群遗传学 |
| 14:10-14:50 | | Edward BRAUN | P7. 雉类进化的全基因组测序研究 |
| 14:50-15:30 | **墙报展示与交流** | **组织人：**董路、李建强 | |
| 15:30-16:00 | 茶歇 | | |
| 16:00-16:40 | **大会报告 8～9**<br>**主持人：**刘阳，John CORDER | 洪志明 | P8. 灰胸竹鸡 *Bambusicola thoracica* 的岛屿与大陆种群分化 |
| 16:40-17:20 | | Rahul KAUL | P9. 印度的鸡形目鸟类保护：在路上 |
| 17:20-18:00 | **闭幕式** | **主持人：**丁平，Keith Chalmers-Watson<br>**会议总结：**Geofrrey DAVISON | |
| 19:00 | **晚宴** | 西郊宾馆赏园餐厅（五号楼二层） | |

# Abstracts

## Content

### Plenary

### Oral

## Poster

# 论文摘要

## 目录

### 大会报告

### 口头报告

## 墙报

# Plenary

Plenary 1

## Evolutionary relationships among galliforms using 1000’s of unlinked loci

## 鸡形目鸟类的进化关系

**Rebecca T. Kimball**
Department of Biology, University of Florida, Gainesville, FL 32611, USA

Galliformes have been studied extensively but a full understanding of their evolutionary relationships within the group has remained elusive. DNA sequence data has been helpful in elucidating many Galliform relationships but there are several relationships that have continued to vary among studies. Here we use next generation sequencing to obtain sequence data from 1000's of loci from throughout the genome. We have sampled over 40% of all Galliform species using this approach, including at least one representative of each genus. Analysis of this resulted in a phylogeny that has strong support for almost every relationship, thus resolving conflicts among previous studies. These results support previous relationships among families, including the position of the African stone partridge as sister to the New World quail. Within the Phasianidae, there were three major clades. Like previous studies, pheasants and partridges were not monophyletic, and multiple clades contained both partridges and pheasants. While most genera were monophyletic, we identified several genera that, as traditionally circumscribed, were not monophyletic. The problematic genera include the Old World quail where large-bodied two partridge genera were intermixed within the quail. Finally, we have integrated this dataset with published mitochondrial and nuclear sequence data to estimate phylogenetic relationships for over 90% of all galliform species where many relationships are well resolved. Overall, these results now allow a more rigorous examination of trait evolution than previous studies.

Plenary 2

# Ecology, behaviour and conservation problems in Siberian grouse *Falcipennis falcipennis* (Hartlaub 1855)

## 镰翅鸡的生态、行为和保护问题

**Siegfried Klaus, Aleksander V. Andreev & Franz Hafner**
Max Planck Institute of Biogeochemistry, Hans-Knöll-Str. 10, D-07745 Jena, Germany

A.T. von Middendorf (1853) was the first who detected this endemic bird in the Stanowoj Mountains/Russian Far East, but failed to find differences to the American sister species. Therefore, he regarded this tetraonide as subspecies *Tetrao canadensis var. franklinii*. Hartlaub (1855) presented evidence for the species character. IUCN 1996 and Storch (2000) considered the Siberian grouse to be at a lower risk (near threatened). In China (recent records missing) and Russia the bird belongs to 1st grade protected in the Red Data Books. We studied this grouse in the Charpin-Baktor area near river Gorin, Bureinsky and Myochan Mountains.

The Siberian grouse inhabits the dark coniferous forests of the Ochotskian taiga and the river depressions between at 100 m to timber line at 1500-1600 m in the Russian Far East. Boreal forests of spruce and fir configured with larch-dominated forests form the typical habitat in most of the species' range. In the mountains, thickets of shrub pine (*Pinus pumila*) were used as well as the border of extended bogs covered by *Ledum pallustre.* Locally, coniferous forests without larch mixed with stone birch (*Betula ermanii*) were inhabited. In the southern part of the range Mongolian oak *Quercus mongolicus,* aspen *Populus tremula,* shrub alder *Alnus fruticosus,* and different willows *Salix* spp. mixed with conifers form spruce grouse habitat. In winter Siberian spruce grouse feed exclusively on spruce needles, mostly on Ajan spruce. In May the young needles of the Dahurian larch is a preferred diet.

The close vicinity of spruce and larch seems to form the optimum habitat. Forest fires result in a cyclic rejunification of both types of conifers. In summer, Siberian grouse feed on ground vegetation (Ericaceae, moss, forbs, grass, fruits of *Cornus canadensis*, ants and other insects). Ants seem to play a major role in the diet of females in the prelaying period.

In optimum habitats an abundance of 6-8 birds / 100 ha (spring) or 15 birds / 100 ha in early autumn have been reported (Hafner & Andreev 1998). The Siberian spruce grouse was observed to form mixed flocks of 2-6 individuals in winter. Flocks break up by late March or early April. The males move to display territories (mean size 7.5 ha) where they prefer to use a territorial center of only 1 ha. The territorial system seems to be flexible ranging from solitarily displaying males to leks (Andreev et al. 2001) depending on density. The mating system is polygyny (Andreev et al. 2001).

The acoustical communication in the Siberian spruce grouse is adapted to dense habitats of the boreal taiga. Different signals acting at very short (few m) and medium and long (>100 m) distances are an adaptation to specific predation pressures. The most conspicuous territorial performance is the two-syllabic flutter-jump on the ground. It starts with a low-pitched, rising, vibrating hooping sound. Then the bird jumps with a 180° turn. This turning-jump is immediately followed by a straight-jump, both 30-50 cm high. In addition, an imposing run is observed with alternating movements of the spread tail feathers producing a rhythmic instrumental hissing sound, similar to the North American sibling species (Boag & Schroeder 1992). In both species, noisy flutter flights were used to demonstrate the territory.

Habitat loss and fragmentation by clear-cutting and/or fire on large scale of the conifer-dominated pristine forests of the Russian Far East seem to be the main cause of population decline in parts of the area.

Plenary 3

# Taxonomy, genetics and evolution in a highly subspecies-rich pheasant *Phasianus colchicus*

**Yang Liu**

State Key Laboratory of Biocontrol, College of Ecology and Evolution/School of Life Sciences, Sun Yat-sen University, Guangzhou, 510275, China

## Background

The Common Pheasant (*Phasianus colchicus*) is an exemplary species with a large geographical range in the Palearctic region and prominent intra-specific divergence in plumage patterns and coloration. Thirty recognized subspecies categorized into five subspecies groups have been defined mainly on the basis of biogeography and morphology. It inhabits varied climatic zones, including northern temperate to subtropical, and from monsoon to semi-desert regions, and is hence expected to have undergone several, and probably parallel local adaptations. The common pheasant has a long history of captivity and being introduced as a common game species in Western Europe, North America and Australia. Therefore the common pheasant is a particularly suitable model for studying evolutionary patterns and processes.

## Methods

In this talk, I review previous studies on the taxonomy, phylogeography and population genetics of the common pheasant based on morphological traits, biogeography and evolutionary genetics approaches using multiple genetic markers. With the advancement of the high-throughput sequencing technology, we are using genomics approaches to study natural populations of the common pheasants.

## Results

I will show morphological-based subspecies delimitation is only partially consistent with results suggested from genetic analyses, with ambiguous boundaries among some subspecies. Levels of divergence of subspecies/ populations varied spatially, depending on geographic arrangements and demographic historis. Further, I show patterns of genetic polymorphism at some loci are likely involved in environmental adaptations along a climatic gradient in Northern China.

## Conclusions

Using complementary data and approaches, our results suggests new insights into the taxonomy, evolution and genetics of the common pheasant, which in turn offers some useful implications for the management and conservation of its wild and captive populations. However, we are only beginning to understand genetic basis of phenotypic traits and ecological adaptations in the common pheasant, which represents a nice model to understand the evolution of diversity in nature.

**Keywords:** *Phasianus colchicus*, subspecies, population genetics, genomics, demography

Plenary 4

# Genomic studies of grouse
# 松鸡的基因组学研究

**Jacob Höglund**

Dept. of Ecology and Genetics, Uppsala University, Norbyv. 18D, SE 75236, Uppsala, Sweden

Since the announcement and publication of the first human draft genome on the 26th of June 2000, biology as we used to know it has changed dramatically. The first bird genome, of the chicken, was published in 2004 and now genomic studies of thousands of organisms have been published including hundreds of bird species. In this talk I will focus on genomic studies of grouse (subfamily Tetraoninae). The first grouse genomes, of the black grouse and Gunnison sage grouse, respectively, were published in 2014 and have since been followed by a few more sequenced grouse species. Even more grouse genomes are in the pipe-line.

This talk will be organised in two parts. First I will present the black grouse genome study which was done by my lab. The focus here have been on identification of immune genes with special attention to comparative studies with other galliform birds but also issues relating to conservation where patterns of genetic variation in large and continuous populations are compared to small and isolated population fragments. The second part will show how genomic data can be used to infer past population changes throughout the history of black grouse and three *Lagopus* species. I will furthermore resolve a phylogeographic enigma previously observed in willow grouse and present data suggesting a few candidate genes that may have played important roles in the divergence within the *Lagopus* lineage.

Plenary 5A

# The European Association of Zoos and Aquaria (EAZA) structure and management programmes for Galliformes

# 欧洲动物园和水族馆协会(EAZA)及其鸡形目鸟类管理项目

**Simon Bruslund**

Member of EAZA Galliformes Taxon Advisory Group & Chair of WPA GERMANY Schuetzenhausstr. 35b, D-69151 Neckargemuend, Germany

The talk aims to set out the structures for population management adopted by the European Association of Zoos and Aquaria (EAZA) and to showcase current priorities in regard to focus species. The author will add historical comments, demonstrate current population developments and provide background information in and outside current breeding programmes.

As governing body the EEP Committee oversees and approves formal changes in breeding programmes. The executing body is the Taxon Advisory Group (TAG) which produces regional collection plans and pre-selects candidates to lead population management in specific taxa.

Zoos are continually increasing their commitment to in-situ conservation and quite a number of zoo based conservation projects are benefitting wild Galliformes.

In recent years the focus in many TAG's has shifted more and more towards maintaining safety populations of severely threatened species with high genetic diversity. This is also the case in the Galliformes TAG and is reflected in working priorities.

The talk will further describe the methods and tools available to make structured and scientifically based decisions on species priorities and will mention past, present and future software support and techniques needed to develop structured and functional studbooks with a focus on the specific challenges concerning Galliformes and especially Pheasants.

The current challenges and future focus areas will include committing to do specific and relevant research on Galliformes for which the TAG needs to investigate and formulate the priorities and needs together with external stakeholders such as field researchers, IUCN and WPA. Also a functioning but still binding model for cooperation with non-EAZA institutions and private breeders must be established. Finally there is an increasing need for global management and cooperation to ensure long-term genetic diversity. The talk describes some of the specific problems involving international cooperation and animal transfers.

As a former chair and current member of the EAZA Galliformes Taxon Advisory Group the author is in a good position to describe the functions of breeding programmes in the major European zoos.

Plenary 5B

# WPA & Conservation Breeding of Pheasant Species in Europe
# 世界雉类协会（WPA）的欧洲雉类饲养繁殖项目

**John Corder**

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WPA's principal aim is to save threatened galliformes species by increasing the effectiveness of our conservation efforts worldwide. Since the foundation of WPA more than 40 years ago we have transformed a passion for wildlife into effective conservation action both by increasing knowledge of galliformes species within WPA and by involvement with other conservation bodies that share our conservation aims.

Within Europe, WPA has seven Chapters, and representatives from these meet regularly to form WPA's European Conservation Breeding Group (ECBG). Focus Groups have been established for many pheasant species to bring together those who are particularly interested in these species and to establish pure, self-sustaining captive populations.

ECBG has initiated DNA research into Cheer pheasants, Green peafowl, Tragopans, Peacock pheasants and, most importantly, Edwards's pheasant. More than €25,000 has been raised for this research so far which will eventually allow a conservation breeding and reintroduction programme to be established in Vietnam using the most unrelated birds.

WPA has good working relationships with many conservation organisations, but particularly values its close liaison with the EAZA Galliformes TAG. We have worked together for many years and look forward to helping to re-establish the Edwards's pheasant in Vietnam in the future.

Plenary 6

# Avian genomes and population genetics
## 野生鸟类基因组和种群遗传学

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### Background

As top predators, falcons possess unique morphological, physiological and behavioral adaptations that allow them to be successful hunters: for example, the peregrine is renowned as the world's fastest animal. To examine the evolutionary basis of predatory adaptations, we sequenced the genomes of both the peregrine and saker falcon, and we present parallel, genome-wide evidence for evolutionary innovation and selection for a predatory lifestyle. Then we utilized the genomics resources to study the population genetics of saker falcons across Eurasia, and to analyze how their transcriptomes have become modified to cope with the stresses of hypoxia on the Qinghai-Tibetan Plateau (QTP) plateau.

Using the Galliformes genomes newly sequenced, we also study the wild pheasants with different traits in order to understand the genetics basis for their trait evolution.

### Methods

Genome sequencing of falcons was carried out using an Illumina HiSeq 2000. A detailed description of library construction, sequencing and assembly, genome annotation, gene prediction annotation, and comparative genomic analysis is included in Zhan *et al*. (2013).

Using 144 SNPs, we examined population genetic differentiation in the saker falcons across Eurasia. The position of each SNP was verified using the saker reference genome with 108 SNPs positioned within introns and 36 SNPs in exons of six genes. The experiment protocols and analytical procedures were described in Zhan *et al*. (2015).

The RNA sequencing of sakers and genome sequencing of galliform birds are similar to that used in *de novo* sequencing of falcon genomes (Zhan *et al*. 2013), but use a single library.

### Results

Falcon genomes were found to have consistent signatures of rapid evolution but less olfactory receptor genes. Gene-based analysis highlighted falcon-specific evolutionary novelties for beak development and olfaction and specifically for homeostasis-related genes in the arid environment–adapted saker.

In saker populations, we found that exonic SNPs were key to resolve genetic differentiation between QTP and non-QTP sakers. The RNA-seq data of sakers further exemplify synergistic responses between DNA polymorphism and RNA expression diversity in coping with common stresses, underpinning the successful rapid colonization of a top predator onto the plateau.

From the Galliformes genomes, we have identified more than 2.6M SNPs (2~9% heterozygous), which were used to reconstruct the phylogenetic tree of galliform birds.

**Conclusions**

Our study provides important genetic resources for the study of raptors and galliform birds, and presents a model for sequencing the reference genome and its application in the research of wild bird populations.

