

GROUSE NEWS



Newsletter of the Grouse Group *of the*
IUCN/SSC-WPA Galliformes Specialist Group



Galliformes Specialist Group

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From the Editor

Greetings from North America. Grouse research and conservation efforts in North America are advancing at an unprecedented rate, and with time I expect that we shall see many more contributions by North American grouse researchers in future Grouse News. I want to continue to encourage my North American colleagues to consider submitting information for upcoming issues. This issue includes recent research results on Greater Prairie-Chickens, Sharp-tailed Grouse, and Spruce Grouse, and also includes an update on the status of Lesser Prairie-Chickens. A research report on the Cantabrian capercaillie is also included in this issue. Additionally, there is a summary of a new management guide on Pyrenean Capercaillie, and a book review on a new and exciting book about Ruffed Grouse, which includes chapters on the biology of the species as well as hunting of this valued game species. Finally, there are announcements of three different awards or honors that were recently bestowed upon some of our members.

The 13th International Grouse Symposium will be hosted by Olafur Nielsen in Iceland in 2015. We will get back to more details on time and place in a later issue. The 7th International Black Grouse Conference will be organized in May 2014 in the Komi Republic, Russia.

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From the Chair

In GN45 (June 2013) I had announced the upcoming re-formation of the Galliformes Specialist Group (GSG) according to regulations of the International Union for Nature Conservation (IUCN), which request to formally renew Specialist Group membership every four years. The new quadrennium 2013-2016 has started this year. In this process, it is the task of SG Chairs to invite new and re-appoint old members on behalf of the IUCN's Species Survival Commission (SSC). Unfortunately, the reformation of the GSG became delayed because of a pending revision of the formal relationships between IUCN/SSC and the World Pheasant Association (WPA), which affects the management of the GSG. A meeting has now been scheduled for mid-December to clarify future relationships. Thereafter, I hope that the Co-Chairs of the Galliformes SG, Peter Garson and I, will be able to send out invitation and re-appointment letters to you without further delay.

Unlike than the re-formation of the GSG, publication of papers from the 12th International Grouse Symposium (IGS) in Japan (2012) will be perfectly in time. Wildlife Biology (www.wildlifebiology.com/) will publish a selection of papers in its December 2013 issue; a few further papers may follow in the next issues. The IGS papers will be "open access" and can be downloaded without costs. The review process was based on the standards that are the norm at Wildlife Biology. Special Editor Rocky Gutierrez (University of Minnesota, USA) has done a remarkable job in securing both the timing of the review process, and high quality of the accepted papers. Thank you Rocky!

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NEWS FROM GALLIFORMES SG

GSG Report 2013

In early 2013 this SG became a full amalgamation of five previous ones, with the inclusion of the Cracids of South and Meso-America. This brings together global concerns about all the 286 Galliformes species, and a worldwide community of about 250 people actively working on their conservation and sustainable use.

The focus of the GSG must be the 25% of species (73) that are currently listed as threatened. Galliformes habitats, especially forests, are being disrupted and many species are also over-hunted. Whilst our tropical and subtropical species of Asia and the Americas remain under-researched, there is a wealth of knowledge and expertise available on the hunted grouse species of the Northern Hemisphere. So the GSG remains dedicated to making up this deficit through capacity-building, making use of its network to transfer knowledge and expertise: recently, for instance, from India to Nepal and Pakistan, and from China and Thailand to Myanmar.

To spread the word more generally, the GSG produces a main newsletter (*G@llinformed*) as well as *Grouse News* and the *Cracid Bulletin*, all of which include project reports, technical pieces and alerts to recent literature. The GSG website (www.galliformes-sg.org) contains an archive of all past issues. Papers from the most recent International Grouse Symposium (Japan 2012) have now been published in the journal *Wildlife Biology*.

A major concern in 2013 has been to seek information and promote action on the plight of Edwards's Pheasant *Lophura edwardsi*, which is Critically Endangered and endemic to a small and heavily impacted area of central Vietnam. Matt Grainger (Newcastle University, UK) is moderating an email consortium for the GSG, designed to bring together key experts including breeders of this species in Europe, Japan and North America. Their aim is to establish the purity and diversity of captives through DNA screening, thereby enabling Chris Holmes (Houston Zoo, USA), as the new International Studbook Keeper, to manage the global captive population to best effect in case re-introductions are necessary in future. Philip McGowan (Newcastle University, UK) has recently led a CEPF-funded workshop under the auspices of the GSG for many different stakeholders in Vietnam. An agreed Strategic Conservation Plan, to be managed by a Vietnam-based Working Group, is imminent. As no wild birds have been recorded since 2000, GIS modelling is being used to identify priority areas for future field surveys.

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CONSERVATION NEWS

U.S. Fish and Wildlife Service Endorses Western Association of Fish and Wildlife Agencies Lesser Prairie-Chicken Range-Wide Conservation Plan, October 23, 2013

Claire Cassel

Range-wide plan provides model for State leadership in conservation of a species proposed for listing under the ESA

Today, the U.S. Fish and Wildlife Service endorsed the Western Association of Fish and Wildlife Agencies' Lesser Prairie-Chicken Range-Wide Conservation Plan, a landmark, collaborative planning effort to conserve a species proposed for listing under the Endangered Species Act (ESA).

The range-wide plan (RWP) represents a dedicated effort by the five range states of Texas, New Mexico, Oklahoma, Kansas and Colorado to conserve the lesser prairie-chicken. After an extensive review, the Service found the plan is consistent with criteria proposed last May for conserving the species, which is proposed for listing under the ESA. The plan calls for providing financial incentives to landowners who voluntarily manage their lands to benefit the species. It also includes a framework for mitigating the potentially harmful effects to lesser prairie-chicken habitat from development activity throughout its range.

"The unprecedented collaborative efforts of WAFWA and the five state wildlife agencies have produced a sound conservation plan for the lesser prairie-chicken," said Service Director Dan Ashe. "We applaud the states' commitment to lead conservation actions across the bird's range."

