Phylogeography of a wide-ranging bird in Asia, the common pheasant *Phasianus colchicus*

Yang Liu¹, Xiaoju Niu², Zhengwang Zhang²

1. School of Life Sciences, Sun Yat-sen University, Guangzhou 510275, China
2. College of Life Sciences, Beijing Normal University, Beijing 100875, China

§ Email: liuy353@mail.sysu.edu.cn

Phasianus colchicus

The common pheasant, *Phasianus colchicus* is widely distributed throughout temperate regions in East and Central Asia, and is well adapted to a wide range of environmental and climate conditions. This species had been introduced into Europe and North America as a game bird. Thirty subspecies belonging to five major subspecies groups have been defined based on substantial variation in male morphology (Fig. 1).

Questions

- Do defined subspecies groups correspond to genetically distinct lineages?
- When and how did these subspecies groups split?

Methods

- Individuals from 29 sites genotyped at 2 mtDNA (1625 bp) and 9 unlinked nuclear introns (5331 bp).
- Phylogenetic relationships -> Networks (mtDNA) & Bayesian framework (mtDNA + nucDNA, BEAST).

Results

- The divergence time: I vs (II, III, IV) : 0.33 (0.19-0.52, 95% HPD) Mya
- IV vs (II, III) : 0.24 (0.14-0.38, 95% HPD) Mya
- II vs III : 0.13 (0.06-0.23, 95% HPD) Mya

The white-winged group (6 ssp)

The black-necked group (4 ssp)

The gray-rumped group (17 ssp)

The Tarim group (1 ssp)

The Kirghiz group (2 ssp)

NE China

E China

C China

Loess Plateau

Qinghai & the Loess Plateau

C China

NE & E China

Xinjiang

Fig. 2 Phylogenetic relationships based on mtDNA and nucDNA sequences of a subset of 49 common pheasants. Asterisks indicate posterior probability > 0.90.

Fig. 3 Unrooted median-joining networks illustrating the phylogenetic relationships of 483 common pheasants. Detailed substructures within “the gray-rumped group” demonstrate genetic introgression between subspecies in E and C China (A), and in the Loess Plateau (B).

Conclusions

- Deep divergent evolutionary lineages and the affinity of subspecies to these evolutionary lineages corresponds with pre-defined morphological groups and a previously undescribed group in Yunnan.
- Divergence times between major lineages corresponded to geographical and climate changes in glacial periods in the Pleistocene (0.33-0.13 Mya).
- Evidence of genetic introgression between contiguous subspecies within lineages.

Acknowledgements: The copyright of the Phasianus artworks belongs to HBW Alive (www.hbw.com). We thank Y. Liu, Y.Y. Liu, D. Chen for their assistance in lab work.