

## Symposium 20 Evolutionary genetics of the Phasianidae

### Introduction

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This symposium updates results of ongoing research projects on evolutionary and conservation genetics of species of Phasianidae. The use of molecular methods is producing growing datasets of DNA sequences and allelic frequencies for pheasant species and their populations. As the papers presented show, these data are being used to infer interspecific phylogenetic relationships, to estimate the extent of intraspecific differentiation and to trace phylogeographic population structuring. Thus the symposium contributes to reconstructing phylogenies and evolutionary processes in pheasants. Moreover, pheasants include a number of highly endangered taxa, particularly in Southeast Asia. Although most of them are kept in captivity,

many are bred without appropriate demographic and genetic management. Accordingly, papers in this symposium evaluate recent results produced by conservation genetics programs. These programs assess levels of gene diversity and inbreeding, and detect cases of interspecific hybridization in captive stocks, all needed for implementing effective conservation strategies and reintroduction programs.

All papers presented are published here, except the fourth by Koon Wah Fok and David Parkin. That presentation covered genetic differentiation and evolution in the eared pheasants, *Crossoptilon*; and its abstract is published in the Abstract Volume for the Congress.