The Service's endorsement is not a decision by the Service that implementing the plan will preclude the need to protect the lesser prairie-chicken under the ESA. The Service will carefully consider the plan, its implementation and effectiveness when it makes a final determination on whether to list the lesser prairie-chicken under the ESA in March, 2014.

Under the plan, agreements with participating landowners will aim to improve habitat conditions for the lesser prairie-chicken, increase populations and provide for long-term conservation of the species. The plan also establishes a framework for mitigating impacts from a wide range of activities with a goal of providing a net conservation benefit to the species.

"We are encouraged to see U.S. Fish and Wildlife Service endorsement of the five-state, range-wide plan to conserve this iconic grassland bird and its native prairie habitat," said Carter Smith, WAFWA president and Texas Parks and Wildlife Department executive director, speaking on behalf of WAFWA and the five state agencies. "Years of due diligence have gone into this plan, guided by scientific research and monitoring, and developed with input from landowners, agriculture, wind and oil and gas interests and other stakeholders. We can now work at the local level to implement the plan, facilitate more conservation for the bird while allowing sustainable land use and responsible economic development, and hopefully preclude the need to list this species."

In the coming weeks, the Service will revise the May 6, 2013, proposed 4(d) special rule for the lesser prairie-chicken to more specifically identify the range-wide conservation plan as one that, when implemented, will address the conservation needs of the species. If the Service ultimately determines that the lesser prairie-chicken should be listed as a threatened species, the revised 4(d) rule would provide a mechanism for ESA compliance. Linking the plan to a 4(d) special rule would offer participating landowners and industry participants regulatory certainty, as actions carried out in accordance with the plan would be in compliance with the ESA, even if the species requires ESA protection.

The lesser prairie-chicken is a species of prairie grouse commonly recognized for its colorful spring mating display and orange eye combs. Once abundant across much of Texas, New Mexico, Oklahoma, Kansas and Colorado (the five range states), the lesser prairie-chicken's historical range of native grasslands and prairies has been reduced by an estimated 84 percent. The substantial decrease in the range of the species is primarily a result of habitat fragmentation and loss caused by development and conversion of the species' native grassland habitat to other uses. Last year, the population declined by an estimated 50 percent, primarily due to drought conditions in the West.

America's fish, wildlife and plant resources belong to all of us, and ensuring the health of imperiled species is a shared responsibility. The Service is actively engaged with conservation partners and the public in the search for improved and innovative ways to conserve and recover imperiled species such as the Working Lands for Wildlife program. To learn more about the Endangered Species program, go to <http://www.fws.gov/endangered/>. The Western Association of Fish and Wildlife Agencies was



founded in 1922. It currently consists of 23 member states and provinces that have primary responsibility and authority for protecting and managing fish and wildlife in the western United States and Canada. WAFWA promotes the principles of sound resource management, as well as strengthening partnerships and cooperation among local, state, and federal agencies, non-government conservation organizations, and private industry. To learn more about WAFWA and other conservation efforts, and to find a copy of the Lesser Prairie-Chicken Range-Wide Conservation Plan, please go to www.wafwa.org.

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RESEARCH REPORTS

Recent pilot study on sharp-tailed grouse summer habitat selection in interior Alaska

Scott M. Brainerd

In spring 2010, a cooperative 1-year pilot project was initiated between the Alaska Department of Fish and Game (ADF&G) and U.S. Army Alaska (USAA) to investigate habitat selection by Alaska sharp-tailed grouse (*Tympanuchus phasianellus caurus*) during nesting and brood rearing on the U.S. Army Donnelly Training Area (DTA; 63° 50' N, 145° 50' W) on Ft. Wainwright, near Delta Junction, Alaska. The project leader was Thomas Paragi. Cooperators included John A. Haddix II (U.S. Army Alaska), Jeffrey D. Mason, and Elizabeth S. Neipert (Colorado State University).

Few studies on sharp-tailed grouse have been conducted in Alaska. This is the first radio-telemetry study conducted by ADF&G on this species. Grouse were captured in walk-in style traps placed at breeding leks in April and May 2010. The two main leks were in scrub-grassland and 11-year post-fire spruce-aspen regeneration. Field crews captured 46 individual grouse (32 males and 14 females), deployed necklace style radio transmitters on 17 males and 12 females, and recorded grouse locations via telemetry and flushes 1-5 times per week from June through September. An ecotype classification from 1994 satellite imagery was condensed to 4 habitat types based on vegetation species and structure (grassland, low scrub, tall scrub, forest) for comparing use by grouse to availability in areas defined by 100% minimum convex polygons. Vegetation type and visual cover were described from each nest and grouse location and from random points. Home range was estimated for 5 females (4 with broods) and 11 males with ≥ 20 relocations each and was used to define habitat type availability by individual.

Ground-based radio telemetry was used to obtain 142 locations on females and 254 on males during 24 May to 23 September 2010. Home ranges overlapped extensively within and between sexes surrounding each of the two leks, in part due to flocking tendencies of males, confounding landscape scale selection (position of individual ranges within a composite range). Within home range both sexes tended to select forest less than other types, but effect of site (difference in vegetative composition between composite ranges) was strong as a confounding factor with the small number of relocations per individual. Visual concealment (% obscured) at 4 m from nests was greater than at random locations ≤ 100 m distant when viewed horizontally at 15 cm after leaf emergence and at 4 m from nests when viewed obliquely from 1.5 m before and after leaf emergence, suggesting selection for greater concealment. Vertical cover (%) at 50 cm above the nest was also greater than at random sites before and after leaf emergence. Visual concealment at relocations of males and females was not different between sexes or within sex between used and random sites during nesting or brood rearing, except that males used sites with slightly greater concealment at 10 m from the site during brood rearing. Within a May 2010 prescribed burn at the scrub-grassland lek, males and females used sites with a similar degree of concealment as nearby random sites (with the exception of slightly greater concealment at 10 m from the site for males in burned areas), suggesting the burn effect on concealment during nesting and brood rearing was not substantial.

