

Conservation genetics of the Black Grouse *Tetrao tetrix* in Poland — distribution of genetic diversity among the last populations

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Rutkowski R., Pałucki A., Dulisz B., Ciach M., Nowak-Życzyńska Z., Kowalewska K. 2018. Conservation genetics of the Black Grouse *Tetrao tetrix* in Poland — distribution of genetic diversity among the last populations. *Acta Ornithol.* 53: 181–204. DOI 10.3161/00016454AO2018.53.2.008

Abstract. The Black Grouse *Tetrao tetrix* populations in Europe have become fragmented and reduced in numbers. These processes affected genetic diversity of the species, altering patterns of gene flow and genetic structure. In Poland, the Black Grouse is one of the most endangered bird species, however very little is known about diversity of this native population, bordering on to the area of Europe in which the species maintains a continuous range. To complete the knowledge of genetic structure of European populations, we analysed microsatellite polymorphism in 97 native Polish birds, along with 39 introduced individuals, originating in Belarus and at a breeding centre in Poland, regarded as representing the gene pool from the north-eastern part of the country. The results confirmed that isolation of populations and recent decreases in their sizes have reduced genetic diversity in Poland's populations of the Black Grouse. The results also indicated the presence of two genetic groups in Poland, involving birds of the north-eastern part of the country and the Carpathians Foothills in a first group, and the population from the Sudetes (Izerskie and Karkonosze Mountains) in a second. We suggest that the conservation effort should treat these two groups as independent units. We also analysed a fragment of the mitochondrial Control Region (CRmtDNA). The comparisons of sequences obtained with data from other Eurasian populations indicate that populations of the Black Grouse in Poland should be included within a large Conservation Unit — the northern *tetrix* — which comprises birds from Eastern and Northern Europe.

Key words: *Tetrao tetrix*, Black Grouse, genetic diversity, genetic differentiation, microsatellite, Control Region, mtDNA, phylogeography

Received — Oct. 2018, accepted — Dec. 2018

INTRODUCTION

Information on the distribution of genetic diversity among populations of endangered species is of a great importance to conservation biology (Frankham et al. 2014), as anthropogenic habitat fragmentation and loss have altered patterns markedly, impacting negatively upon both genetic connectivity and population size (Keyghobadi 2007, DiBattista 2008). The consequent genetic drift gives rise to: (i) random fluctuations in allele frequencies, and increasing genetic differentiation among groups of individuals inhabiting fragmented patches of suitable habitat; and (ii) a loss of

genetic diversity, with the likelihood of extinction increased by negative genetic effects. Against this background, comparisons of genetic diversity among populations of differing sizes and levels of isolation help with the identification of those units most vulnerable to negative genetic processes (Hoban et al. 2013, Kahilainen et al. 2014, Díez-del-Molino et al. 2018). On the other hand, analysis of genetic structure allows basic conservation units to be identified, former and current patterns of gene flow inferred and the severity of the fragmentation and loss of habitats assessed (Moritz 1994, Palsbøll et al. 2007, Habel & Schmitt 2012, Keyghobadi et al. 2013, Epps & Keyghobadi 2015).