**Keywords:** Falcons - Galliformes - Genome - Population genetics

Plenary 7

# Insights into the evolution of pheasants from whole genome sequencing
# 雉类进化的全基因组测序研究

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Recent large-scale whole genome sequencing efforts in birds have elucidated broad patterns of avian genome evolution. However, despite the importance of Galliformes for agricultural, conservation, and behavior we have limited genomic information from this clade outside of the chicken (*Gallus gallus*) and turkey (*Meleagris gallopavo*). The decreasing costs of genome sequencing have resulted in the recent addition of two new galliform genome sequences (the Northern bobwhite *Colinus virginianus* and the Japanese quail *Coturnix japonica*). We decided to assess the potential to assemble galliform genome sequences using a single insert library, allowing substantial cost savings. We assembled draft genome sequences for the Chinese bamboo partridge (*Bambusicola thoracicus*) and three additional junglefowl (*Gallus*) species, all of which can provide information about the evolution of the chicken genome. All of our genome assemblies were sufficient to generate high-quality data for evolutionary analyses. We examined the impact of selection on coding regions by examining shifts in the average nonsynonymous to synonymous rate ratio (*dN/dS*). There were substantially more protein-coding genes with elevated *dN/dS* ratios in *Bambusicola* than in *Gallus*, and those proteins had many different cellular functions. These results are consistent with the hypothesis that selection has been less efficient in the *Bambusicola* lineage than in the *Gallus* lineage. Our analyses suggest this likely reflects a larger long-term effective populations size in the *Gallus* lineage. These results demonstrate that genome assemblies generated using a single library have the potential to be a valuable tool for testing evolutionary hypotheses and provide new resources for comparative studies of galliforms.

Plenary 8

# Species delimitation in the Chinese bamboo partridge *Bambusicola thoracica*

## 灰胸竹鸡的岛屿与大陆种群分化

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Although tropical and subtropical Asia harbor a high level of species diversity, their species richness can be underestimated because species which are in fact distinct have not been separately identified. In this study, we delimit *Bambusicola thoracica* into two full species, the Chinese bamboo partridge (*B. thoracica*) in continental Asia and the Taiwanese bamboo partridge (*B. sonorivox*) on the island of Taiwan, using coalescent-based multilocus division and diagnosable vocalization patterns. Isolation with migration analysis indicated that the two bamboo partridges diverged approximately 1.8 million years ago, with gene flow present most probably during the early stages of their divergence. This conclusion supports the hypothesis that diverging lowland lineages spread across the Asian mainland and continental islands have more opportunities for secondary contact than highland ones when the sea level was low. Our results imply that conservation of biodiversity in tropical and subtropical Asia could be hindered by overlooking numerous “hidden” species, and highlight the importance of re-examining the taxonomic statuses of species in this region traditionally defined as polytypic.

**Key words**: species delimitation, coalescent, species tree, bamboo partridge, vocalization

Plenary 9

# Conservation of Galliformes of India: a journey
# 印度的鸡形目鸟类保护：在路上

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The British left a rich legacy of knowledge in the Indian sub-continent about its flora and fauna including the galliformes which largely pertained to the natural history of these species. Post independence, the work was consolidated by Ali and Ripley in their Handbook of the Birds of Indian subcontinent. This work was compiled from the volumes already published by the British explorer and naturalists, supplemented by their personal observations.

With the advent of the WPA International Galliformes Symposia – Pheasants in Asia – first in 1979 in Kathmandu, Nepal and then in Srinagar, Kashmir, in 1982, interest was rekindled in this group of birds and kickstarted research on Indian galliformes. Over the last 30 years, we now know where most of our galliformes are and how they might be faring. There was substantial increase in the rate of publications on galliformes after 1980, with over 550 publications (all forms) listed since then, indicating growing interest in galliform research. Most of this work has been on the distribution and status as was the need then. This was followed by subjects like ecology and behavior and other aspects such as like management, followed. With the availability of technology, projects involving landscape level distributions (use of GIS/RS) and genetics became common. We also see a move towards initiation of on ground conservation projects especially in areas under private or community ownership where traditional ways of conservation have borne less impact. This period also saw the inclusion of other tools such as conservation breeding, especially in the Himalaya to try and breed threatened species in captivity to aid *in-situ* conservation.

Despite all this work, there are still gaps in our knowledge. For instance is the Himalayan Quail still alive or is *molesworthii* really a sub-species of Blyth's to more complex issues such as how are the galliformes responding to challenges of climate change?

Research is an important part of conservation for it allows us to take informed decisions but in the wheel of conservation, research is one cog. We need to initiate ground level, long-term conservation projects that actually stop the declines in the number of galliformes by bringing in synergies of other dimensions of conservation such as policy, awareness, enforcement to achieve better conservation and secure our galliformes for the future.

# Oral Presentation

Oral 1

## Survey of the Blyth's Tragopan *Tragopan blythii* in western Myanmar
## 缅甸西部灰腹角雉调查

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**Background**

Blyth's Tragopan *Tragopan blythii* is the most endangered species in the genus Tragopan, and information about it is least amongst the five species. The boundary between Myanmar and India was recorded to be one of the main areas of the birds' distribution. But no survey had been taken out in this area, and the status of the bird was unknown.

**Methods**

In April-June 2014 and April-May 2016, a survey of Blyth's Tragopan was undertaken in the boundary area between Myanmar and India at Mount Kennedy, Chin Division, and Mount Saramati, Sagaing Division, Myanmar. The distance between the two mountains is 290km. We camped and walked in the forest along the paths to find Blyth's Tragopan. Morning and evening calling site and encountered sites of the birds were recorded for analyzing the density and potential distribution. DNA samples were collected from the dead birds hunted by local people for analyzing the Genetic distance of the two populations in the two mountains. Photos of the birds were taken to compare the outsight.

**Results**

In Mount Kennedy, Seven sites were recorded to be Blyth's Tragopan habitat. We undertook a survey in two of them and 15 locations were recorded for Blyth's Tragopan. In Mount Saramati, we undertook a survey in two sites, and 58 locations were recorded. All of the birds appeared at the habitat above 2000m with steep slope and old forest. In Mount Kennedy shift cultivation is the main reason for Blyth's Tragopan habitat loose, and the landscape is dominated by young second growth forest and shrub which could not provide habitat for Blyth's Tragopan. In Mount Saramati, pressure on Blyth's Tragopan was not so serious as in Kennedy. Adult male Blyth's Tragopan in Mount Kennedy is red check, which is different from the yellow check of the Saramati population. DNA analysis shows that the two populations could be identified as two subspecies, and the potential distribution of the birds shows a broad gap between the two populations.

**Conclusions**

Habitat for Blyth's Tragopan in Mount Kennedy is much less than in Saramati, and Mount Saramati keeps a healthy population. The genetic distance of the two population is because of the broad low altitude area between them.

**Key words:** Blyth's Tragopan; Myanmar; Subspecies; Potential Distribution; genetic distance

Oral 2

# Activity rhythm of Green Peafowl (*Pavo muticus*) in Konglonghe Nature Reserve based on camera-trap data

# 利用红外相机技术分析恐龙河保护区绿孔雀活动节律

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Behavior activity patterns of wild Green peafowl (*Pavo muticus*) were studied from January to May 2016 using camera trap in Shuangbai Konglonghe Nature Reserve of Yunnan, China.16 infrared cameras were laid to monitor the Green peafowl and 418 identification photos were obtained after 1838 work days. The camera data showed that the higher months of RAI (relative abundance indexes) of Green peafowl are higher from February to March, which coincide with the time of courtship by field study, and the maximum group size during the 2 months is 13. *Pavo muticus* complied with strict diurnality, the activity peaks ware at 8:00-10:00 and 17:00-19:00, there was no significant difference of the activity intensity of different time quantum between female and male peafowl (÷2=10.57, df=13, P=0.35)

**Key word:** *Pavo muticus*-camera trap- activity rhythm

Oral 3

# Studies on Unusual Incubation Behavior and Embryonic Tolerance of Hypothermia by the Sichuan Partridge (*Arborophila rufipectus*)

# 四川山鹧鸪奇特孵卵行为及其胚胎耐受低温研究

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**Background:**

Temperature profoundly affects avian incubation behavior and embryonic development. During incubation, it is assumed that birds restrict their foraging activities as much as possible in order to avoid embryonic hypothermia. In most species of birds, the optimal temperature for embryo development is between 35.5°C and 38.5°C, and development is suspended below 26°C [i.e. the physiological zero temperature (PZT)]. Single-sex incubators are often faced with a direct conflict between incubation and foraging. The Sichuan Partridge (*Arborophila rufipectus*) is a globally endangered species that inhabits subtropical evergreen and deciduous broadleaf forests at 1100–2250 m a.s.l. We reported an unusual incubation behavior of the Sichuan Partridge, with long recesses of females and embryonic hypothermia, at Laojunshan National Nature Reserve, southwest China. The aims of this study were to (1) describe the incubation behavior of Sichuan Partridge, (2) test whether human activities and weather condition were associated with the long incubation recesses, and (3) assess Sichuan Partridge embryonic tolerance of hypothermia in relation to the adaption in cold montane environments.

**Methods:**

We used Tinytag Plus 2 temperature data loggers (TGP-4520, Gemini Data Loggers, UK) to monitor incubation rhythms (i.e. departure time, return time, recess duration and nest attentiveness). Effects of nest sites (Groups High Disturbance *vs* Low Disturbance) and weather condition on incubation rhythms

of the Sichuan Partridge were tested using general linear mixed models (GLMM).

**Results:**

Female partridges incubated eggs alone, and typically took one long incubation recess of 4.5 ± 1.2 hr (mean ± SD) per day. They left the nests at 07:36 am (± 50 min) and returned at 12:06 pm (± 70 min). Nest attentiveness was 81.2 ± 5.2 % of the entire incubation period. Females prolonged the recess duration and decreased nest attentiveness significantly in response to high disturbance risk and bad weather. Although eggs experienced ~4.2 hr below PZT for each recess, the total hatching rate was 88.4%, suggesting that embryonic hypothermia seemed to have little negative effect on the hatching rate. For Sichuan Partridges, the ability to withstand embryonic hypothermia may be an adaptation to the cold montane environments.

**Keywords:** Incubation; long recesses; embryonic hypothermia; Sichuan Partridge *Arborophila rufipectus*

Oral 4

# The Breeding Behavior and Nest Selection of Sclater's Monal (*Lophophorus sclateri*) at Mt. Gaoligong in Yunnan

## 云南高黎贡山白尾梢虹雉(*Lophophorus sclateri*)繁殖特征和巢址选择

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This project is supported by Forestry Department of Yunnan Province.

**Background:**

Sclater's Monal is a vulnerable species (Vu) in IUCN Red List, and it is also protected by China's Wildlife Protection Law (Class I). This species distributes from across Himalayan southern slopes to the Hengduan Mountains in China. Mt. Gaoligong is a reliable site for its breeding populations. However, the field study on this pheasant is extremely difficult, causing an extremely poor understanding on its population trends, habitat preference, and ecological needs, especially during the breeding season.

**Methods**:

During the breeding season of 2015 and 2016, we recorded the display and fighting behavior by digital cameras. When the nests were found, data logger was used to monitor the temperature in and out of the nest. From which we illustrated the incubation rhythm of the bird. The topographic characters of the nest site were also described and measured. All the field work was done at Mt. Gaoligong, Lushui County, Yunnan Province, China.

**Results:**

It is the first time to record the displaying behavior of this monal in China. The male always approached the female from behind, trotting around back and forth, and then stopped when getting closer, spreading its wings and tail with its head lower down, finally dashed to the female with its feathers fluttering. We recorded four attempts like this of different males, however, none of them succeeded to mate with the female. The male-male fighting was recorded from late March to early June, so did the displaying behavior. Egg-laying was also initiated from late March, but ended in early May.

We found 6 nest sites in total, of which 3 were used in 2015-2016, while the other 3 were used in the

former years. One nest site was reused both in 2015 and 2016, indicating that “nest site reuse” was not occasional for this bird. The clutch size was (mean ± SD) 2.75±0.5 (n=4), the hatchability was 100% (n=11). The incubating bird left the nest from twice per day to once for 3 days, the interval averaging 62.17±26.76 (n=47) min. All the 6 nests located on the ledge on the side of large boulders, averaging 6.97±1.49 m (n=3) above the ground. The distances between these nests varied from 150m to 1500m.

**Conclusions:**

Compared to the southern populations, this population has a prolonged breeding time. Sclater’s Monal has strict selection on the nest site, for which the slope direction, larger boulder, and nesting ledge are critical. These sites are limited resources at Mt. Gaoligong, resulting in that the population mainly distributes around these nest sites and some sites are reused for several years. The protection of nest sites is critical for the conservation of this species.

**Keywords:** Sclater’s Monal; Breeding Behavior; Nest site Selection; Mt. Gaoligong

Oral 5

# Selection and overlap of dust bathing habitat among three sympatric montane Galliform species

## 三种同域高山鸡形目鸟类沙浴生境的选择与重叠分析

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**Background:** Niche theory predicts that non-limiting resources (i.e. supply>demand) does not necessarily lead to severe interspecific competition and niche partitioning. However, this hypothesis has little been tested in the topic of habitat use, since habitats in natural environment are limited supply in most cases. Dust bathing site represents a non-limiting behavior-specific habitat subset, as its particular characteristics of non-consuming, short use duration and low use frequency allow species to satisfy own bathing needs without exclusively and long period occupying.

**Methods:** We tested spatial niche partitioning in terms of dust bathing habitat, using three sympatric montane Galliform species on the Qinghai-Tibet Plateau in China: Blood Pheasant (*Ithaginis cruentus*), Buff-throated Partridge (*Tetraophasis szechenyii*), and White Eared-pheasant (*Crossoptilon crossoptilon*), by recording bating scrapes and measuring habitat characteristics of bating sites, 10 × 10 m quadrats with the scrape as the center, along 10 transects established in Gexigou nature reserve, Sichuan, China, from April to August in 2015.

**Results:** In total, 117 dust bathing scrapes were detected. A high proportion of dust bathing scrapes and sites (35.7% of bathing scrapes, and 20.7% of bathing sites) were co-used by multiple species. The three species did not significantly differ in the dimensions of bathing scrapes, vegetation type, and habitat features of bathing sites, and the habitat overlap indexes between them were higher than 0.6 which is proposed as an ecologically significant threshold. All the three species preferred to select fir forests with dense tree stratum and good concealment that could provide sufficient safety and suitable bathing substrate for bathing.

**Conclusions:** Our study supports the hypothesis that sympatric species do not necessarily partition a non-limiting habitat subset between them. Further studies on monitoring Galliformes' use of dust bathing sites are needed to test potential temporal partitioning that minimizes competition between inter- and con-specific individuals.