The authors noted goshawks frequently at leks, including observations of goshawks attacking sharp-tailed grouse, and 8 of 11 predation mortalities in this pilot study were attributable to avian predators. Goshawks were documented feeding on sharp-tailed grouse during the 2010 study as well as during 2011 lek monitoring surveys on DTA.

The authors reviewed literature on best management practices for sharp-tailed grouse habitat and summarized pertinent biological information from this pilot study (7 nests were ≤ 1.3 km from their associated breeding leks and 4 females observed with broods were ≤ 1.6 km from associated leks). Until further study of reproduction and survival response to habitat management at DTA, they recommend that the military should avoid human presence or other disturbance at existing leks during breeding display and nesting (late March to mid-June) to minimize displacement of females and should avoid extensive vegetative disturbance within 2 km of existing leks to maintain cover for nesting and brood rearing.

The full report can be downloaded here:

http://www.adfg.alaska.gov/static/home/library/pdfs/wildlife/research_pdfs/wrr_2012_1.pdf.

Please reference as:

Paragi, T. F., J.D. Mason, and S.M. Brainerd. 2012. Summer habitat selection by sharp-tailed grouse in eastern interior Alaska. Alaska Department of Fish and Game, Division of Wildlife Conservation, Final Research Technical Report. Project 10.1. Juneau, Alaska.





Male sharp-tailed grouse with radio collar on breeding lek south of Delta Junction, Alaska (ADF&G photo, Scott Brainerd).



ADF&G Biologist Tom Paragi radio-tracking sharp-tailed grouse on a study area lek (ADF&G photo, Scott Brainerd).

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New research: Spruce Grouse Habitat Use in Northern Michigan — revisiting after 40 years

Laurel Hill and Pat Brown

Introduction

Spruce grouse *Falcipennis canadensis* were once abundant in Michigan, United States, but are now scarce (Amman 1963, McCormick and Corace 2011). Spruce grouse are found in conifer-dominated forests throughout its range. Jack pine *Pinus banksiana* and lodgepole pine *Pinus contorta* are common in the boreal and western habitats (Boag and Schroeder 1992). In Michigan, typical spruce grouse habitat consists of upland jack pine and wetland black spruce, generally interspersed with ericaceous shrub cover.

The goal of my research is to address the principal threat of spruce grouse habitat degradation. I am investigating the effects of forest connectivity, structure and human alterations as measured by indices of habitat use by spruce grouse on the Yellow Dog Plains (YDP). The YDP area is nearly 6,500 ha of glacial out-wash plain and is found in north-western Marquette County in the Upper Peninsula of Michigan (USA). The area has sandy soils and the dominant vegetation is jack pine forests that have been subject to logging and fires during the last 100 years. In some places, fire suppression and silvicultural practices have favored red pine and other species in recent decades.

Background

Studies of spruce grouse began on the YDP in 1965. Robinson's (1980) work addressed the life history of spruce grouse including habitat requirements, breeding behavior, physiological questions, and mortality factors. The spruce grouse population there has not been investigated since the 1980's.

The YDP historically has been an area of heavy forest harvesting. Since the 1970's the area has gradually become more populated with private camps used for hunting and recreation. Off road vehicles (ATVs) are becoming more prevalent in once remote reaches of the plains. These vehicles destroy vegetation, create new trails, and may cause problems with high levels of noise. Recently a large nickel-copper mine has been established that may cause large scale changes to the forests on the mine's company land that could be detrimental to spruce grouse populations on the YDP.

Research objectives

To better understand the effects of habitat degradation on forest patch occupancy, I plan to characterize habitat patches based on their connectivity, forest structure and human alterations, such as road density and presence of recreational camps. Patch connectivity and changes over the last 40 years will be explored using satellite imagery and historical aerial photography from 1960s-2012. Forest structure will be determined from a combination of density measurements, three-dimensional vegetation classification (MDNR 2007), and forest age. The extent of human alteration will be measured by analyzing road density and relative road impact (e.g. dirt road vs. paved road), as well as presence of recreational camps or structures.

Spruce grouse are protected in Michigan so we are measuring relative habitat use using observational counts to minimize disturbance and stress to the species. Variable-width transects based on flushing distance are used to systematically survey for spruce grouse (a variation of Robinson's 1980 method). In addition to counts, scat pellet density and frequency in study plots are being used as an index to habitat preference.

Large-scale changes in human land use, and landscape patterns likely have significant effects on the habitat use of spruce grouse. Spruce grouse are threatened by habitat fragmentation and degradation, small population size and global climate change. This study seeks to investigate the current spruce grouse population its habitat use on the Yellow Dog Plains in relation to current and cumulative human disturbances.

This project began in the summer of 2013 and field work will continue through summer of 2014, with project conclusion planned for late 2014.

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Distribution and landscape attributes of greater prairie-chickens and sharp-tailed grouse outside of their traditional range in South Dakota

Mandy Orth, K.C. Jensen and Charles Dieter

Grasslands play a critical role in providing habitat for greater prairie-chickens (*Tympanuchus cupido*) and sharp-tailed grouse (*Tympanuchus phasianellus*). Due to increased conversion of grassland to cropland, South Dakota is losing this critical habitat. This study identifies areas of eastern SD where populations of prairie-chickens and sharp-tailed grouse were suspected to reside, characterizes landscape attributes within 3,000 m of leks, and analyzes landscape characteristics using Geographic Information System (GIS) modeling to develop a model to predict the probability of prairie grouse presence across eastern South Dakota. Survey routes were developed in areas of potential suitable habitat and were sampled beginning ½ hour before sunrise and ending 2 to 2½ hours after sunrise during the breeding period of mid-March to early June of each year. Listening points were established at 1.6 km intervals. All detected leks were located and recorded. All land and land-uses within 3,000 m of identified leks and randomly selected non-use points were digitized and labeled into a GIS. Land-use attributes for all of eastern South Dakota were obtained from the Habitat and Population Evaluation Team (HAPET) office of the US Fish and Wildlife Service (USFWS Region 6); and land use around all identified leks and random non-use points were analyzed at 7 scales (400, 800, 1200, 1600, 2000, 2400, and 3000-m).

