

RAPD molecular markers to study populations of black grouse *Tetrao tetrix* in the Alps

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The black grouse *Tetrao tetrix* is declining in most of the Alps where it historically occurred. A better knowledge of the genetics of the wild populations and of captive-reared birds is necessary for future reintroduction into areas where they historically occurred or where they are endangered. DNA-markers are the choice of method to study genetics of wild populations, but it is difficult to get blood samples from wild birds to extract DNA. A technique based on feathers as the DNA source was developed. DNA extracted from blood and feathers from seven birds was tested by PCR, 80 10-base primers. Only seven primers showed a repeatable amplification profile between DNA sources and polymorphic variation within the population. The selected primers were

used to amplify the DNA extracted from wild black grouse feathers in different areas (Trentino, Cuneo, Maritime Alps). The Trentino population presented a reduced genetic variability with an average band sharing (ABS) of 0.76 ± 0.145 in the captive-reared birds vs 0.70 ± 0.17 in all birds. The birds from Cuneo and the Maritime Alps had an ABS of 0.48 ± 0.07 and 0.35 ± 0.10 , respectively, and were quite different from the average genotype.

Key words: black grouse, genetic variability, RAPD molecular markers, *Tetrao tetrix*, the Alps

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Do sage grouse *Centrocercus urophasianus* exhibit metapopulations in northcentral Washington, USA?

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Metapopulations can be considered populations of subpopulations, each with characteristic patterns of gene flow, extinction, and recolonization. Increased understanding of metapopulations is essential if wildlife managers are to maintain populations in altered environments. Management of sage grouse *Centrocercus urophasianus* has often been conducted with the tacit objective of managing subpopulations; this objective typically includes the delineation of high priority habitats within a defined proximity of known lek locations. This procedure has been defended by research and conjecture: 1) most females nest close to leks; 2) most females visit only one lek; and 3) each lek appears to represent a distinct population of females. Between 1992 and 1995 the possible existence of metapopulations was examined by observing 110 radio-marked sage grouse in northcentral Washington, USA. The 2,000 km² study area consisted of a variety of altered

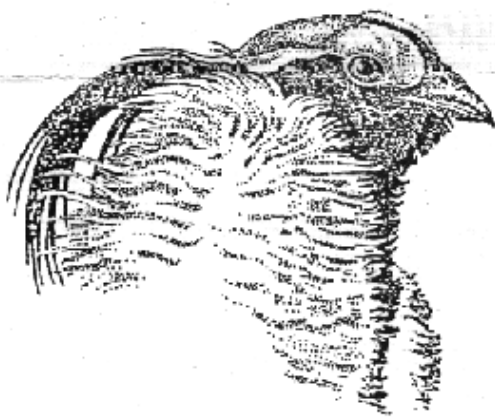
habitats, configured in a highly fragmented landscape. The results indicate that the sage grouse in this area comprise a single population, not several subpopulations: 1) distances between nest locations and lek locations are large; 2) visits by females to more than one lek are common; 3) movements by birds within the population indicate that genetic transfer throughout the region is unhindered by distance, geography, and habitat. The lack of distinct subpopulations in northcentral Washington indicates that this sage grouse population should be managed as a single unit. Nevertheless, it is possible that the lack of evidence for subpopulations may reflect the scale of these observations; sage grouse may exist in a metapopulation at a larger scale, perhaps consisting of northcentral and southcentral Washington subpopulations.

Key words: *Centrocercus urophasianus*, management, metapopulation, sage grouse, Washington

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RAPD MOLECULAR MARKERS TO STUDY POPULATIONS OF BLACK GROUSE

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Abstract: The black grouse (*Tetrao tetrix*) is declining in most of the Alps where it historically occurred. A better knowledge of the genetics of wild populations and of captive-reared birds is necessary for future reintroduction into areas where they historically occurred or where they are endangered. DNA markers are the choice of method to study genetics of wild populations, but it is difficult to get blood samples from wild birds to extract DNA. We developed a technique based on feathers as a DNA source. We extracted DNA from blood and feathers from 7 birds which we tested by PCR, 80 10-base primers. Only 7 primers showed a repeatable amplification profile between DNA sources and polymorphic variation within the population. We used the selected primers to amplify the DNA extracted from wild black grouse feathers in different areas (Trentino, Cuneo, Maritime Alps). The Trentino population presented a reduced genetic variability with an average band sharing (ABS) of 0.76 ± 0.145 in the captive-reared birds vs. 0.70 ± 0.17 in all birds. The birds from Cuneo and the Maritime Alps had ABS of 0.48 ± 0.07 and 0.35 ± 0.10 , respectively, and were quite different from the average genotype.