**Keywords:** Overlap, Phasianidae, Spatial niche, Coexistence, Ground-dwelling birds

Oral 6

# Male vigilance and presence are important for foraging by female Chinese Grouse in the pre-incubation period

## 雄鸟警戒对斑尾榛鸡雌鸟孵化前期的重要性

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In some monogamous birds, males invest more time in vigilance than females, especially during the pre-incubation period. As behaviors are time costly, there is a trade-off between vigilance and feeding behavior. Male vigilance can be regarded as a male investment in their female mate and may benefit the female by reducing the danger of predation, increasing her probability of survival, and allowing more time for her to forage to obtain more resources for egg production and incubation. In this study, we documented the proportion of time spent in vigilance and feeding by Chinese Grouse (*Tetrastes sewerzowi*) with their mates and alone during the pre-incubation period, and then estimated male vigilance under more severe predation pressures through predator call playback. Our results indicated that paired male Chinese Grouse spend more time in vigilance than unpaired males and paired females and could alter their activity budgets in response to the social context (i.e., with and without their mate) and an experimental encounter with an important predator. Male vigilance behavior and presence allowed females to spend more time foraging. We therefore conclude that vigilance behavior by their male partners by may play an important role in promoting the females' survival and probably the reproductive success. The proportion of time allocated for vigilance by males and foraging by females of Chinese Grouse during the pre-incubation period was the highest recorded among monogamous grouse species, perhaps because the Chinese Grouse is the smallest grouse species and has the highest relative reproductive investment.

**Key words**: male investment; vigilance; Chinese Grouse; playback experiments; predation risk

Oral 7

# Habitat association and availability of Snow Partridge *Lerwa lerwa* on the Qinghai–Tibet plateau

## 基于生态位模型的雪鹑栖息地选择和预测

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### Background

Understanding habitat use is important for species protection and conservation, particularly for species such as Snow Partridge *Lerwa lerwa*, one of the little known birds distributed along the Himalayas with high altitude and harsh climate. Tibetan Snowcock (*Tetraoganllus tibetanus*), with many similarities of habitat, distribution and niche with Snow Partridge, was also available and of interest in exploring this phenomenon. Species distribution models (SDMs) have been widely used to predict available habitat and potential distribution. Additionally, ENMTools, an online free software available, has been accepted to compare quantitatively the similarity of environmental niche models (ENMs).

### Methods

We conducted a field study of Snow Partridge at Balangshan in August 2013, at Shangri in January 2015 and Mount Yulong in August 2016 on the Qinghai–Tibet plateau of west central China. We used models of Random Forests to determine the micro-habitat variables that Snow Partridges might select based on 25 presence and 27 absence locations with 18 micro habitat variables and a maximum entropy algorithm (MaxEnt ver. 3.3.3.e) to predict the distribution for three counties (Wenchuan, Xiaojin and Baoxing, Sichuan Province) adjacent to our main study site, with a total area of 12800 km$^2$. We compared the distribution and niches between Snow Partridge and Tibetan Snowcock from meso-scale of the three counties and macro-scale of the whole distribution based on MaxEnt and ENMTools.

### Results

We found a total of 15 flocks of Snow Partridge in the study area, on pyramidal peaks, arêtes and steep rock slopes above 4300 m. The species was associated with habitats of the top of high cliffs or flatter terrain closed to high cliffs, less steep slope and high altitude. Slope angle was the main factor affected the species' micro-habitat selection while vegetation was a more important factor at meso-scale, with

altitude being consequential at both scales. Only approximately 6.64% of study areas had the features that might provide the suitable habitat for the species. At meso-scale, the suitable habitat of Tibetan Snowcock was larger than the Snow Partridge's and the overlap area of them about of 761.57km$^2$ occupied 89.97% of Snow Partridge's and 79.63% of Tibetan Snowcock's habitat respectively. At macro-scale, they clearly occupied different ecological niches such that Tibetan Snowcock occurred on the Tibet plateau and Snow Partridge was distributed the southeastern margin of the Qinghai–Tibet plateau, where a higher overlap range of 72.33% of Snow Partridge's areas with Tibetan Snowcock.

**Conclusions**

We suggest that the abatement of human-induced activities such as grazing and herb gathering should be taken into account in developing long-term protection strategies for Snow Partridge and other wildlife species in the area, particularly with the concerns that global warming may further reduce the availability of suitable habitat for these species associated with high altitude and cool climate conditions.

**Keywords:** *Lerwa lerwa, Tetraoganllus tibetanus,* Habitat selection, Random Forests, Maxent, overlap, scale

Oral 8

# Progress of the national bird monitoring program in China and results review of Galliformes

# 中国鸟类观测网络进展与鸡形目鸟类结果回顾

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Biodiversity monitoring is a repeated survey of biodiversity in a certain period and area, and it is the most important means to detect the trends and status of most species and habitats. Since 2011, Nanjing Institute of Environmental Sciences, Ministry of Environment Protection of China has established a national bird monitoring trial program (including breeding bird survey and wintering waterbird survey) in order to build the bird monitoring network in the country. By the end of 2015, there were 201 bird survey sample areas (counties) in 31 provinces, covering 99 national nature reserves. There were 917 transect lines with a total length exceeds 2000 km, and 914 survey points in the bird monitoring program.

During the past five years, we have recorded 970 species, more than 70% of China's bird species (1371 species). Among them, 41 species were Galliformes accounting for 66.13% of China's Galliformes species, 9 species were protected as the national first class and 12 species were as the national second class. From 2011 to 2015, the analysis of 10 common breeding bird species, such as Great Tit (*Parus major*) showed that their distribution and population had no obvious change. The analysis of the inland wetlands waterfowl monitoring data indicated that there was no obvious change in bird species and with a fluctuation in population, but without significant change trend. Nevertheless, through the data analysis of seacoast wetland waterfowl monitoring, it reflected that the populations of six sample areas were in declining trend among the 11 sample areas. Overall, due to enclosing tideland for cultivation and exploitation, a large number of seacoast wetland waterfowl habitats had lost and fragmented which facing a serious threat. In the future，we need more volunteers and new equipments to establish a moreperfect national biodiversity monitoring network.

**Keywords:** Biodiversity monitoring, Galliformes, population, distribution

Oral 9

# Reconstructing the phylogeographic patterns of *Chrysolophus* pheasants by multilocus DNA sequence data

## 基于多位点 DNA 测序数据的锦鸡属（*Chrysolophus*）谱系地理重建

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To explore the phylogeographic patterns of *Chrysolophus* pheasant species pairs (*C. pictus* and *C. amhersitiae*), we sequenced 36 nuclear genes and mitochondria cytochrome *b*(cyt *b*) gene in Golden pheasant (*C. pictus*) and Lady Amherst's pheasant (*C. amhersitiae*) sampled from multiple localities across their ranges in China. DNA polymorphism analyses showed that genetic diversity of *C. pictus* is higher than *C. amhersitiae*, and the diversity of cyt *b* gene from both of them is lower than expected, as a result of strong genetic drift or natural selection. Baysien trees constructed by mitochondria cyt *b* gene, Z-link genes and autosome genes, respectively, reflected different phylogenetic patterns. Mitochondria cyt *b* gene tree revealed the apparent geographic patterns of *C. pictus*, inferring distinct genetic differentiation between the two populaitons in north-west (Sichuan and Shaanxi) and south-east (Hubei, Hunan and Guizhou). However, no alike patterns were showed by nuclear genes trees. All trees constructed by different kinds of genes showed no obvious geographic patterns of *C. amhersitiae*. Divergence time of the two species was estimated to be 0.89 Myr (95%HPD: 0.57-1.24 Myr) ago according to mitochondria cyt *b* gene, but was shorter according to nuclear genes,with 0.64 Myr (95%HPD: 0.27-1.08 Myr), 0.40 Myr (95%HPD: 0.28-0.52 Myr), 0.42 Myr (95%HPD: 0.30-0.54 Myr) ago according to Z-link genes, autosome genes and all 37 genes (both nuclear genes and mitochondria cyt *b* gene), respectively. Both haplotypes networks and phylogenetic trees indicated gene flow between the two species. Our study indicates the importance of using multiple data sets in a genomic level for reconstructing phylogeographic patterns as well as detecting interspecific gene flow during speciation, and thus deepening our understanding of the divergence history of the species.

**Key words：***Chrysolophus* , phylogeographic patterns , gene-flow , species divergence

Oral 10

# Microsatellites in Genome and Application in Genetic Diversity Study of Sichuan Hill Partridge *Arborophila rufipectus* in Laojunshan Reserve

## 微卫星在老君山保护区四川山鹧鸪基因组和遗传多样性研究中的应用

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### Background

The *Arborophila* only distributed in Asia from the Himalayas eastwards to Taiwan and south to Java, is a very diverse genus, while data of molecular as well as morphology is deficient to figure out relationships among these species. In this study, we firstly sequenced the whole genome of the Sichuan Hill partridge (*A. rufipectus*) and the phylogenetic relationships were analyzed based on the mitochondrial genome sequences.

### Methods

The Sichuan hill partridge samples were obtained from Sichuan Laojunshan Natural Reserve and its genome was sequenced on Illumina HiSeq platforms. Sanger sequencing platform was applied in determination of mitochondrial genomes. Together with 42 other mtDNA sequences of closely related species, we reconstruct highly resolved phylogenetic trees with combined datasets composed of 13-protein coding sequences applied in maximum likelihood (ML) and Bayesian inference (BI) analyses. The divergence time of each taxon was calculated in BEAST with four fossil calibrated points.

### Results

A total of 124.4Gb sequence raw data were generated. The assembled genome size of the Sichuan hill partridge is 1.11Gb with GC content 46.7% and scaffold N50 4.75Mb. The three mitochondrial genomes of *Arborophila brunneopectus*, *A. rufipectus* and *A. ardens* are 16719~16728 bp in size and have a GC content of 43.71~ 45.52%, which is similar to the two previously published *Arborophila* mito-genomes. A total of 43 potential positive selective positions were identified while 31 of them were located in NADH subunits genes which are also mutable most in all mito-genes. The results also indicated that CYTB is a more conversed marker than COXI. Phylogenetic relationships together with geographical distribution of the five Hill partridges whose mito-genomes have published as well as status

of *Arborophila* in Phasianidae were discussed intensively: (1) Bar-backed Partridge is surely closed to Hainan partridge in relationship; (2) while the Genus Arborophila locates root of Family Phasianidea, *Arborophila* was supposed to be the oldest group in Phasianidae; (3) Hainan Partridge and Bar-backed partridge show a closer relationship and diverged later after Sichuan partridge. Hainan partridge diverged at around 5 Mya with Bar-backed partridge and experienced a migration along the Latitude direction before arriving at Hainan Island.

**Conclusions**

The whole genome of Sichuan hill partridge was firstly sequenced. Positive selective pressure has contributed to diversity of mito-genes, and that these genes with more positive loci are easily affected by environment and could be important for speciation and divergence among Hill partridges. The discrepancy between phylogenetic relationships and geographic distribution suggests a more complex population diffusion model of these Hill Partridges.

**Keywords**

Sichuan hill partridge， *Arborophila rufipectus*， genome, mitogenome, phylogeny,

Oral 11

# The Conflict between Conservation and Development: the case of the Cabot’s Tragopan in Wuyanling National Nature Reserve

# 乌岩岭国家级自然保护区的黄腹角雉保护

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As the only protected area mainly focus on Cabot's Tragopan in China, Wuyanling National Nature Reserve has been supporting a Cabot's Tragopan population that is suffering from several threats such as low fertility, delayed sexual maturity, and the low success in natural breeding. Moreover, their eggs and chicks are easily and frequently destroyed or prey on by Yellow-throated Martens, King Rat Snakes and other predators. With the expanding scope of artificial coniferous forests and bamboo forests, the fragmentation of the Cabot's Tragopan habitat has been a serious threat to the populations. On the other hand, the contradiction between development and conservation has made some local people lived in the natural reserve became "ecological refugees”. In view of these factors, a series of positive countermeasures were developed. Firstly, 150 infrared cameras were set to monitor the dynamics of Cabot's Tragopan in the reserve during the breeding season. In addition, 200 artificial bird's nests were established, with a utilization rate of 18%. Since 2010, with the support of Beijing Normal University, a program of artificial insemination was conducted. Five Cabot’s Tragopans were successfully hatched out for the first time in Wuyanling, with increased success year by year. The implementation of more than 0.4 $KM^2$ broad-leaf forest project, more than 5,000 *Daphniphyllum macropodum* seedlings cultivation project, and 0.08 $KM^2$ habitat modification project would be helpful to resolve the problem of habitat fragmentation of Cabot’s Tragopan. To carry out such conservation actions, the ecological emigration work has been carried out covering 665 households, 2,385 people of the Huang Qiao Town by the “whole village relocation project". Finally we are aiming to propaganda of conservation in Cabot’s tragopan and crack down the illegal hunting and logging in the reserve. The first Museum of *Tragopan Caboti* in China was established in 2015 in the reserve, with the purpose of introducing the life history and conservation of Cabot's Tragopan to spread the culture from generation to generation.

**Key words:** Wuyanling ; Cabot's Tragopan; habitat, conservation action

Oral 12

# The status assessment and conservation of Nepal's galliforms
# 尼泊尔雉类的保护与现状评估

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Work was carried out to assess nearly 800 species of birds of the country applying IUCN Red List Categories and Criteria for regional assessment. For this as many as 3000 references were collected, mostly citizen science reports. Two national workshops were orgnaised for wider inputs to the work. A total of 167 species was found to be threatened. Of these seven species were galliforms; one regionally extinct, one critically endangered, two endangered, and three in vulnerable category. In addition to these threatened species, five additional species of galliforms were considered near-threatened. Hunting, trapping and anthropogenic disturbance were identified as main threats to the galliforms of Nepal. Strict protection to minimise hunting and trapping, anthropogenic disturbance, and conservation education are recommended tools for Nepal's galliform conservation.

Oral 13

# Recent developments in the reintroduction of pheasant species

## 雉类再引入项目进展

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WPA is involved in a number of pheasant conservation breeding programmes where reintroduction or reinforcement of an existing wild population is planned. Current knowledge of pheasant release programmes is largely limited to Cheer pheasants in Pakistan during the 1980s and game pheasants for shooting. Many lessons were learnt from WPA's many attempts to re-establish the Cheer pheasant in Pakistan, and in subsequent years a more scientific approach to conservation breeding and reintroduction has suggested many new areas for consideration. This presentation will discuss some of these, particularly related to recent pheasant programmes in Malaysia, India, Vietnam and China.

Two key factors that seem to be apparent are the need to parent-rear pheasants that are scheduled for release, and the importance of establishing release protocols which relate to specific species.

Beyond the two IUCN key documents "*IUCN Technical guidelines on the management of ex situ populations for conservation"* and "*Guidelines for Reintroductions and Other Conservation Translocations"*, we have attempted to underline key elements in conservation breeding of pheasants for release. We have compiled a paper entitled, "A Philosophy for rearing threatened pheasant species for reintroduction" which defines current thinking and practice, but we recognize that further experiences are likely to modify current thinking and practice.