In eastern South Dakota, greater prairie-chickens and sharp-tailed grouse utilize the same habitats and often can be found displaying on mixed leks containing males of both species; hence results apply to both species within this study area. Seventy grouse leks were found outside of their traditional range in eastern South Dakota. Significantly more grassland cover was found around grouse leks than randomly-selected non-use points. Conversely, there was less cropland surrounding lek locations than non-use points. The combination of the proportion of total grassland cover (grassland, undisturbed grass and hayland) and the number of habitat patches on the landscape was a strong predictor of grouse lek presence at all 7 spatial scales. Undisturbed grass is land with a mix of cool-season grass and forb species planted on previously cropped land, and is generally undisturbed but may be hayed or grazed intermittently.

An avoidance of trees and wetlands was evident at the 800-m scale. We then developed and tested models utilizing habitat factors at multiple scales around identified leks and randomized non-use points. Multi-scale modeling revealed that the number of patches at the 3000-m scale, and the total amount of grass on the landscape at the 2000-m scale to be the strongest predictors of lek presence. Within the multi-scale models, grasslands were determined to be most important at the 2000-m scale, and undisturbed grass was most important at the 1600-m scale. The important scale for hayed land was variable, but appeared to be most important at the 1200-m scale. These results suggest that when acquiring land for grouse habitat in eastern South Dakota, roughly 1250 ha (3100 acres) is optimal to meet the spatial needs of grouse; with about 50% of that total composed of grassland habitat. Additionally, we determined that the minimum amount of land that is required to support a grouse population is about 809 ha (2000 acres), with approximately 404.5 ha (1000 acres) of that being grassland habitat. We used multi-scale models in a GIS to then develop a predictive model that showed the likelihood of grouse presence and/or absence for the use of wildlife habitat managers and planners (Figure 1).



Habitat Suitability Index based on the All Grass category

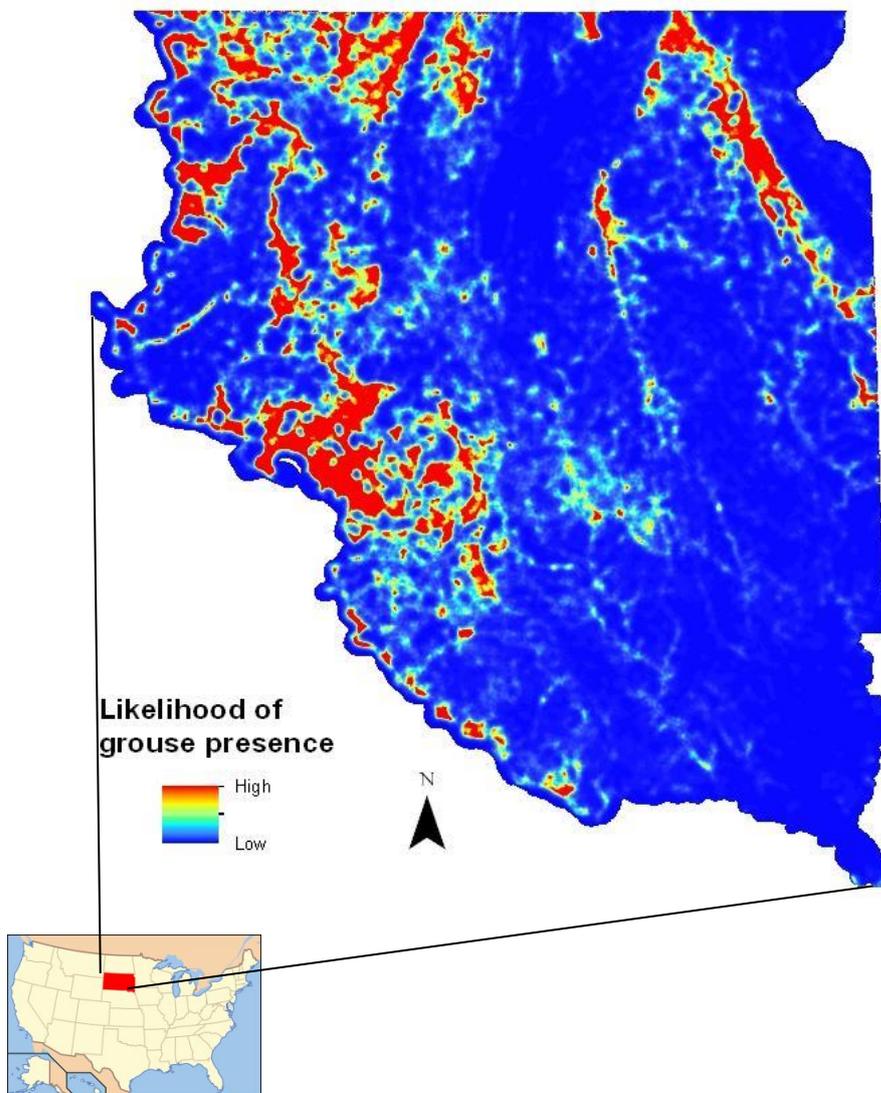


Figure 1. A predictive model created from multi-scale logistic regression equations showing the likelihood of grouse presence and/or absence in eastern South Dakota.

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Brood Habitat and Invertebrate Biomass of the Greater Prairie Chicken (*Tympanuchus cupido pinnatus*) in Northwestern Minnesota

Jennifer Syrowitz

M. Sc. Thesis, University of Manitoba

Abstract

This study assessed the influence of terrestrial invertebrate abundance and vegetation characteristics on northwest Minnesota greater prairie chicken brood success. Radio telemetry was used to determine movements of greater prairie chicken hens and their broods. Invertebrate abundance indices were collected using a sweep net and vegetation data were recorded with overhead and dot-board photographs. Invertebrates were dried, sorted by size and order, and weighed and counted. Vegetation was classified according to life form and height was measured. Greater prairie chicken broods appear to use those habitats most readily available with increased invertebrate resources. Invertebrate biomass was not related to the occurrence of uncultivated forbs which averaged < 17% in Minnesota habitats where greater prairie chicken broods were located. Relatively undisturbed grasslands produce sufficient invertebrate resources to fledge greater prairie chicken chicks. However, location data and invertebrate-habitat indices suggest increased brood success would be likely with improved habitat placement/availability and irregular disturbance regimes that produce beneficial mixed grass/forb vegetation attractive to both greater prairie chicken broods and their invertebrate prey.

