S17 Avian Phylogeography in East Asia

**Phylogeography and population genomics of a wide-ranging bird in**

**Eurasia, the Common Pheasant *Phasianus colchicus***

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The Common Pheasant, *Phasianus colchicus* is distributed throughout temperate regions in East and Central Asia, and had been widely introduced into Europe and North America as a game bird. This species is well adapted to a wide range of environmental and climate conditions. Thirty-one subspecies have been identified based on substantial variation in male morphological ornaments. We investigated the phylogeography and genetic diversity patterns of Common Pheasant in Asia using two mitochondrial and nine nuclear genes, and male morphological characters. Our analyses revealed six highly divergent evolutionary lineages and the affinity of subspecies to evolutionary lineages corresponds with five pre-defined morphological groups and a previously undescribed group. The distribution of these lineages reflects geographical breaks of mountains, plains and deserts, and the estimates for the divergence times between these lineages probably predate the last glacial maximum. We further found evidence of extensive genetic introgression between contiguous subspecies within lineages. Further, genome-wide patterns of population structure and admixture were assessed by analyzing tens of thousands SNPs derived from RAD-sequencing approach. Taken together, these results suggest that the divergence of Common Pheasant has been shaped by ancient colonization events and isolation during postglacial periods. This study system provides a favorable framework to understand the speciation processes under biogeography, local adaptation and sexual selection.

4

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