We will also emphasise the importance of DNA research, using Edwards's Pheasant as an example, to select the best birds for reintroduction, and we will indicate how reintroduction projects require international cooperation.

Oral 14

# Bird quality, origin and predation level affect survival and reproduction of translocated common pheasants *Phasianus colchicus*

## 鸟类质量、来源和反捕食能力对雉鸡迁地重建种群存活与繁殖的影响

**Heidi Kallioniemi, Veli-Matti Väänänen, Petri Nummi and Juha Virtanen**

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We investigated the survival and breeding success of common pheasants *Phasianus colchicus* of two origins and in two predator densities. We translocated hand-reared and wild pheasant hens to southern Finland (60N, 24E) and hand-reared ones to central Finland (63N, 27E). Both groups of birds were treated similarly before release and translocated to areas with no local pheasant populations. Both areas appeared similar, the only major difference being the amount of predators. The red fox *Vulpes vulpes* was the major predator of pheasants present in the southern study, where it was abundant, whereas it was almost non-existant in central Finland. In accordance with earlier studies, the wild birds survived much better than the hand-reared ones in the area with a high red fox density. The hand-reared birds located in the low red fox density area survived better than the hens in the area of high red fox density. However, no significant difference was observed in the survival of the hand-reared birds in the low fox density area and wild birds in the high fox density area. Interestingly, after the first two weeks, the survival of pheasants in different groups was equal. We additionally found no significant differences between the bird-groups in terms of hatching success when comparing hens that managed to initiate nesting. No difference was also observed between the hand-reared birds in the low fox density area and the wild in the high fox density area in brood survival to the age of six weeks. We conclude that even hand-reared pheasants can succeed in brood production in an area with low fox densities. We furthermore suggest that pheasants that survive the two first weeks after translocation have good chances of producing a brood whether they are wild or hand-reared.

**Keywords:** *Phasianus colchicus*, common pheasant, survival, hand-reared, translocation, red fox density, predation

Oral 15

# Recent investigations on distribution and threats of Western Tragopan *Tragopan melanocephalus* in Pakistan: Challenges for conservation
# 巴基斯坦黑头角雉的分布与受胁因素调查：保护的挑战

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**W**estern Tragopan, a red-listed species, is endemic to Pakistan and India. In Pakistan the species is found in three main areas i.e. Azad Kashmir, Kaghan Valley and Palas Valley. For the current assessment, we established surveys plots in Azad Kashmir and Kaghan Valley. We present our call count survey data collected between 2008-15 at 86 survey plots (Azad Kashmir, N= 58 and Kaghan valley, N= 28). Western Tragopans were confirmed at 52 plots in Azad Kashmir whereas in Kaghan Valley the species could not be confirmed at any of the survey locations. Deforestation, road construction, unsustainable natural resource utilization, unmanaged nomadic migration and illegal hunting are the major threats to the Western Tragopan and its associated ecosystem. Drawing attention to government authorities as well as local communities to help reduce anthropogenic pressures on the species' habitat is a big challenge along with implementing standardized methodologies to help obtain authentic scientific data needed for better conservation and management planning.

**Key words:** Western Tragopan, *Tragopan melanocephalus*, distribution, threats, conservation challenges, Pakistan.

Oral 16

# Conservation breeding programme for Edwards’ Pheasant *Lophura edwardsi*, Vietnam

## 越南爱氏鹇（*Lophura edwardsi*）的保育繁殖项目

**Dang Gia Tung**

VietNature and Hanoi zoo，Vietnam

Edwards’s Pheasant *Lophura edwardsi* is an endemic species to Central Vietnam, only distributed in the lowland wet evergreen forest from Ha Tinh to Thua Thien Hue provinces. The species was upgraded to CR in 2012 as a result of BirdLife Internation Forum. The last recorded in 2000 through a male confiscated from hunter in Hai Lang district, Quang Tri province.

From 2013 to now, Vietnam Nature is working together with partners in its distribution range to focus conservation efforts for EP species as the followings:

- Establishment of Vietnam Edwards’s Pheasant Working Group and Viet Nature was nominated as coordinator of the group;
- The Action Plan 2015-2020 with vision to 2030 developed and endorsed by: the management bodies in its range from Ha Tinh to Thua Thien Hue provinces; managers of protected areas throughout its range; Institute of Ecology and Biology Resources, Hanoi zoo; Preventing Extinctions Programme BirdLife International;
- Continuing to search EP in the wild by using camera trap surveys in its distribution range
- Viet Nature made efforts to contact the ex-situ conservation communities to express the conservation breeding programme;
- Search the station's location for conservation breeding station in Quang Binh and Quang Tri provinces

Promising results can launch the programme's conservation breeding in 2017 - Year of the Chicken in the sense of a number of Asian countries including Vietnam:

- Provincial leaders of Quang Binh province was agreed to offer land for conservation breeding station and support the construction of aviary.
- Ha Land IUCN has agreed for a period of approximately $ 6,000 to rent / buy land for conservation breeding station;
- Berlin Zoo, Germany and Viet Nature has signed an agreement to support about 5,000 Eur / year for conservation programme of Edwards’s Pheasant;
- WPA agreed to support $ 26,000 for EP conservation breeding programme.

However, most traditional donors agreed that conservation breeding programme is costly and not urgent / possible delay, the process of raising capital is difficult; need access to corporate and the help of individuals, the general public that the Zoo is one ideal bridge. Ex-situ conservation communities, especially WPA and EAZA, Galliformes TAG can do to support the implementation of the Action Plan, including supporting the conservation breeding programme. Viet Nature is expecting more support for conservation breeding programme as the following:

1. Seeking a Zoo/organization committed to funding seed, cost / technical assistance for conservation breeding programme (with Hanoi Zoo); or funding commitments as Berlin Zoo did?
2. Awareness Campaign and Fundraising for the EP during Christmas of 2016 - beginning of 2017?
3. Assisting Vietnamese Nature to access to European businesses mobilize financing for conservation EP: L'Oreal? (e.g The Body Shop is a subsidiary of L'Oreal is funding habitat conservation project in Khe Nuoc Trong- one of the potential locations to release EP in the future)
4. Volunteer producing publications, videos, website upgrade and propaganda on EP conservation
5. Other initiatives?

**Key words:** Edwards' s Pheasant, Conservation, Vietnam

Oral 17

# Are Blyth’s tragopans(*Tragopan blythii*) secure in community conserved landscapes of Nagaland?

# 灰腹角雉在 Nagaland 景观保护群落中是否安全？

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**Background**

The goal of preserving nature is often in conflict with economic needs and aspirations of the rural poor. The pressure escalates even more in the mountains, where the land and usable water is limited for agriculture. Food security drives farmers to bring more forest lands under cultivation (shifting slash - and - burn agriculture, locally known as *Jhum*), further catalyzing deforestation. Amidst all this crisis, there are few fine examples of conservation being exemplified by people of Nagaland, a northeastern state of India.In order to assessthe current status of Blyth’s tragopan and particularly the tenure of such conservation efforts, a scoping survey was initiated.

**Methods**

We surveyed three such sites across Nagaland to assess, in addition to the abundance of Blyth’s, peoples’ attitudes and perceptions on conservation to prepare comprehensive site specific conservation plans.Single - season (March - April 2016) data to quantify the abundance of tragopans, were collected employing call count sampling technique. Peoples’ perception was assessed using participatory SWOT analysis with community stakeholders and state forest department.

**Results**

Based on pooled mean of calls heard from each station across a single site and radius of 500m, the population density (calling groups/km$^2$) of the species from Khonoma, Satoi range and Saramati range is calculated to be 2.128/km$^2$, 3.132/km$^2$ and 2.992/km$^2$ respectively. Based on all the calls heard, call timing pattern of the species was skewed more towards dusk (n=82), than during dawn (n=80).

**Conclusions**

Although Blyth’s are thriving inside this ‘protected areas’, but internal threats (habitats conversion for jhumming or customary and game - hunting practice) from non - empathetic section of the community still lurks. Our consultations with the communities across the sites showed a slew of initiatives to set aside and maintain areas for wilderness,tragopans in specific and a willingness to conserve more. However, there are also threats from the prospect of commercial gains from lumbering forests which need to be offset by accrual of tangible benefits from conservation. Initiatives like eco - tourism, alternate livelihoods for hunters, introduction of cleaner technologies and also community - based enforcement are some common suggested initiatives by the locals.

**Keywords:** Blyth’s tragopan, Nagaland, Call count sampling, Abundance, Community conservation

Oral 18

# Genetic Evaluation of Ex Situ Conservation Breeding Projects of Cheer Pheasant (*Catreus wallichii*) and Western Tragopan (*Tragopan melanocephalus*) in India

## 印度彩雉和黑头角雉易地保护繁育项目的遗传学评估

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When setting-up a captive population, genetic assessment of founders is essential to formulate effective breeding strategies that minimize the negative effects of inbreeding in the successive generations caused by mating between genetically related individuals. We carried out molecular genetic analysis of Cheer Pheasant and Western Tragopan populations of Chail and Sarahan Pheasantries in the State of Himachal Pradesh. The results revealed that the captive stock of Cheer Pheasant is sustaining well and does not exhibit signatures of inbreeding. Conversely, inbreeding is strongly evident in Western Tragopan population. Our study adds new dimensions to the captive management of Cheer Pheasant and Western Tragopan populations and contradicts with a previous study conducted on the same Western Tragopan population of Sarahan Pheasantry using studbook data. This study demonstrates strong evidence for retaining genetic assessment as an integral part to formulate policies/strategies for conservation breeding projects and proposes refining existing studbook records by incorporating microsatellites data and genetic analyses.

**Keywords:** Cheer Pheasant; Western Tragopan; captive management; studbook records; microsatellite analysis

Oral 19

# How to track Galliformes
# 如何遥测鸡形目鸟类

**Sean WALLS**

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How birds use their environment is essential for understanding them and managing populations for wildlife management. For many years Galliformes have been tracked using conventional VHF radio-tags, helping to determine what habitats are important and their survival. In the last decade new technologies have become available for tracking these species, which can reduce the human effort and time to follow the birds, and giving more accurate locations. However, choosing the right technology for your species and project aims is not so easy. In this talk we look at the different technologies and discuss which species and which projects they are most appropriate for.

# Poster

Poster 1-1

## Habitat use of pheasant *(Phasianus colchicus)* broods in southern Finland
## 芬兰南部雉鸡*(Phasianus colchicus)*的栖息地利用

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We studied habitat use of pheasant broods in southern Finland (60° N, 24° E) in 1995-1998. We released both hand-reared (N=33) and wild (N= 31) ring necked pheasant hens at the end of May. Both groups were translocated to the study area and kept in similar pens and fed similarly before release. We followed the hens with broods by radio-tracking for four weeks after hatching.

Because hand-reared hens succeeded to rear only two broods, we combined the data of wild and hand-reared hens. First we analyzed the overall habitat use of surviving broods (n = 14). We included only those broods for which we had at least 23 observations, altogether 318 observations. Compared with the overall availability of the six most important habitat types, pheasant hens with chicks seem to prefer certain environments, while avoiding others (G-test, $G^2$=146.4, $P < 0.001$). Most broods were detected in the most common habitat type, cereal field, but compared to availability of different habitats, the highest number of brood observations was made in field banks (14.1 %), which comprised only 2.5% of the study area. Then we more closely analyzed the use of cereal fields. We included altogether 190 observations of 10 hens. 64.7 % of the pheasant broods in cereal fields were found closer than 20 m to the field edge, and 70.1% to the nearest edge zone. During the study period the amount of field margin area (under 20m from field edge) averaged 23.5 ha, representing 36% of the available cereal field area. Hens were found in this area 123 times, compared with the expected 68, indicating a high preference of margin area ($G^2$=65.7, $P < 0.001$).

Our results indicate that pheasant broods prefer banks, margins and strips to pure field lands. Special game fields should be placed near field margin areas to benefit pheasants. Improving habitats for broods can lead to a better game yield later in autumn, which decreases the need for introductions

**Keywords:** *Phasianus colchicus*, common pheasant, habitat use, translocation, brood survival

Poster 1-2

# Red Jungle Fowl are surviving only in a small pocket in Pakistan: Conservation opportunities.

## 狭域分布的巴基斯坦红原鸡种群：保护的机遇

**Muhammad Naeem Awan[1,2] and Chaudry Muhammad Razzaq[3]**

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Red Jungle fowl *Gallus gallus* is categorized as least concern as the species does not approach the thresholds for Vulnerable under the range size criterion (Extent of Occurrence <20,000 km$^2$ combined with a declining or fluctuating range size, habitat extent/quality, or population size and a small number of locations or severe fragmentation). Although species has an extremely large range but in Pakistan it is found only in a small pocket of Azad Kashmir where a population of n=109 birds has been estimated and species is facing severs anthropogenic pressures. We reviewed the recent research on the RJF in Pakistan besides conducting field surveys to gather information on the threats to this isolated population. Habitat destruction, eggs collection, illegal and over hunting, capturing of live birds, environmental contamination through excessive use of fertilizers and genetic contaminations are some of the threats to RJF in Pakistan. Training of local communities, capacity building of field staff for regular monitoring and development of conservation action plan could help protect the species from local extinction.

**Key Words:** Red Jungle Fowl, Isolated population, Threats, Conservation opportunities, Pakistan.

Poster 1-3

# Are cheer pheasants' (*Catreus wallichii*) survival dependent only on grassland habitats or are they more adaptive?

## 彩雉只依赖于草地类型栖息地还是具有更高的适应能力

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**Background**

Galliformes occupy the central position in the food web making them one of the best indicator species to inspect habitat changes and abiotic pressure. Cheer pheasant is one of such habitat specialist species of grasslands. To record the status of cheer in the districtsof Shimla, Solan and Sirmaur of Himachal Pradesh and identify new microsites of its occurrence, an intensive reconnaissance survey was initiated.

**Methods**

In all, 15 sites were elected for ground truthing, on the basis of earlier record of cheer presence (Sharma & Pandey, 1989), elevation (1500－2500m asl), aspect (south facing), and habitat (grass/scrub lands). Owing to their territoriality during breeding season, call count sampling technique (dawn & dusk) was used to evaluate the presence of cheer and also its abundance. To estimate the abiotic human－induced pressure, locals were interviewed in addition. A three－decadal spatial imageries were tested to understand the change in grassland cover for each microsites pertaining to its habitat.

**Results**

Interestingly, cheer is recorded to be extantfrom all earlier surveyed areas. Moreover four new sites were also found containing cheer in fair numbers.A minimum of 48 calling groups was documented to be extant from all the sites consolidated. One site, appeared to have lost its cheer population in the last two decades on the basis of discussions with locals and our call count surveys.The change－detection study revealedadecrease in grass/shrub cover, in 7 sites. Considerable increase in the grassland from 2000 to 2014 was evidenced from another 3 locations. Grassland area have shown a decreasing trend in three locations (one of them being Chail WLS) owing to increase in construction activities.