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Census and effective population size of the endangered Cantabrian capercaillie (*Tetrao urogallus*) estimated from non-invasive samples

José F. Vázquez, Trinidad Pérez, Jesús Albornoz and Ana Domínguez

Abstract

Non-invasive genetic identification can be used to estimate census (N_C) and effective population size (N_e) and has several advantages upon traditional demographic estimators. We compared eleven models to estimate N_C and two methods of estimating N_e over the basis of feather and faecal samples in the endangered population of Cantabrian capercaillie. A total of 253 samples collected during the year 2006 were genotyped and from them we identified 97 specimens, 53 males, 37 females and 7 undetermined. Animal abundance varied between 147 and 557 depending on the method of estimation. The models including heterogeneity in detection probability were the most appropriate to estimate N_C from our data. The best fitting model was Chao's lower bound estimator that yielded an overall $N_C=297$ (CI 95%: 191-496), with a sex ratio of males to females of 0.41. Abundance estimates confirm the small population size that was revealed by field surveys. Estimates of effective population size (N_e) from two single-sample methods were compared. The effects of rapid population fragmentation were apparent from the linkage disequilibrium estimation of N_e ($LD-N_e=17$) as compared to the value based on multiple summary statistics obtained from ONeSAMP ($N_e=80$). The ratio of effective to census size ($N_{e\text{ ONeSAMP}} / N_C$) was 0.27. Our study demonstrates the importance of single sample genetic studies to monitor threatened populations. The fragmentation into isolated nuclei is the main threat of the population, hence protection of local demes and interconnection of suitable patches are crucial for conservation management.

Keywords: *Tetrao urogallus*, Cantabrian capercaillie, Conservation, Census size, Effective size, Fragmentation, Bottleneck, Linkage disequilibrium, Microsatellites, Non-invasive genotyping.

Introduction

Population census size (N_C) and effective population size (N_e) are among the most important parameters in wildlife management because they are tightly related to extinction risk due to demographic stochasticity and genetic erosion (Brook et al. 2002; Luikart et al. 2010). Traditional estimates of census are difficult because they are based either on direct field surveys, or on capture-mark-recapture (CMR) using physical marks to identify individuals (Seber 1973). Estimation of N_e directly from demographic data such as variance in reproductive success is even more difficult than the estimation of census (Frankham et al. 2010). The advancement of non-invasive genetic techniques has made it possible to identify individuals without capturing them by using DNA extracted from hair, feathers or faeces collected in the field (Taberlet et al. 1999). This allows the estimation of both N_C and N_e from genetic tagging of individuals, which complements traditional demographic estimators (Luikart et al. 2010).



Advantages and disadvantages of non-invasive genetic sampling are now well known and have been discussed (Miller et al. 2005; Marucco et al. 2011). In the context of estimation of population parameters, it is relevant to highlight that genetic tagging allows the collection of suitable data for populations or species that are difficult to study using traditional methods, such as endangered or elusive ones. On the other hand, there are technical problems of the method associated with low quality and quantity of DNA in samples that require the adoption of special measures to avoid misidentification that would lead to erroneous inferences (Miller et al. 2002; Valière 2002; Waits and Paetkau 2005).

The method to estimate population size through non-invasive genetic sampling is simple in concept. A large number of samples are collected in the field and subsequently genotyped. The number of unique multilocus genotypes observed is recorded and serves as a minimum population size (Taberlet et al. 1999). More refined estimates of census size can be obtained using several standard approaches that have been modified to fit genetic identification such as genotype accumulation methods (rarefaction indices) or CMR analysis (reviewed in Luikart et al. 2010).

Effective size can be estimated from data of one single sample of the population by different methods (Luikart et al. 2010) that are being widely used in natural populations (Beebee 2009; Skrbinsek et al. 2012; Schregel et al. 2012). One method, LD- N_e (Waples and Do 2008), is based on the linkage disequilibrium (LD). The principle of the method is that, as N_e decreases, genetic drift with few parents generates non-random associations among alleles at different loci, i.e. LD (Waples and Do 2010; Waples and England 2011). The method is susceptible to be down-biased by processes other than small N_e including population subdivision, immigration or admixture (Luikart et al. 2010; England et al. 2010; Waples and England 2011). The Bayesian method ONeSAMP, proposed by (Tallmon et al. 2008) uses LD plus seven other summary statistics and thus more information from the data, is therefore a less biased estimator (Luikart et al. 2010). We compared estimates obtained with these two methods and discussed differences considering possible violations of assumptions of the models.

The goal of this work is to study N_C and N_e in the endangered Cantabrian capercaillie. The capercaillie *Tetrao urogallus* is a large grouse that is widely distributed across Eurasia. Twelve subspecies have been described since the 1760s, mostly based on morphological and behavioural characteristics (de Juana 1994). The species has a continuous distribution in the boreal forest from Scandinavia to eastern Siberia; however, distribution in western and central Europe is scattered, primarily because of the patchy distribution of coniferous forest. The Cantabrian capercaillie, *T. u. cantabricus* in the Cantabrian Mountains (Castroviejo 1967; Castroviejo 1975) occupies the south-western edge of the grouse family distribution range in Eurasia (Figure 1) and is genetically differentiated from other European capercaillie (Duriez et al. 2006; Rodríguez-Muñoz et al. 2007). The Cantabrian capercaillie is the only subspecies of capercaillie that qualifies as endangered, according to the International Union for Conservation of Nature (IUCN) Red List Categories (Storch et al. 2006). The population is marginal to the area of distribution of the species, its habitat is highly fragmented and covers approximately 26% of the original montane forest distribution (García et al. 2005).

