

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

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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).

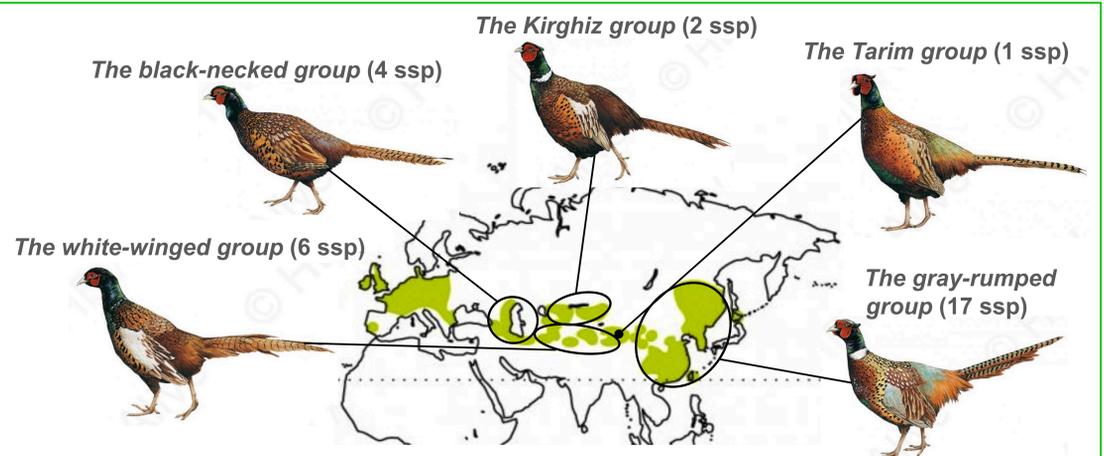


Fig.1 Geographically separated subspecies groups (no. of subspecies) are associated with substantially morphological variation in male common pheasants.

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).

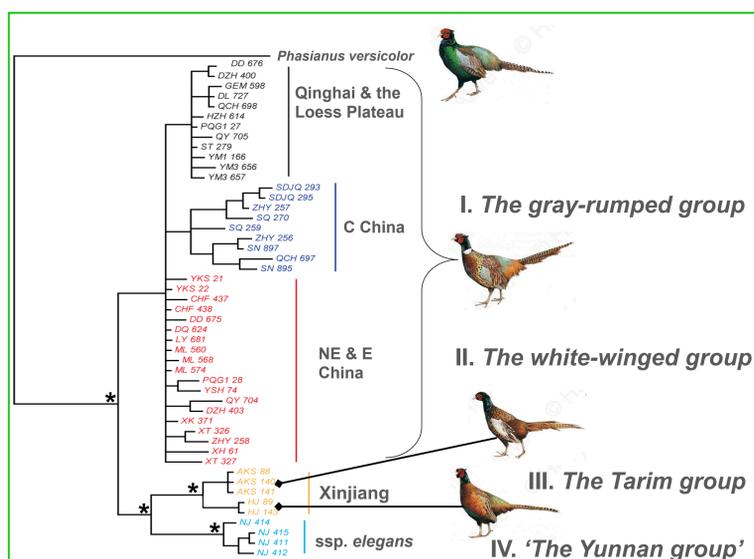
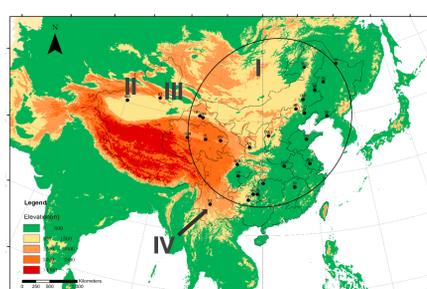


Fig. 2 Phylogenetic relationships based on mtDNA and nucDNA sequences of a subset of 49 common pheasants. Asterisks indicate posterior probability > 0.90.

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

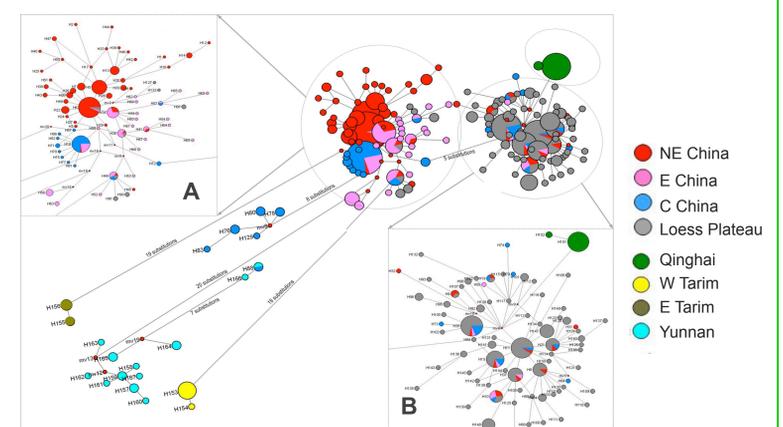


Fig. 3 Unrooted median-joining networks illustrating the phylogenetic relationships of 483 common pheasants based on mtDNA sequences. Detailed substructures within "the gray-rumped group" demonstrate genetic introgression between subspecies in E and C China (A), and in the Loess Plateau (B).

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.