**Conclusion**

The paucity of baseline data, limited the possibilities of comparison of their population status.The cheer population is seen to be stable in these three districts, however proper measures need to be taken to sustain their population by keeping a check on the anthropogenic pressures. However, the hypothesis of cheer being a resilient species apparently holds true.

**Keywords:** Cheer pheasant, change detection analysis, land－use land－cover, Himachal Pradesh, call count sampling

Poster 1-4

# Status of Galliformes of Pipar/Santel in Annapurna Conservation Area, Nepal

# 尼泊尔 Annapurna 保护地的鸡形目鸟类现状

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The Galliformes of Pipar, within the Annapurna Conservation Area in Central Nepal, have been surveyed 11 times since 1979 and most recently in 2011, 2013 and 2014. The nearby area Santel has been surveyed 4 times using identical methods since 2001 and most recently in 2012. In continuance of this long term monitoring at Pipar and to provide a fourth count at Santel dawn call counts were conducted at both sites in April-May 2011-2014. The aim of the surveys was to obtain information on the pheasants and partridges especially population status of satyr tragopan *Tragopan satyra*, koklass pheasant *Pucrasia macrolopha* and common hill partridge *Arborophila torqueola*. The secondary aims were to gather information on the presence of birds and mammals of both areas, and to gather information of the human disturbances on the forests.

20 satyr tragopan, two koklass pheasant and 21 common hill partridge were recorded by dawn call count at seven listening stations at Santel in 2012. Likewise, 15 satyr tragopan, six koklass pheasant and seven common hill partridge were recorded by the same method at six listening stations at Pipar in 2014. Both forests are rich in birds and mammalian species. A total of 152 bird species in Pipar forests and 116 species in Santel forests was recorded during the surveys which include Himalayan monal (*Danphe*) *Lophophorus impejanus*, blood pheasant *Ithaginis cruentus*, Tibetan snow cock *Tetraogallus tibetanus*, kalij pheasant *Lophura leucomelanos*, rufous–throated partridge *Arborophila rufogularis* in both forests and black fancolin *Francolinus francolinus* in the lower altitudes. A checklist of total 295 birds recorded so far in Pipar was prepared which represents 11 orders 38 families and 146 genera. Himalayan tahr *Hemitragus jemlahicus*, Himalayan pika *Ochotona roylei*, orange-bellied Himalayan squirrel *Dreomys lokriah*, barking deer *Muntiacus vaginalis,* leopard *Panthera pardus*, Himalayan black bear *Ursus thibetanus* were the wild mammals recorded during survey periods.

Buffalo and sheep grazing, Yarsha Gumba/Caterpillar fungus *Ophiocordyceps sinensis,* medicinal plants and bamboo shoots collections, firewood and timber materials collections, and very newly introduced tourist trekking route through the Pipar forests were the major human pressures in the areas.

Poster 1-5

# Research of the endemic White-necklaced Partridge
# 特有种白眉山鹧鸪的研究现状

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The White-necklaced Partridge *Arborophila gingica*, which is endemic to China, is categorized as a near-threatened species by IUCN. The present research status of this species was assessed based on publications and field studies, which includes: 1) A newly discovered subspecies, *A. g. guangxiensis*, was identified in 2008 based on geographic and phenotypic differences between this subspecies and *A. g. gingica*. The taxonomic validity of this subspecies was further supported by genetic evidence, and it was suggested that *A. g. guangxiensis* be considered as a conservation unit. 2) With small and isolated wild populations, the distribution of *A. g. guangxiensis* is restricted in Jiuwandashan of north Guangxi and Damingshan of south-central Guangxi. *A. g. guangxiensis* was found only at the western and southern margins of the species' distribution range. Besides, the new distribution record of *A. g. gingica* from Luofushan, Guangdong, updated the southern limit of the distribution of this subspecies, which is at similar latitude to that of *A. g. guangxiensis*. 3) Only two research articles focusing respectively on the ecological characteristics and winter feeding sites selection have been published so far on the habitat selection of *A. gingica*. To sum up, little is known about this species, which would be a disadvantage factor for the conservation of this endemic species. Here we started the study on the habitat selection and genetic structure of the two subspecies of *A. gingica*, including studies on their feeding sites, nesting sites, breeding sites, genetic diversity, effective population size and inbreeding coefficient, which would be valuable for the conservation of *A. gingica*, especially for the new subspecies *A. g. guangxiensis*.

**Key words:** *Arborophila gingica*; subspecies; habitat selection; genetic structure

Poster 1-6

# Current status and distribution of Green peafowl *Pavo muticus* in China

# 中国绿孔雀现状与分布

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**Background:** Understanding the latest status of endangered species is important for making effective conservation plans. The endangered Green peafowl as the largest pheasant species has undergone a substantial decline in both China and other countries in East Asia since 1990s. To a certain degree, deficient of field data hampered the conservation efforts. In this study, we tried to explore the current population and distribution status of green peafowl in China for better protecting of this specie.

**Methods:** From 2014 to 2016, we carried out comprehensive field surveys of green peafowl in Yunnan and Tibet, China. Totally, we investigated all the historical distribution range in central, western and southern Yunnan covering nearly 10000 km and the 3000 km journey in Tibet were mainly distributed in Motuo and Chayu County, SE Tibet. We used integrated methods in the study including questionnaire, interview, singing and line transect survey. We collected information from 1046 questionnaires, 200 interviewers and 71.25km line transects.

**Results:** Our results indicated that there were no peafowl in the Motuo County and Chayu County in Tibet and the current distribution range of green peafowl in China were scattered in the central, western and southern Yunnan province. Only 117-145 individuals were recorded in 11 counties and cities of 8 districts in Yunnan. Comparing with historical records of 1990s, both population (364-460 recorded individuals and 800-1100 estimated individuals) and distribution range (35 counties) of green peafowl decreased a lot in China. We also found that the population structure changed from 5-10 individuals twenty years ago to 2-5 individuals per flock in our study.

**Conclusions:** We found significant decline of population, distribution range and flock size of green peafowl in China during the past twenty years. Four kinds of threat factors were determined including habitat loss, alternation of traditional cultivation, pesticide poisoning and hunting.

**Keywords:** Green peafowl; China; Endangered species; Population; Distribution range

Poster 1-7

# Survey of geographical populations of White Eared-pheasant

# 白马鸡地理种群调查

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## Background

The White Eared-pheasant *Crossoptilon crossoptilon* has an extensive range in south west China. Its fragmented distribution and apparently specialized habitat requirements suggest that the birds inhabit areas below 4600m, and that high altitude areas act as barriers between populations. Four subspecies of White Eared-pheasant are currently recognized: *C. c. dolani, C.c. drouynii, C.c. crossoptilon,* and *C.c. lichiangense*. Their physical appearance and distribution have been described only briefly. But the range of each subspecies has remained unclear, and the populations in remote areas remain undescribed. To compare the appearance of geographically isolated populations of this species will be helpful to understand the dispersal history of the bird.

## Methods

Surveys of White Eared-pheasants covered all of the four subspecies' distribution and their connecting areas. We photographed birds to record their characteristics. Locations of birds were recorded by GPS to analyze their potential distribution.

## Results

Eye colour of the four subspecies show differences. *lichiangense* is red; *dolani* and *drouynii* are white; *lichiangense* showed a variety of eye colours from white to yellow and red. Wing colour of *crossoptilon* and *lichiangense* are black, and differences cannot be detected; *drouynii* is grey to white; *dolani* is black. Body colour of *dolani* is grey and the other three subspecies are white. At the border area between *dolani* and *drouynii,* characters of both subspecies appear in different individuals within the same population. Populations ascribed to *C. c. drouynii* show local differences: wing colour tends to be darker towards the east and south; the tails tend to be white towards the north west. *Dolani* also show partially white tail. Mapping of potential distribution showed that in the centre of the Tibetan plateau White Eared-pheasants are likely to inhabit mainly the valleys of five rivers: Nujiang, Lancangjia, Jinshajiang, Yalongjiang and Daduhe.

## Conclusions

*C. c. crossoptilon* is distributed along the rivers Yalongjiang and Daduhe, *drouynii* along the Lancangjia and Jinshajiang. *C. c. lichiangense* might be a hybrid or intermediate population between them. *C. c. drouynii* could be identified comprising two populations: eastern population has grey wings and black tail; western population is characterised by white wings and partially white tail. *C. c. dolani* might be a hybrid zone between the western population of *C. c. drouynii* and Tibetan Eared-pheasant *Crossoptilon harmani*.

**Key words:** Eye colour; White Eared-pheasant; geographical population; Subspecies

Poster 1-8

# Dominance hierarchy of White Eared-pheasant: implications on reproduction

# 白马鸡社群等级制对其繁殖成效的影响

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**Background**

Dominance hierarchy is widespread in the group of social animals. It is mainly due to differences in behaviors, which led to the different social status of the group members, produce certain dominant relationship and form a stable hierarchy structure. The hierarchy relationship can maintain animal community structure relatively stablility and health, save energy and strength of population and promote the development of animal community. To find the relationship with sex, age and reproduction in flocks, we analysed the domination hierarchy of wild White Eared-pheasant (*Crossoptilon crossoptilon*) flocks.

**Methods**

We recorded hierarchy behavior of four wild flocks of White Eared-pheasant in Daocheng County, Sichuan, China. DomiCalc, a software, was used to measure the linearity degree of interaction relationship matrix. Mathematical ranking algorithms( *I&SI* ) was used to quantify dominance and to find an optimal ordering of the individuals involved in linear dominance hierarchies. We compared the rank orders with the reproductive status and age to find their correlation.

**Results**

The rank of adult males is higher than females and yearling males. Male and female in high rank tend to be paired, and pairs brooded tend to be in higher rank than single ones and pairs without brooded. Single adult males, females and yearling males tend to be in low rank.

**Conclusions**

Gender and age are correlated with the domination hierarchy of White Eared-pheasant. The dominance hierarchy of White Eared-pheasant has an effect on mate and reproduction.

**Key words:** White Eared-pheasant; dominance hierarchy; reproduction;

Poster 1-9

# Density estimation and habitat evaluation of the Chinese Monal (*Lophophorus lhuysii*) during breeding season in Xiaozhaizigou National Nature reserve

# 小寨子沟自然保护区绿尾虹雉繁殖期密度调查及栖息地评估

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## Background

The Chinese Monal (*Lophophorus lhuysii*) is a vulnerable species with great conservation value endemic to western China. However, knowledge about the biological and ecological traits of the species is limited. The latest field investigations focused on the Chinese Monal were carried out in 1980s, which made brief descriptions on its population density and habitat use. At present, the status of the Chinese Monal are little known, constraining effective conservation management. Therefore, to update new information benefiting conservation targeting the species, it is necessary to use new methods to evaluate current status of population and habitat of the Chinese Monal.

## Methods

We used line transect method to survey Chinese Monal populations in Xiaozhaizigou National Nature Reserve, Sichuan, China from July 2015 to July 2016. The population density of the species was estimated based on repeated line transect surveys. Habitat preference of the Chinese Monal was analyzed at two spatial scales using different methods: at the landscape scale, we modeled current habitat in the nature reserve using MaxEnt approach; and at the local scale, we determined its habitat preferences by comparing environmental factors between used sites and available sites (systematically sampled) using generalized linear models.

## Results

In the study area, population density of the Chinese Monal was estimated as 4.86 adults/ km$^2$. The results of Maxent showed that suitable Chinese Monal habitat in Xiaozhaizigou National Nature Reserve covered 44.82 km$^2$, and high habitat suitability was found in meadows and shrubs with about 975 mm of annual precipitation and elevations between 3500 - 4000 m. At the local scale, the sites used by the

species had significantly lower elevation and slop and significantly higher grass coverage than the available sites. Based on the density estimation and MaxEnt habitat modeling, the total population size of the Chinese Monal in the nature reserve was calculated as about 217 adults.

**Conclusion**

Our population density estimation suggests a higher density of the Chinese Monal compared with the studies conducted in 1980s at the same region, which likely implies the effective conservation during the past thirty years. Habitat preference analysis suggest that sites with lower elevation, gentle slope and well-developed grass stratum are favored by the Chinese Monal at the local scale, which is also ideal Yak pasture for local people. For further conservation, we recommend some managements to restrict grazing activities on subalpine meadows, so that to reduce the potential threats from local disturbances.

**Keywords:** *Lophophorus lhuysii*, Population density, Habitat preference, conservation, habitat modeling.

Poster 1-10

# Revival of the genus *Tropicoperdix* Blyth 1859 (Phasianidae, Aves) using multilocus sequence data

## 基于多位点测序数据对树鹧鸪属（*Tropicoperdix*）的重新确立

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**Background**

*Tropicoperdix* has been considered to be either a full genus or a species complex within the Phasianidae genus *Arborophila* (hill partridges), however, there is long-standing uncertainty regarding the degree of difference that warrants generic separation, including reported anatomical cranial differences. As well, the intra-generic taxonomy is under dispute. Most studies hypothesize that *Tropicoperdix* comprises three species, while others postulate from one to four species. However, no molecular study has been performed to clarify the systematic and taxonomic uncertainties surrounding *Tropicoperdix*.

**Results**

In our study, we performed a series of molecular phylogenetic analyses of *Tropicoperdix* and *Arborophila* taxa based on two mitochondrial genes and five nuclear introns. All of the results are consistent with the finding that *Tropicoperdix* and *Arborophila* are phylogenetically distinct and distant genera, although the precise phylogenetic position of *Tropicoperdix* remains undetermined. Retrospective examination of external characteristics also supports the generic separation, as well as providing evidence of remarkable multiple character convergence. We propose that *Tropicoperdix* is comprised of at least two full species based on mitochondrial data obtained from museum specimens by using a next generation sequencing method.

**Conclusions**

Our phylogenetic analyses support the conclusion that the *T. chloropus* complex is not the member of hill partridges (genus *Arborophila*). We suggest the genus *Tropicoperdix* should be revived and this lineage represents a distinct lineage within the family Phasianidae.