Over the last decades, the population has declined dramatically (Pollo et al. 2005) and genetic analysis has shown a pattern of isolation by distance and a recent decline in population effective size (Alda et al. 2011; Vázquez et al. 2012). Although precise estimates of population census size are not available, the area occupancy has declined by more than 50% in 25 years, and there is evidence of a 30% decline in lek occupancy in the northern watershed of the range from 2000 to 2005 (Quevedo et al. 2006b). A total of 280-300 males was estimated in 1998 (Pollo et al. 2003). Assuming a sex ratio of 1:1 with adults making up 70-80% of the population, the Cantabrian capercaillie metapopulation was estimated at about 630 individuals in 2000-2003; of those birds, about 500 would be adults (Storch et al. 2006). Male counts at leks are a widespread method to estimate abundance. However, such estimates may be biased because of individual differences in attendance at the lek sites and unknown sex ratio. In the present study we compare different approaches to estimate the census size of the Cantabrian capercaillie population using non-invasive genetic samples (feathers and faeces) taken during 2006. In addition, we make estimates of the number of males and the number of females in the population and hence the sex ratio. Different recently developed methods to estimate the effective population size are compared and the estimated N_e is compared with N_C to improve understanding of the N_e/N_C ratio in the species.



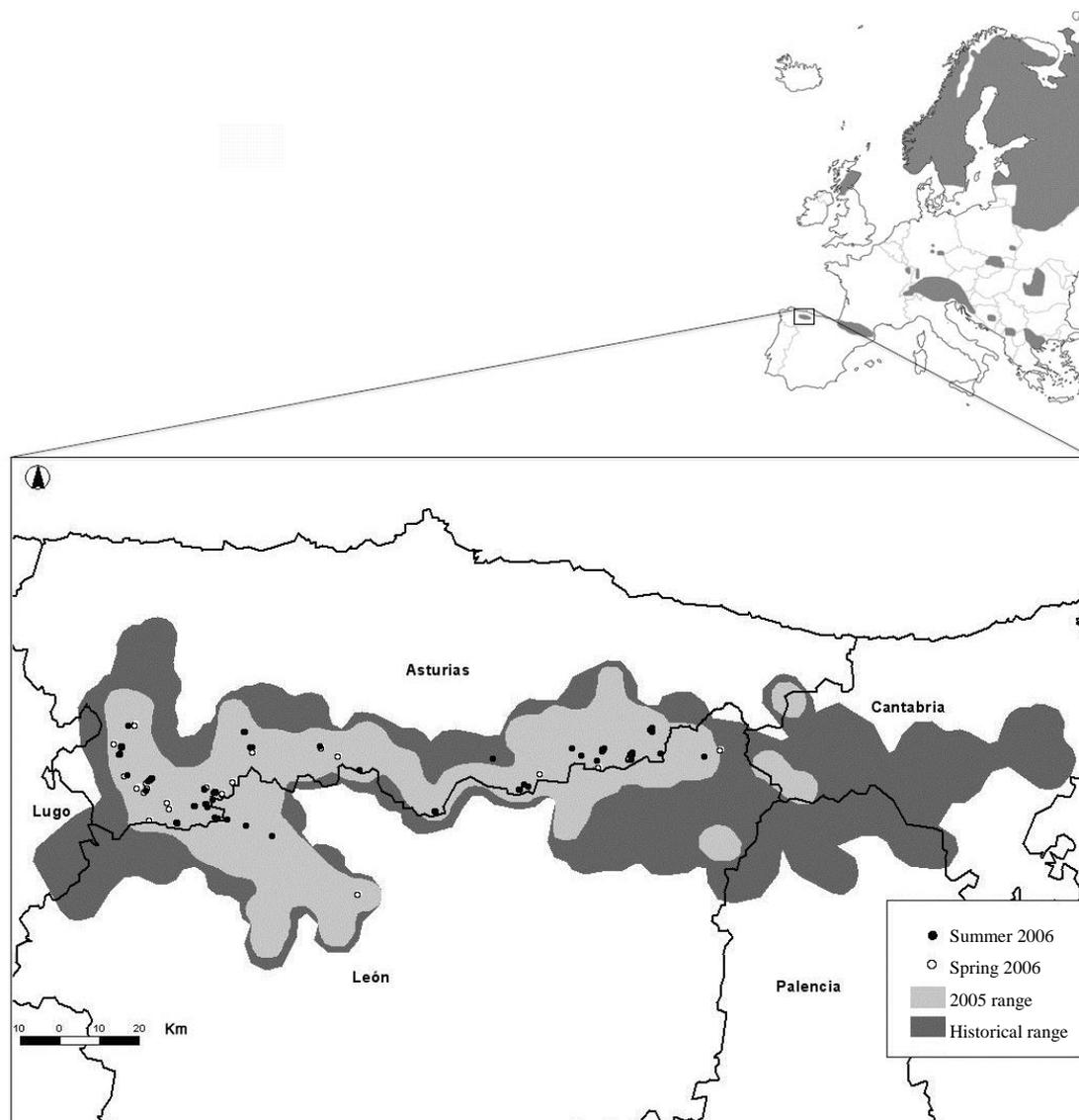


Figure 1. Distribution map of capercaillie in Europe. Inset: Area of occupancy in the Cantabrian Mountains based on <http://www.lifeurogallo.es>. Approximate area of historical occupancy (dark gray) and in 2005 (light gray) and location of the 253 samples genotyped in this study: in gray spring samples and in black summer samples.

Materials and methods

Study area and sampling

The study area included the entire landscape in the range of the bird in the Cantabrian Mountains. At the time of this study, the range occupied an area of 1,700 km² (Figure 1) that is fragmented by several transportation ways in its central sector. The landscape combines both limestone and siliceous soils and is crisscrossed by steep cliffs, ravines, and rocky peaks. Forests are highly fragmented, and the size distribution is strongly skewed towards fragments of <10 ha; the area is composed mostly of semi-natural forests with a long history of human use (García et al. 2005). Beech *Fagus sylvatica* forests are the most abundant in the area and form the largest patches, followed by sessile oak *Quercus petraea* forests with a much lower mean fragment area (Bañuelos et al. 2008). Forest cover becomes scarce at altitudes above 1,500 m.

