

# Genetic analysis of migration in two avian influenza vectors: tufted duck and common pochard

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## Key words

Tufted duck, Common pochard, Avian Influenza, Dispersal, Migration, Population structure, Switzerland

## Aim of the study

We investigated the genetic population structure of two common long-distance migratory ducks in both their breeding and wintering grounds across Eurasia using molecular markers. This provides the first quantitative assessment of the extent of population mixing among East Asian and European ducks and contributes to a better understanding of possible transmission pathways of pathogens associated with these birds (e.g. H5N1).

## Material and methods

We collected tissue samples from 366 tufted ducks and 345 common pochards from major breeding and wintering grounds in more than 16 countries across Eurasia spanning Portugal to Japan. The samples were analysed at the mitochondrial DNA control region (mtDNA) and 14 autosomal microsatellite loci (nuclear DNA). The resulting genetic data were statistically analysed using state-of-the-art phylogeographic and population genetics methods.

## Results and significance

Analyses of mtDNA and nuclear DNA showed relatively high genetic variation and significant genetic differentiation among breeding populations in both species. However, the level of genetic differences between populations was not associated with geographical distance and, in particular, there was no strong genetic divergence between ducks sampled in Europe and East Asia. Differentiation was higher for maternally inherited mtDNA than for bi-parentally inherited nuclear DNA, pointing towards male-biased gene flow and relative female fidelity to breeding colonies. No evidence of genetic substructure was detected for ducks sampled on the European wintering grounds. Taken together, our results suggest some breeding site fidelity in the two duck species leading to genetically structured population during the summer months but population admixture on the wintering grounds. Consistent with the high mobility of these migratory ducks, movements of individuals and gene flow appears to take place across large geographic distances. The specific role of both species as natural vectors of zoonotic pathogens and avian influenza in particular remains to be clarified but the mixing of individuals from different geographical regions during winter shows the potential for pathogen spread and stresses the importance of targeted surveillance measures.

## Publications, posters and presentations

Liu, Y.; Keller, I.; Heckel, G. 2008. 1st International Workshop of the Anatidae Network, Beijing, China. Talk.

Liu, Y.; Keller, I.; Heckel, G. 2009. 2nd Pan European Duck Symposium. Camargue, France. Poster.

Heckel, G. 2009. Friedrich-Loeffler-Institut, Riems, Germany. Talk.

Liu, Y., Keller, I.; Heckel, G. 2010. 25th International Ornithologists' Congress, Campos do Jordão, Brazil. Talk.

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