**Keywords**: *Arborophila* - generic separation - historical DNA - multilocus - next generation sequencing - *Tropicoperdix*

Poster 1-11

# Incubation behaviour of Chinese Grouse at Lianhuashan, Gansu, China
# 甘肃莲花山斑尾榛鸡孵化行为研究

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Parental investment is parents making efforts to benefit the offspring, enhancing their condition, survival, and reproductive success. For female incubation species, male investment during incubation is important for reproductive success. Chinese grouse (*Tetrastes sewerzowi*) is an endemic species distributed in alpine coniferous forest in central and western China. Before incubation, Chinese grouse pairs are mostly together with all the activities. Females spend more time to search for nutritious food while males spend more time in vigilance behavior around females within 5m. During 2013-2016, we studied incubation behavior of the Chinese grouse at Lianhuashan Nature Reserve, Gansu, China, using radiotelemetry and infrared video surveillance cameras. We monitored 5 females and 8 males. Males were normally far from females during incubation (d=117.87±59.4m, n=8) with no guard when females leaving nests for feeding. We suggest this may reduce the probability of predator tracking. Instead males wandered around territories, with the chance of extra-pair copulation to increase reproductive success and looking for a better territory for next breeding season. According to our video-camera data from 5 incubating females, the hens mostly sat still (86.04%±3.62%, n=5), with other behaviors of rearranging eggs (2.3%±1.27%), tidying nest (1.04%±0.97%), taking vigilance (5.46%±1.25%), preening (3.62%±2.57%) and taking reposition (1.54%±1.32%); there were time allocation differences among individuals, however, taking vigilance and rearranging eggs were essential ones. So, the Chinese grouse females took charge of incubation alone, with males giving no nest defence in the incubation period.

**Keywords:** Chinese grouse, incubation behaviour, parental care, Lianhuashan

Poster 1-12

# Multi-scale patterns of habitat use by three sympatric rare high-mountain Galliformes
# 三种同域高山珍稀鸡形目鸟类生境利用的多尺度分析

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**Background**

The high-mountain Galliformes are a group of birds higher threatened, but poor knowledge regarding interspecific differences of habitat use by typically sympatric species has previously limited the development for a regional multiple-species conservation strategy. We examined seasonal patterns of habitat use by three typically sympatric high-mountain rare Galliformes, Blood Pheasants (*Ithaginis cruentus*), Buff-throated Partridges (*Tetraophasis szechenyii*), and White Eared-pheasants (*Crossoptilon crossoptilon*), at the plot and home range scales.

**Methods**

We positioned signs of species including sightings, calls, faeces, footprints, and feathers along 17 line-transects established in Gexigou nature reserve, Sichuan, China, during the spring, autumn and winter seasons between Apr 2014 – Jan 2015. We measured habitat characteristics in terms of topography and vegetation architecture based on 10 × 10 m plots. At the home range scale, we took environmental variables associated with topographic irregularity and habitat heterogeneity in 0.5 × 0.5 km squares from a 30-m resolution digital elevation model via GIS and a landuse map derived from a supervised classification from six Landsat 8 imagery scenes using ERDAS. Using multinomial and logistic regressions with AICc-based model selection, we examined habitat differences among species and determined the habitat use pattern of each species during each season (presence vs. randomly chosen non-presence sites).

**Results**

We detected 240 species signs at the home range scale, and 192 at the plot scale. Percentages of sites that were co-used by multiple species were similar among the seasons at both the scales (on average, 33.8%

for home range scale, and 5.7% for plot scale). Habitat differences were significant among the three species during all the three seasons. In spring and winter, Blood Pheasants preferred sites with lower elevations, suggesting seasonal vertical migrations. Without wintering at lower elevations, Buff-throated Partridges and White Eared-pheasants showed preferences for oak thickets at the home range scale. At the plot scale, Buff-throated Partridges preferred sites with good canopy, and White Eared-pheasants preferred sunny slopes. In autumn, Blood Pheasants preferred sites that were characterized by lower percentage of rhododendron or other miscellaneous shrubs and grasslands at the home range scale, and correspondingly avoided higher shrub cover at the plot scale, while Buff-throated Partridges and White Eared-pheasants had no obvious selection on variables we measured.

**Conclusions**

The three Galliform species partitioned their habitat niches, but with some overlaps. The extent of partitioning or overlap changed spatially. The patterns of habitat use by a specific species changed across seasons, but were compatible at the different spatial scales. We suggest managers to maintain a mosaic of habitats in conservation planning.

**Keywords:** Conservation, Habitat, Scale, Seasonal, Threatened species

Poster 1-13

# The importance of willow to Chinese grouse in the conifer forest: evidence from analysis on the breeding territory

# 针叶林中柳树对斑尾榛鸡的重要性：繁殖领域的证据

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Breeding territory habitat features have important adaptive significance on survival and reproduction of its owners, and thus breeding territory habitat selection influence population sustainability and dynamic. Chinese grouse (*Tetrastes sewerzowi*) is a rare and endemic species with confined distribution and decreasing population trend. Elucidating breeding territory habitat needs of male Chinese grouse has significant importance for its habitat management and conservation. Using radio-telemetry and field observations of 48 radio-tagged and 19 untagged male Chinese grouse from 20 April to 20 May, 2009 - 2012. We determined the core areas of their breeding territories. 2 to 3 samples were selected in each core breeding territory as used sites and compared with nearby sites with no grouse occurrence using logistic regression. Our model showed a high accuracy in prediction of core breeding territory use by males (AUC = 0.998), which preferred stands with more small deciduous trees and bushes (3900.0 ± 90.9 trees / ha vs 1143.9 ± 67.1 trees / ha, mean ± SE), more small willow trees (2328.1 ± 128.3 trees / ha vs 64.7 ± 16.0 trees / ha), greater willow cover (0.22 ± 0.009 vs 0.02 ± 0.002) and greater herb cover (0.12 ± 0.006 vs 0.01 ± 0.003). Number of small willow trees had the biggest influence on males' core breeding territory selection. Dense shrubs was also chosen compared with unused sites. Tall conifer trees was important determinant in the distribution of Chinese grouse at the landscape scale, and was relatively important in univariate model, but not included in our final multivariable model. Male Chinese grouse established territories at sites with abundance food resources, which not only met its own use, but also for paired females. From the landscape scale, Chinese grouse occurred in alpine conifer forest. In the territory scale, small willow trees had the most important effects on male's core breeding territory selection. So we recommended increased forest gaps in conifer forest to facilitate breeding territory establishment of Chinese grouse.

**Keywords:** *Salix* spp., Chinese grouse, territory, core area, conifer forest, logistic regression

Poster 1-14

# Studies on population status and habitat suitability evaluation of Brown Eared Pheasant in Shanxi Province

# 山西省褐马鸡种群现状与栖息地适合度评估

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Brown Eared Pheasant (*Crossoptilon mantchuricum*) is an endemic species of birds in China, and has been listed as vulnerable species by the IUCN red list and the first class State Protected Animals in China. As one of the main distribution areas, Shanxi Province plays an important role in the persistence and development of the population of Brown Eared Pheasant. From May 2015- June 2015, we used both Line transect method and sound-playback method to investigate the distribution, population density and habitat utilization of Brown Eared Pheasant in Shanxi Province. Field work was carried out in the Pangquangou National Nature Reserve, Luyashan National Nature Reserve, Wulushan National Nature Reserve, Lingkongshan National Nature Reserve and Choulengshan Nature Reserve. We set 51 transect lines in the study area, with a total length of 156.4km. During the investigation, we recorded 35 entities, 101 crowing and 30 feather, faeces or other traces of Brown Eared Pheasant. We found the main distribution range is the Lvliang Mountain, while the Lingkongshan Nature Reserve of Taiyue Montain is a new distribution site for Brown Eared Pheasant. The results of line transect surveys show that average density of Brown Eared Pheasant was 8.54 individual/km$^2$ in the survey area. The highest density reaching 20.06 individual/km$^2$ in Luyashan Nature Reserve, while in Pangquangou Nature Reserve, Wulushan Nature Reserve and Lingkongshan Nature Reserve, the densities were 8.26 individual/km$^2$, 5.97 individual/km$^2$, and 4.79 individual/km$^2$ respectively. We did not find any traces of Brown Eared Pheasant in Choulengshan Nature Reserve. During the breeding season, Brown Eared Pheasant tended to select gentle shady slope with coniferous forest or coniferous and broad leaved mixed forest at 1600-2200m altitude as their habitat. Using the Maxent model, we made a prediction of the potential distribution area of Brown Eared Pheasant in Shanxi Province, figured out that the most suitable habitats focus on the Lvliang mountain, with a total area of 2961.91km$^2$, while Datong basin, Xinding basin, Yuncheng basin are the least suitable for Brown Eared Pheasant, possible related to the loss of forest and high intensity of human activities in these areas.

**Key words**: Brown Eared Pheasant, population density, Maxent, habitat suitability evaluation

Poster 1-15

# The new geographical distribution for Chinese Monal pheasant *Lophophorus lhuysii* of Liangshan mountain in Sichuan province

# 四川省绿尾虹雉凉山山系地理分布新记录

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## Background

As we currently know, the Chinese Monal pheasant is a endemic specie, which has distributed in Gansu province, Sichuan province and Yunnan province. Because of human disturbance, their habitats are constantly narrowing, leading to the threat of population extinction. It's amazing we found the Chinese Monal pheasant in pheasant monitoring, which located in Heizhugou Nature Reserve (E102°54′29″-E103°04′07″, N28°39′54″-N29°08′54″, 1054m-4288m) of Ebian county in Sichuan province, it's a new geographical distribution in Liangshan mountain that has never reported.

## Methods

We laid 4 line transects randomly in alpine meadow habitat from May to August, which measured almost 20 kilometers totally, and kept 2-3 kilometers per hour. We judged if there were the Chinese Monal pheasant according to their sound, excrement, feather and object. Finally, we recorded their sound and object and we distinguished different ones from the orientation of sound. We made the farthest distance of sound as the width of belt transect, which was 500m, then used belt transect method to estimate their density preliminarily.

## Results

We recorded 3 females foraging together at 3490m on 25 May, 2 males, 1 female foraging together at 3566m on 20 May and we recorded 6 males sings in foggy weather and it sound like "guo-guo". The density was 1.2 per km$^2$.

## Conclusions

This area did not appear the bird on 2008 at the last local investigation in Heizhugou nature reserve while our investigation may show the improvement of ecological environment. This survey area was connected with Maanshan Nature Reserve and Dafengding Nature Reserve and they had the same habitat, so, we thought it should be caused more attention and better management. Otherwise, we found some grazing behaviors and traps to arrest pheasant, it may hurt the population, so, it was necessary to further explore their survival status.

**Keywords:** *Lophophorus lhuysii,* Liangshan Mountain, New record, Sichuan province

Poster 1-16

# Studies on winter habitat characteristics of the Sichuan Partridge (*Arborophila rufipectus*) at Laojunshan National Nature Reserve in Sichuan Province, China

## 四川老君山国家级自然保护区四川山鹧鸪冬季栖息地特征研究

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**Background**

Understanding of habitat requirement is necessary for conservation of endangered species. The Sichuan Partridge (*Arborophila rufipectus*) is a globally endangered species endemic to the mountains of Southwest China. So far, little information is known about its winter habitat. We studied the winter habitat characteristics of Sichuan Partridges at Laojunshan National Nature Reserve in Sichuan Province, China in January, 2013 and from January to February, 2014.

**Methods**

We compared the microhabitat attributes between the used and control plots. We used principal components analysis to determine the most important variables influencing winter-habitat-selection by the Sichuan Partridge.

**Results**

The habitat characteristics of a total of 48 plots used by the Partridge and 30 control ones were measured. It was found that Sichuan Partridges preferred the habitats with lower altitude, gentle slopes, smaller coverage of trees, shorter bamboos, less herbs, larger coverage of 1.0 m layer, smaller coverage of 4.0 m and 5.0 m layers, and close to trails and forest edge. In addition, Sichuan Partridges also preferred the sites close to water resources and with rich dry leaves. Security and food condition might be the key factors influencing winter-habitat-selection by the Sichuan Partridge.

**Keywords:** Sichuan Partridge *Arborophila rufipectus*; habitat characteristics; winter; principal components analysis; Laojunshan Nature Reserve.

Poster 1-17

# Nest predation experiment of *Tragopan caboti* in Jiangxi Wuyishan
## 江西武夷山黄腹角雉巢捕食实验

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From December 5, 2014 to April 29, 2015, we selected two nest predation experimental plots in Jiangxi Wuyishan National Nature Reserve. Experimental plot 1 was in *Pinus taiwanensis* and evergreen broad-leaved mixed forest at the altitude from1 270 m to 1 345 m, and experimental plot 2 was in *Tsuga chinensis* var. *tchekiangensis*-*Cryptomeria fortunei* and evergreen defoliate broad-leaved mixed forest at the altitude from 1 805 m to 1 920 m.We placed 20 artificial nests on branches that 2.0 m to 5.4 m high above the floor at both two experimental plots. The nests have got into the environment after 110 days. Infrared cameras were used to monitor each nest that we placed 2 chicken eggs into it at experimental plot 1 from March 28 to April 25, 2015, and from April 1 to April 29, 2015 at experimental plot 2. In the same time, we installed 3 infrared cameras to monitor other animals at each experimental plot. After 28 days of experiment: a total of 12 losted eggs for 20 nests, incuding 10 nests were preyed by *Macaca thibetana* at experimental plot 1; a total of 5 losted eggs for 20 nests, incuding 3 nests were preyed by *Garrulus glandarius* at experimental plot 2; *Macaca thibetana* eated both 2 eggs in one time and *Garrulus glandarius* eated one. There were 15 species animal appeared the 2 experimental plots such as *Ursus thibetanus*, *Paguma larvata*, *Callosciurus erythraeus*, *Niviventer coninga*, *Urocissa erythrorhyncha*, *Picus canus*, *Garrulax monileger* and so on, and them could be the potential nest predators.