Feather and faecal samples were collected across the capercaillie distribution range in the Cantabrian Mountains during the year 2006 (Figure 1). Samples were collected through systematic surveys around historically known lekking grounds and surrounding areas one time during the spring (April-June) and one time during the summer (July-September) by forest rangers as described in (Robles



et al. 2005). During the spring the males and females aggregate around the leks (Storch 1997), facilitating the collection of samples. The summer is the moulting season and this makes it easier to get feather samples. Samples from adult birds were collected and the GPS coordinates were recorded. Feathers were placed on individual envelopes and dry stored until DNA extraction. Faeces were either dry stored with silica after ethanol soaking following (Roeder et al. 2004) or simply stored directly in silica.

Methods used to estimate both N_C and N_e assume closure of the population. Geographic closure is reasonably met in our data given that the study area covered the area of distribution of the population and the nearest capercaillie population in the Pyrenees is 300 km apart. The sampling elapsed over a six months period; during this time the number of deaths of adults must be limited, the new-borns are unlikely to be accidentally sampled given that their faeces and feathers are easily distinguishable, then we can also assume demographic closure as reasonable. Further, considering two different seasons would yield a more comprehensive picture of the whole population, given that combining two or more different sampling strategies would reduce sample bias due to individual differences in capture probability dependent on the sampling method (Ebert et al. 2010).

Laboratory analysis and genotyping

We extracted DNA from feathers using a DNeasy Tissue Kit (Qiagen, Hilden, Germany) as previously described (Vázquez et al. 2012). DNA from faeces was extracted with the Qiaamp DNA tool kit (Qiagen, Hilden, Germany) according to the manufacturer's instructions, as described in (Pérez et al. 2011). All DNA extractions were carried out in a separate room used exclusively for processing samples of this type. We used 14 microsatellites and a sex-specific gene as described in Pérez et al. (2011) plus two additional microsatellites, BG4 and BG14 (Piertney and Höglund 2001) to give a total of 16 microsatellites for genetic individualization. Amplifications were performed on a GeneAmp PCR 9600 (Applied Biosystems). All the PCR reactions included a positive and a negative control. Fluorescently labelled PCR products were visualized on an ABI3130 analyzer (Applied Biosystems). We examined microsatellite patterns both visually and using the software GENESCAN ANALYSIS 3.1 (Applied Biosystems). A second experienced genotyper scored at least 20% of microsatellite genotypes, as recommended (Morin et al. 2010). Four PCRs resulting in an amplification product were first analysed, a consensus genotype was assigned using the software GIMLET v.1.3.2 (Valière 2002), and its reliability was tested using the software RELIOTYPE (Miller et al. 2002).

If we found a multilocus genotype with reliability lower than 95%, more repetitions were carried out until achieving that level of reliability and a new consensus genotype was assigned with GIMLET. We discarded samples that could not be reliably typed for at least 13 of the 16 microsatellite markers after the entire process was completed. We inferred individuals empirically from the mismatch distribution of pairs of genotypes obtained with the software GENALEX 6.4 (Peakall and Smouse 2006), as has been described (Vázquez et al. 2012). We computed the probability of identity of the multilocus genotypes for unrelated individuals (P_{ID}), and of identity among siblings (P_{ID-Sib}) with GENALEX 6.4 (Peakall and Smouse 2006). In addition, we computed the minimum P_{ID} and P_{ID-Sib} for genotypes with only 13 microsatellites by combining the probabilities of the 13 markers with the larger probabilities of identity by locus. We estimated diversity, mean number of alleles and mean effective number of alleles with GENALEX 6.4. Global test for heterozygote deficiency and pairwise test for LD were performed with GENEPOP 4.2 (Raymond and Rousset 1995) using the Fisher method.

Census size (N_C) estimates

Population size estimates were performed using several rarefaction indices and CMR estimators. The sampling scheme included recaptures within the same day and location and was considered both in Recapture and in CAPWIRE. Nonetheless, the resampling in the same session and at the same location actually contained multiple replicate observations of the same animal and falsely increases precision (Harris et al. 2010). In order to limit resampling of the same individual at the same location and session, calculations to infer the census were made after condensing replicate observations of the same animal into one capture event. The minimum distance between two samples from the same bird to be considered two captures was set after analysing the frequency distribution of the distances between samples of the same animal (Figure 2). In fact, most recaptures of the same individual in the same day were within a distance of 20 m and were considered resampling of the same capture event. Detection of the same individual more than 20 m apart was considered as recapture in the abundance analysis. Estimates of N_C from the whole set of samples were also obtained to check for the effect of resampling over the estimates.



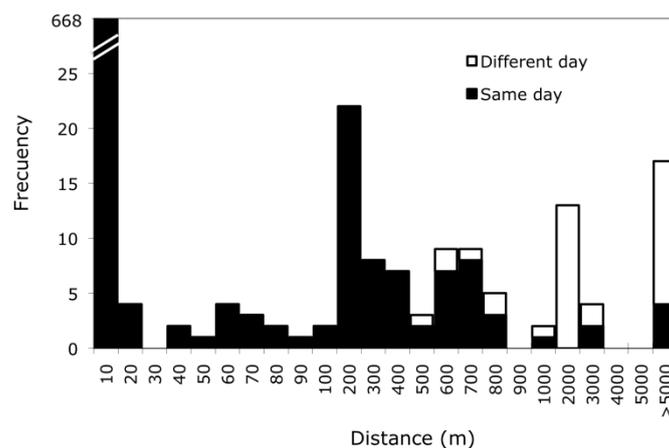


Figure 2. Distances between different captures of the same individual. If lower than 20 m they were considered as resampling and condensed in one capture event, if higher, they were considered recaptures.