**Key words**：*Tragopan caboti* , Nest predation, Artificial nest experiment, Jiangxi Wuyishan

Poster 1-18

# Breeding Ecology of the Black-billed Capercaillie *Tetrao urogalloides* in China

# 黑嘴松鸡的繁殖生态

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To bridge the gap in the breeding ecology of the Black-billed Capercaillie (*Tetrao urogalloides*) in China, during May 2011 and October 2015, we conducted field investigations in the Heilongjiang Zhongyangzhan National Nature Reserve (125°44’57”~126°13’31”E, 50°38’23”~50°48’10”N) and the Inner Mongolia Hanma National Nature Reserve (122°23’34”~122°52’46”E, 51°20’02”~51°49’48”N), which respectively maintain China’s southernmost and the most concentrated capercaillie’s natural habitats. Specifically, based on currently known knowledge about the Black-billed Capercaillie, we determined and then investigated the areas with high possibility of the capercaillie’s occurrence; after leks and nests were located, we set trap cameras and cover (tents) for continuously observing and subsequent banding. The field observations indicated that the Black-billed Capercaillie courted during late March to late May, showing a peak of courtship display and mating between late April and early May; the incubation period lasted from mid May to early June, and eggs were solely incubated by the females; the clutch size of the Black-billed Capercaillie in China was recorded from 3~10 (mostly 6), and chicks usually hatched between 2:30 am and 1:00 pm around 10th June. We also found that the Black-billed Capercaillie mainly fed on twigs, leaves and buds of Asian White Birches (*Betula platyphylla*) and Dahurian Larches (*Larix gmelinii*), as well as the catkins of the birches and cones of the larches; Bog Bilberries (*Vaccinium uliginosum*), roses (*Rosa davurica*), grass seeds and insects may also be used as food by the capercaillie during summer and autumn. Sable (*Martes zibellina*), Red Fox (*Vulpes vulpes*), Siberian Jay (*Perisoreus infaustus*), Common Raven (*Corvus corax*), Eurasian Jay (*Garrulus glandarius*), Great Grey Owl (*Strix nebulosa*) and Eurasian Goshawk (*Accipiter gentilis*) posed a potential risk of predation to the Black-billed Capercaillie. Moreover, based on our filed research, we speculated that the Black-billed Capercaillie may secure the nest via utilizing other birds as indicators for the predators and other potential threats – Olive-backed Pipit (*Anthus hodgsoni*), Black-faced Bunting (*Schoeniclus spodocephala*), Radde’s Warbler (*Phylloscopus schwarzi*), Yellow-throated Bunting (*Schoeniclus *elegans*), Silver-throated Tit (*Aegithalos caudatus*) and Great Spotted Woodpecker (*Dendrocopos major*) were found nesting within 100 meters to the capercaillie's nests in an unusually great density. Furthermore, the Black-billed Capercaillie showed highest chick mortality during July and next February, which mainly caused by the rugged weather conditions (continuous rainfall, low temperature), predation, nest sabotage and food shortage. The ongoing population descent was further aggravated by the confined and decreasing natural habitats and poaching. Consequently, for the habitat maintenance and ultimate population persistence, regionally, we propose the conservation suggestions for the Black-billed Capercaillie with urgency, specifically as the control of the current predatory plucking of the wild cranberry and reduction of the fire lane burning frequency.

**Keywords:** Black-billed Capercaillie; *Tetrao urogalloides*; Breeding Ecology; China.

Poster 1-19

# Multiple-scale Priorities Areas Identification and Management for Vulnerable Reeves's Pheasant *Syrmaticus reevesii* conservation: A Case Study in Central China

# 白冠长尾雉保护的多尺度优先保护地确定与管理：中国中部的案例

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Deciding which areas should be protected priority, where and how to manage to enhance threatened species persistence is critical for successful conservation and management. With the development of geographic information system and increasing remote sensing imagines, habitat suitability modeling and habitat change analysis has become a very helpful tool in the priority areas identification and management effectiveness evaluation. Numerous studies provided initial insight into the broad-scale patterns of species distribution, but they could not reflect more accurate and fine-resolution habitat suitability for at-risk populations. Moreover, previous research has mainly focused on species conservation related to changes in land cover and habitat fragmentation while few studies have examined changes in microhabitat structure.

Here we used a habitat suitability model and habitat change analysis across space and temporal framework to identify the priorities areas and assess the effectiveness of current nature reserve management for the habitat protection of the Reeves's Pheasant (*Syrmaticus reevesii*), a vulnerable, forest-dwelling species. With multi-scale habitat models, we analyzed the effect of climatic variables and identify priority areas on the national scale, and then predicted land cover and other factors that affect patterns of habitat selection within the potential distribution in the regional and landscape scales. We also measured land use/land cover changes inside and outside the Dongzhai National Nature Reserve (DNNR). And we compared differences in habitat fragmentation patterns and microhabitat structure and composition between 2002 and 2013 corresponding to the times at and after the establishment of the DNNR.

Results show that the habitat suitability models among three scales were quite robust. In the national scale of bioclimatic model, the species is primary limited to the mountains of Dabie, Qinling, Daba,

Wushan, Wuling and Dalou, which extrapolated little beyond the known distribution in the central of China. And in the regional scale, the variables only derived from topography and land-use data and the distance to the nearest evergreen forest was the most informative variable which account to 65.6% of the model performance. Moreover, compared the national-scale model in the Dabie Mountains, the regional model prediction was more fragmentation in a fine resolution of land-cover data. The landscape-scale model also included the anthropogenic variables and most of the predicted suitable habitat was located in the center of the DNNR. According to the land cover change analysis, the forest coverage has slightly increased both inside and outside DNNR, and habitat fragmentation metrics have not changed substantially since the establishment of DNNR. Significant differences were detected in microhabitat structure and composition between 2002 and 2013. After more than 10 years of no disturbance, canopy cover and density of the shrub layer increased, while herbaceous plant height declined. The observed changes reduced resource availability resulting in increased foraging time for pheasants and increased predation rates.

As wildlife habitat has been regarded as a hierarchically nested organization of conditions and resources required by an organism, the habitat models need a comprehensive analysis of the influences of different environmental variables across multiple spatial scales. To many imperiled wildlife, knowledge of their global, regional, and even local distributions is very useful for their network of priorities areas construction and management. This study also suggests that current nature reserve management systems may have negative impacts on the conservation of the Reeves's Pheasant. We propose that the Regulations of Nature Reserves in China should be revised to account for the habitat requirements of different threatened species with varied life history traits.

**Key words：** Priorities Areas Identification; Reeves's Pheasant; *Syrmaticus reevesii*; central China

Poster 1-20

# Evaluating the conservation effectiveness of Brown Eared Pheasant in the nature reserve and its functional zoning

# 自然保护区及其功能区的褐马鸡保护成效评估

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Nature reserves have played extraordinary importance role in animal population and their habitat, particularly the suitable functional zonings are essential for effective conservation of threatened species. However landscape change and unreasonable zoning designations cannot give enough protect. These protect areas are also rarely evaluated for their effectiveness on the threatened species. Using the Species distribution models and GAP analysis to evaluate the effectiveness in different spatial-temporal scales was a new approach. Here we used the species distribution models to predict the suitable habitat of the Brown-eared Pheasant in the west of Beijing in 2010 and 1995. Then we made a GAP analysis between the suitable habitat with the functional zoning of Baihuashan National Nature Reserve (BNNR), as well as BNNR and Xiaowutaishan National Nature Reserve (XNNR). Results show as follows: 1) the functional zoning of BNNR is yet unable to satisfy the conditions required for the protection of Brown-eared Pheasant. According to the model, the potential distribution area of the Brown Eared Pheasant is 34.86km$^2$, making up 8.70% of the whole area. Then through the GAP analysis, we can conclude that the suitable habitat in the core zone about 17.75 km$^2$, taking up 14.36% of the whole area; And in the buffer zone about 4.22 km$^2$, taking up 5.42%; in the experimental areaabout 12.89 km$^2$, taking up 6.41%. What's more the suitable habitat in the core zone in all takes up 50.92% of the entire suitable area. 2) the suitable habitat of Brown-eared Pheasant have changed a lot from 1995 to 2010 and these two national nature reserves need to change their range for a better conservation of this flagship species. The results show that the area of suitable habitat is 248.54 km$^2$. Compared with 1995, the suitable habitat in 2006 reduced about 83.37 km$^2$, accounts for about 36.9% of the total area suitable in 1995, and the new distribution area covers an area of 125.91 km$^2$, accounts for about 46.8%. Compared with 2006, the suitable habitat reduced about 141.76 km$^2$ in 2010, accounting for 52.7% of the total area of 2006. The new distribution is 121.02 km$^2$ in 2010. 3) The fragmentation degree decreased from 1995 to 2010. It can be show up from the increased of concentration area and the decreased of patch area. The concentration area of suitable habitat increased from 25.26km$^2$ in 1995 to 67.17 km$^2$ in 2010. The patch area decreased from 35.07 km$^2$ in 1995 to 20.93 km$^2$ in 2010. Also a new functional zoning was designed. The suitable habitat area in the new core zone is 88.30%, compare it in the current core zone is 49.91%. Our study provided a new viewpoint to evaluating the efficacy of functional zoning in other nature reserve or other flagship species facing similar challenges with balancing landscape change and conservation goals, not only in China but also around the world.

**Key words：** Conservation effectiveness; Brown Eared Pheasant; nature reserve; functional zoning

Poster 1-21

# Social behavior and cooperative breeding in a precocial species: The Kalij Pheasant (*Lophura leucomelanos*) in Hawai‘i

# 早成鸟的社会行为与合作繁殖：夏威夷黑鹇为例

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Cooperative breeding in birds occurs mostly in altricial species, in which the offspring require substantial parental care to survive. However, its occurrence in precocial species affords unique opportunities to examine factors influencing cooperative breeding free from the constraint of extensive offspring needs. We examined social behavior and documented cooperative breeding in Kalij Pheasants (*Lophura leucomelanos*) in an introduced population in Hawai`i, only the third reported instance of cooperative breeding in Phasianidae. Birds in 31 distinct social groups occupied overlapping home ranges, and group composition remained relatively constant over the 3-year study period. Each social group contained one female and one to six males. All adults exhibited cooperative behavior including caring for chicks, agonistic behaviors against conspecific intruders, and vigilance against predators. Within each group, one male was dominant. Age was the only factor found to determine within-group dominance, suggesting that subordinate males may gain dominance and breeding status by staying in the group. Average population density was high (3.21 residents per ha), which may lead to habitat saturation in this population. The adult sex ratio was male-biased with an average M:F ratio of 2.1:1.0. Genetic sex identification of egg samples revealed unbiased primary and secondary sex ratios and suggests that the bias in adult sex ratio may be caused by differential survival and/or dispersal. Paternity analysis of 13 broods revealed that 68.4% of offspring were fathered by the dominant male of the social group, while 16.5% were fathered by the subordinate males of the group, suggesting that helpers gained some direct benefit by sharing reproduction. We suggest that cooperative breeding may be more common in precocial species than conventionally recognized.

**Keywords:** Cooperative breeding, precocial species, *Lophura leucomelanos*, social queuing, habitat saturation, mate limitation, parentage assignment, microsatellite genotyping

Poster 1-22

# Flocking Behavior Analysis of Reeves's Pheasant (*Syrmaticus reevesii*) using Infrared Cameras

# 基于红外相机技术的白冠长尾雉集群行为研究

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The flocking behavior of animals has long been an important topic in wildlife research. Such information should be helpful to develop a comprehensive understanding of the natural ecology and biology of wildlife, including pheasant species, which should be beneficial to protecting pheasants in the wild. However, some species of pheasants are naturally vigilant with concealed behaviors, making it rather difficult to conduct field studies on their flocking behavior. One such pheasant species is Reeves's pheasant (*Syrmaticus reevesii*), and sparse quantitative information on its flocking behavior in the field has been collected to date. In order to survey the flocking behavior and its geographic variation of Reeves's pheasant, we used camera trapping to monitor the flocking behavior at two sites: Pingjingguan Village, Hubei Province and Dongzhai National Nature Reserve, Henan Province. These infrared cameras were set up in the field from March 2013 to March 2014, which provided an opportunity to understand the annual rhythm of flocking behavior of this pheasant at these two sites. Based on the results of radiotracking studies previously conducted at the same study sites, we established a 1 ×1-km plot in each site, and then placed 25 infrared cameras in each plot. The working days of all cameras added up to 12,412 days, and we obtained 24,374 video clips in the field from these cameras. In particular, a total of 1361 of these clips captured Reeves's pheasant, including 525 clips and 836 clips in Dongzhai National Nature Reserve and Pingjingguan Village, respectively. We determined the ratio of the numbers of individual clips showing flocking behavior of the pheasant ($m$) to the total number of clips ($M$), and the ratio of the number of pheasants captured by the clips ($n$) to the total number of clips showing pheasant flocking behavior ($m$). Our results showed that a flock with two individuals occupied the largest portion of all flocks at these two sites, accounting for 68.23% and 72.79% of the total in Pingjingguan Village and Dongzhai National Nature Reserve, respectively. Three types of flocks, i.e. only-males, only-females, and mixed males-females, occurred in these two sites, and single-sex flocks dominated the flocks in the field, whereas the mixed male-female flocks accounted for only a small portion of the total flocks. In particular, Pearson's chi-squared test showed that there were no significant differences in the numbers of flocks between the two sites, whereas a significant difference was found in flocking types between the two sites. Moreover, the encounter rate of only-female flocks in Pingjingguan Village was higher in summer and autumn, and that of only-male flocks was higher in spring and autumn. Similarly, the only-female flocks in Dongzhai National Nature Reserve appeared occasionally in summer and autumn, and only-male flocks mainly appeared in spring. In addition, the flocking intensity of the whole year reached the peak in the non-breeding period at both study sites. On the other hand, the lowest flocking intensity at Pingjingguan and Dongzhai National Nature Reserve occurred in the breeding period and at the early stage of the breeding period, respectively. In the breeding period, these two study sites showed similar flocking intensities. The peak of the flocking rate of this pheasant in Dongzhai and Pingjingguan occurred in winter and the early stage of the breeding period, respectively. Reeves's pheasant showed a highly significant preference for shrub and bamboo, while avoiding broadleaf mixed forests, fir, and arbor in Pingjingguan Village. It had a highly significant preference for theropencedrymion and coniferous forests, while avoiding fir and broadleaf forests in Dongzhai National Nature Reserve.

**Key words:** Reeves's pheasant; flocking behavior; camera trapping

Poster 2-1

# Capture and handling Pheasants: sharing the learning experiences
# 雉类的捕捉与保定：经验共享

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Capture and handling of birds is pre-requisite for a wide range of purposes for monitoring and management of pheasants in wild as well as in captivity. Most commonly, birds are captured either for setting up a population for ex-situ conservation programme or for deploying transmitters to study habitat use, ranging, survival, migration and behavioral patterns. Capture is also necessary for breeding projects, zoo exchange programmes, health check-ups and for releasing birds back into the wild habitats. Though, there are guidelines available on live trapping of pheasants from Pheasant Specialist Group Code of Practice, we will discuss about causality that often occurred however, gone unreported in many cases. In this article, we will present the learning experiences that workers have gained while working with pheasants. In addition, we interviewed several zoo keepers (n=20) and pheasant biologists (n=13) in India and compiled findings in a way -*'Do's and Don'ts* for handling and capture pheasants in wild as well as in captivity. Several learning experiences on capture and handling of pheasants will be presented and discussed.

**Key words:** Capture, handling, casualties, experiences, recommendations

Poster 2-2

# Effect of illumination on blood physiological and biochemical indexes and blood reproductive hormone of the Chinese monals

# 光照对绿尾虹雉血液生理生化指标、生殖激素水平的影响

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## Background

The low reproductive rate of the Chinese Monals (*Lophophorus lhuysii*) is an obvious characteristics under artificial feeding conditions. A long time in the resting state, the less activity, less sunlight, not getting sufficient light might be extremely important reasons for the low reproductive rate, Under artificial feeding conditions,it may be extremely important measures for improving reproductive performance to regulate the light periods of reproductive period. To explore the effect of illumination on the reproductive performance of the Chinese monals from the mechanism, we conducted artificial supplementary light test in this study.

## Methods

Artificial supplementary lighting test was conducted during the period during February 26 to May 26, 2016. We chose 8 adult Chinese monals(4♂、4♀) with the similar weight and size. And we randomly divided them into an experimental group and a control group, each group had 4 Chinese monals(2♂､2♀). and each group had 2 replicates, each repeat had 2 Chinese monals（1♂、1♀).In the control group, we used natural lighting, and in the experimental group, we combined the natural lighting with artificial supplementary lighting and the illumination time reach to 16 (16 L:8 D) hours every day.

## Results

Under the experimental condition, adopting the light regime of 16L: 8D in the breeding season, the bloody physiological index difference were not significant between the experiment group and the control group ($P>0.05$). The content of total protein, albumin, globulin, glutamic-pyruvic transaminase, alkaline phosphatase, Ca, inorganic phosphorus, cholesterol, triglyceride of the blood biochemical index in the

experiment group were higher than those in the control group (P>0.05), the content of uric acid were lower than that in the control group (P>0.05). Female blood estradiol (E2), male blood testosterone (T) of the experiment group were significantly higher than those of the control group (p<0.01). The luteinizing hormone (LH), prolactin (PRL) of female of the experiment were significantly higher than those of the control group (P<0.05). The blood follicle stimulating hormone (FSH) of female of experiment group was higher than that of the control group (P>0.05).

**Conclusions**

Based on the seasonal spawing habits of the Chinese monal and in the local sunshine environment, artificial supplementary light combing natural illumination to 16 h (16L:8D) every day, the effects on the blood physiological index were small or not significant, and there were some effects on the blood biochemical index and the reproductive hormone.

**Keywords:** Illumination，*Lophophorus lhuysii*，Breeding season，Blood physiological and biochemical indexes，Blood reproductive hormone

Poster 2-3

# A non-invasive system to evaluate physiological status of brown eared pheasant

# 褐马鸡生理状态非损伤性评估体系的建立

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**Background**

Brown eared pheasant (*Crossoptilon mantchuricum*) is a critically endangered and endemic avian species in China. Due to its dramatic decline in population size, the species has been listed as endangered by IUCN. For conserving endangered species, one of the important work is to monitor their physical health indicators. However, due to the ecological habits of the brown eared pheasant, researches on the monitoring of its Immune Physiological Indexes Monitoring are still in the initial stage.

**Methods**

Using non-invasive sampling and ELISA techniques, this study measured and monitored the indexes of immune physiology of captive brown eared pheasant chicks and adults in the Pangquangou National Nature Reserve, Shanxi Province, from 2011 to 2012. Through measuring the proportion of fecal immunoglobulin in feces, and comparing it with individual development characteristics of the chicks, the study proposed a primary noninvasive heath evaluation system for the physiological status of brown eared pheasant.

**Results**

The study showed that when brown eared pheasant chicks were infected, the proportions of the fecal IgA, IgM, and IgY changed regularly, and that the changes were consistent with their body characteristics. The proportion of the fecal IgA of the brown eared pheasant chicks that died within three weeks after their birth was significantly lower than that of the ones survived. Also, the proportion of the fecal IgA, IgM, and IgY of the dead young and adult brown-eared pheasants before their death were significantly different from those of the ones survived.

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The results suggest that: 1) the heath condition of brown eared pheasants at 3-13 days old can be predicted by measuring their proportions of fecal IgA.; 2) brown-eared pheasant chicks with body masses smaller than 35 g have a higher risk of death; 3) the fecal IgM can be used as an indicator for warning the health status, the fecal IgA for disease infection, and the fecal IgY for intestinal mucosal damage.

### Conclusions

The techniques proposed in this health evaluation system for brown eared pheasant would have wide application in areas like selecting the healthy individuals of captive brown-eared pheasants when releasing them to the field and improving the success of reintroduction programs.

**Keywords:** Brown eared pheasant，Fecal immunoglobulin，Non-invasive technology,

Poster 3-1

# Interspecies heterologous chicken microsatellites of high cross species utility with special reference to Cheer Pheasant, Western Tragopan and Himalayan Monal

## 彩雉、黑头角雉和棕尾虹雉雏鸟的微卫星种间异质性

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Isolation and development of new microsatellite markers for any species is still labour-intensive and requires substantial inputs of time, money and expertise. Therefore, cross-species microsatellite amplification can be an effective way in obtaining microsatellite loci for closely related taxa in bird species. We have successfully transferred 7 chicken microsatellites in Cheer Pheasant (*Caterus wallichii*) & Western Tragopan (*Tragopan melanocephalus*) and 15 chicken microsatellites in Himalayan Monal (*Lophophorus impejanus*) for which previous no previous genetic information was available. In Cheer Pheasant, 17 different alleles were found with 2.43 ±0.79 and 2.03 ±0.67 mean observed and effective number of alleles per locus, respectively. The mean Ho and He was 0.72 ±0.27 and 0.47±0.15), respectively. The mean FIS (inbreeding coefficient index) of the analyzed samples was different significantly from zero ($F_{IS}$ -0.52±0.37). In Western Tragopan, 7 loci yielded 39 alleles with 5.57±0.84 and 3.34±0.61 observed and effective number of alleles per locus, respectively. The mean Ho was lower (0.41±0.11) than the mean He (0.64±0.06) and inbreeding coefficient supported a strong signature of inbreeding in Western Tragopan population ($F_{IS}$ 0.39±0.16). All the tested 15 microsatellite markers in Himalayan Monal were polymorphic, with mean allelic number of 4±1.51, ranging 2–7 per locus. The observed heterozygosity in the population ranged between 0.285 and 0.714, with mean of 0.499±0.125, indicating considerable genetic variation in this population. The present study has been the first exhaustive attempt to test and ensuring the applicability of chicken microsatellites in Cheer Pheasant, Western Tragopan and in Himalayan monal. These loci could be employed for further studies on ecological traits such as kin selection and mating systems in these species, and the study would suggest measures for better conservation of species. These results suggest that time, effort and funds spent in investigating the cross-species amplification of these microsatellite loci in non-target species is being well justified, and the results in getting heterologous markers will be of use to other researchers to work on Galliformes. These markers could play a major role in studying genetic variation, evolution, phylogeny and genetic divergence of different taxa.

Poster 3-2

# Whole genome sequences and microsatellites distribution patterns of Chinese monal (*Lophophorus lhuysii*)

# 绿尾虹雉全基因组测序及微卫星分布规律分析

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## Background

Chinese Monal（*Lophophorus lhuysii*）is endemic to south-west China and has been listed as vulnerable in IUCN red list. Its genome sequence and microsatellites distribution pattern were not available.

## Methods

The blood samples of Chinese monal were obtained from Sichuan Fengtongzai Nature Reserve. The de novo sequencing were performed using Illumina HiSeq platform. The distribution information of microsatellites in the genome was calculated by custom Python scripts, and all genes containing microsatellites were annotated by using the programs of Blast2Go.

## Results

A total of 174.66 Gb (158.78x coverage) genome sequences were generated and the genome （1.01Gb） was de novo assembled by ALLPATH, with the N50 6939kb, GC concent 41.47% . The final gene set contained 18676 genes, compared with 15508 in chicken，14123 in turkey and 17488 in Zebra Finch. A total of 286 479 simple sequence repeats (SSRs) with 1 – 6 bp nucleotide motifs were identified and there is a locus per 3.53 kb. Among different types of microsatellites, mono-nucleotides (209 448, 73.11%) were the most, followed by tetra-nucleotides (26 625, 9.29%), di-nucleotides (20 077, 7.01%), tri-nucleotides (17 526, 6.12%), penta-nucleotides (10 480, 3.66%) and hexa-nucleotides (2 323, 0.81%). The predominant repeat types are A, C, AAAC, AT, AAAT, AC, AAT, AAC, AG, AAAG, AAAAC, with a total number of 261 867, accounting for 91.41% of the total SSRs. The number of each of these 11 categories is greater than 2 500. There were 1 661 microsatellites in exons, 107 241 microsatellites in introns and 177 648 microsatellites in intergenic regions. Tri-nucleotide microsatellites (1 411) were the most in exons, accounting for 84.95% of the total SSRs in exons. Mono-nucleotide microsatellites were the most, whether it’s on the intergenic regions or introns, followed by tetra-nucleotide microsatellites. The results of GO annotation indicated that 753 GO terms were classified as cellular component, 359 GO

terms were related to molecular function and 1100 GO terms were related to the biological process. In the molecular function, they were mainly involved in the binding, catalytic and transcription regulator.

**Conclusion**

The whole genome of *Lophophorus lhuysii* was firstly sequenced with 1.01Gb in size. The number and distribution pattern of the microsatellites in genome were analyzed. This study will certainly facilitate the development of microsatellite markers and lay the foundation for further in-depth analysis of microsatellite function of *L. lhuysii*.

**Key words:** *Lophophorus lhuysii*; genome; microsatellites

Poster 3-3

# Phylogenomic inference place three enigmatic phasianid genera (Aves: Galliformes)

## 系统基因组学探索 3 种雉科鸟类的进化地位

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The phylogeny of the Phasianidae (pheasants, partridges, and allies) has been studied extensively. However, these studies have largely ignored three enigmatic genera because of scarce DNA source material and limited overlapping phylogenetic data: blood pheasants (Ithaginis), snow partridges (Lerwa), and long-billed partridges (Rhizothera). Thus, phylogenetic positions of these three genera remain uncertain in what is otherwise a well-resolved phylogeny. Previous studies using different data types place Lerwa and Ithaginis in similar positions, but the absence of overlapping data means the relationship between them could not be inferred. Rhizothera was originally described in the genus Perdix (true partridges), although a partial cytochrome b (CYB) sequence suggests it is sister to Pucrasia (Koklass Pheasant). To identify robust relationships among Ithaginis, Lerwa, Rhizothera, and their phasianid relatives, we used 3692 ultra-conserved element (UCE) loci and complete mitogenomes from 19 species including previously hypothesized relatives and representatives from all major phasianid clades. We used DNA extracted from historical specimen toepads for species that lacked fresh tissue in museum collections. Maximum likelihood and multispecies coalescent UCE analyses strongly supported Lerwa sister to a large clade which included Ithaginis at its base, and also including turkey, grouse, typical pheasants, tragopans, Pucrasia, and Perdix. Rhizothera was also in this clade, sister to a diverse group comprising Perdix, typical pheasants, Pucrasia, turkey and grouse. Mitogenomic genealogies differed from UCEs topologies, supporting a sister relationship between Ithaginis and Lerwa rather than a grade. The position of Rhizothera using mitogenomes depended on analytical choices. Unpartitioned and codon-based analyses placed Rhizothera sister to a tragopan clade, whereas a partitioned DNA model of the mitogenome was congruent with UCE results. In all mitogenome analyses, Pucrasia was sister to a clade including Perdix and the typical pheasants with high support, in contrast to UCEs and published nuclear intron data. Due to the strong support and consistent topology provided by all UCE analyses, we have identified phylogenetic relationships of these three enigmatic, poorly-studied, phasianid taxa, and found that previous attempts have been hampered by cyto-nuclear discordance.

**Keywords:** ultraconserved elements, mitochondrial genome, Ithaginis, Lerwa, Rhizothera.

Poster 3-4

# Polymorphism in some birds of Galliformes
# 鸡形目鸟类多态性

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The phylogenetic and taxonomic status of galliform birds is difficult to ascertain. This study reviews previous research on molecular techniques and morphological characteristics (e.g., plumage color) of Tragopan, Ithaginis, and Perdix to elucidate the polymorphism and taxonomic criteria of some galliform genera. Taxonomic criteria include genetic and morphologic characteristics (e.g., body color). Plumage color is associated with sexual selection and environmental factors and, therefore, is an important criterion in bird taxonomy. The results of this study reveal the polymorphism of some galliform birds and the difficulty in ascertaining the taxonomic status of these birds.

**Keywords:** Morphology, Taxonomic criteria, Colour

Poster 3-5

# Population Genetic Analysis of Widespread bird Common Pheasant (*Phasianus colchicus*)

## 分布广泛的雉鸡（*Phasianus colchicus*）的种群遗传分析

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### Background

Common pheasant (*Phasianus colchicus*) is widely distributed in Eastern and Mid-Asian region, such as China, Mongolia, North Korea, Russia and Afghanistan, Iran, Turkey and so on, with 30 subspecies according to in male morphology and geographic settings. As its wide distribution, large populations and morphologically geographic variation, common pheasant is an ideal model to biogeography and evolutionary studies.

### Methods

Based on multiple nuclear and mitochondrial genes and 13 pairs of microsatellites from more than 20 subspecies, we inferred the population genetic structure and history of common pheasant.

### Results

By analyzing the phylogenetic relationships, five subspecies groups including Grey-rumped group, Olive-rumped, Kirghiz group, White-winged group and Black-necked group were supported. Furthermore, the subspecies *Phasianus colchicus elegan* from Grey-rumped group is likely to be the base taxa of all subspecies. However we also found that introgression with various degree exists among different subspecies and subspecies groups.

### Conclusion

Common pheasant might originate from Southwest China, expanding to Eastern and Mid-Asian region. Geographical isolation led to subspecies divergence, yet population admixture mediated by recent expansion and in gene flow, causing indistinct genetic boundaries of parapatric subspecies.

**Key Words:** *Phasianus colchicus*; population genetic; nuclear genes; mitochondrial; microsatellite; subspecies; gene flow

Poster3-6

# High altitude adaptation in Eared-pheasants based on transcriptome data
# 基于转录组数据的马鸡属对高海拔的适应性研究

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The main characteristics of extreme environment in high altitude are hypothermia, hypoxia and strong ultraviolet radiation, which are both great challenges that local animals confronted with. Eared-pheasants, a genus of pheasants in the Phasianidae family, are typical birds mainly living in the Plateau, and long-time high altitude life may promote them to develop a specific gene expression pattern adapting to the surrounding environment. In this study, we conducted blood transcriptome sequencing and comparative analysis about four species from zoo, for the purpose of understanding the different adaptive mechanism. The results were displayed as follows: i) The phylogenetic tree reconstructed based on all 476 DEGs was perfectly conformed with the ideas that *Crossoptilon harmani* is closely related with *Crossoptilon crossoptilon*, and *Crossoptilon mantchuricum* is sister group to *Crossoptilon auritum*. ii) *Crossoptilon harmani* had more specifically expressed genes, in which, 22 up-regulated genes were mainly involved in “Cardiac muscle contraction”, “energy metabolism” and disease resistance. This study preliminarily showed that the increased expression level of key genes may lay the foundation for *Crossoptilon* birds to adapt to the extreme condition in Plateau, and long-term adaptive evolution made the genetic mechanisms of genes expression and regulation appear differentiation gradually.

**Key words:** *Crossoptilon*; high altitude adaptation; transcriptome