Rarefaction indices

We employed the three methods (Chessel, Eggert and Kohn) implemented in GIMLET (Valière 2002) to calculate the population size through rarefaction approaches. Data were analyzed in the software R (version 1.6.2) using the script file (small program) wrote by GIMLET, with 1000 random iterations of the genotype sampling order. We calculated the 95% confidence intervals (CI) for each estimate from the 1000 random iterations.

CMR estimators

Estimates of population size from capture-mark-recapture-based methods were obtained manually using the traditional formulae of Lincoln-Peterson and with two software packages based on individual capture histories, Rcapture (Baillargeon and Rivest 2007) and CAPWIRE (Miller et al. 2005). In every case we used closed population models, that is, the population size is assumed to be constant throughout the experiment. First, we used the traditional CMR method of Lincoln-Peterson considering the spring sample as the marked individuals and the summer sample as the second sampling session where marked individuals can be recaptured. We applied the modification of Bailey (Bailey 1951), appropriate when the number of marked individuals to be recaptured is not decided prior to recapturing. The equation to estimate the population size N is: $N = M(n+1)/(m+1)$ where M is the number of animals marked (in our case number of individuals identified in spring), n is the sampling size and m the number of individuals recaptured. The standard error (SE) of the estimate was computed as $SE = [M^2(n+1)(n-m)/(m+1)^2(m+2)]^{0.5}$. For the other census estimates, with the software Rcapture and CAPWIRE, data were treated as multiple observations within a single session. In Rcapture we used the function closedp0 which fits five loglinear models: M0, Mh Chao, Mh Poisson2, Mh Darroch and Mh Gamma3.5, from the distribution of the number of specimens captured i times. The number of capture sessions (t) was set to infinite as appropriate when dealing with repeated captures within the same session. The model M0 does not consider heterogeneity in capture probability while heterogeneity is incorporated in the other four models. The several models were fitted and compared based on the Akaike Information Criterion (AIC). Confidence intervals were obtained using a profile log-likelihood with closedpCI.0. In addition, we calculated the population size with a CMR-based program specially designed to work with non-invasive genetic sampling, CAPWIRE (Miller et al. 2005). The program appears to work well, especially for small populations (<100 individuals). The likelihood ratio test (with $P < 0.1$) was used to choose between the even capture probability model (ECM) and the two innate rates model (TIRM).

Effective size (N_e) estimates

We compared two one-sample estimators, (1) the LD- N_e estimator (Waples and Do 2008), and (2) the Bayesian method implemented in ONeSAMP (Tallmon et al. 2008). Both methods rely on the assumption that the markers are not subject to selection. In a previous study (Vázquez et al. 2012) we have shown a large excess of heterozygotes for TUD7 that was explained by overdominant selection of linked genes. Therefore the microsatellite marker TUD7 was excluded from the analysis of N_e . Also the markers are supposed to be unlinked; although there are no data on map location, these markers have been used in



numerous studies and found to be in linkage equilibrium (Segelbacher 2002; Segelbacher and Storch 2002; Segelbacher et al. 2008). The methods also assume non-overlapping generations; when individuals in the sample belong to several generations, the estimates relate more to the number of effective breeders (N_b) than to N_e but it was found that, although the relations between N_b and N_e can be complex, N_b is in many cases a useful comparable measure (Waples 2005). The assumption of population closure can be reasonably met in our study and it was argued that the estimation of N_e from one generation is generally free of the assumption that populations are closed (Beebee et al. 2009). The estimator LD- N_e is highly sensitive to population fragmentation and has been proposed as an indicator of this (England et al. 2010). For LD- N_e we obtained separated N_e estimates after excluding alleles with frequencies less than three different critical values 0.05, 0.02 and 0.01. Confidence intervals were computed using the jackknife option. To estimate N_e with ONeSAMP, the marker TUD6 had to be excluded after there were too many missing data. Two estimates of N_e were obtained with ONeSAMP using different priors on lower and upper limits. We used either 2-200 or 2-500 as lower and upper limits, respectively.

Results

Genetic identification

We collected and genotyped 362 samples taken across the Cantabrian capercaillie range. From them, only the 253 samples (199 feathers and 54 faeces) rendering reliable multilocus genotypes for at least 13 microsatellite markers were retained for further analysis. The mean number of markers (including sex) successfully typed in those samples was 16.10. Different multilocus genotypes differed for a minimum of 4 markers with a mean of 10.21 mismatches between pairs. From the 253 positive samples, we identified 97 individuals, 41 from the spring samples and 61 from the summer samples, 5 of them were sampled in the two sampling periods (Table 1).

Table 1. Summary of the number of samples genotyped and the number of specimens identified from them.

	Spring				Summer				Total			
	M	F	?	Tot	M	F	?	Tot	M	F	?	Tot
Total samples	31	23	4	58	142	50	3	195	173	73	7	253
Resampling condensed	26	18	4	48	66	34	3	103	92	52	7	151
IDs	20	17	4	41	37	21	3	61	53	37	7	97
Nsamples/ID	1.55	1.35	1.00	1.41	3.84	2.38	1.00	3.20	3.26	1.97	1.00	2.61
Ncaptures/ID	1.30	1.06	1.00	1.17	1.78	1.62	1.00	1.69	1.74	1.40	1.00	1.56

Resampling condensed: samples from a given individual in the same day and location were condensed into one unique capture event; IDs: number of unique specimens; Nsamples/ID: mean number of observations per individual; M: males; F: females; ?: sex undetermined; Ncaptures/ID: mean number of captures per individual

Identical genotypes were always found within a diameter of 7 Km. We have determined the sex in all but 7 of the samples, 173 samples were from 53 males and 73 samples were taken from 37 females. The number of observations per individual ranged from one to 22 in males and from one to 7 in females. The theoretical probabilities of identity (P_{ID}), and of identity among siblings (P_{ID-Sib}) for the 16 microsatellite genotypes were $P_{ID}=2.3E-11$ and $P_{ID-Sib}=2.0E-5$. The corresponding values for the 13 microsatellites with the lowest individualization power were $P_{ID(13)}=2.4E-8$ and $P_{ID-Sib(13)}=3.1E-4$, respectively. The locus TUD7 showed a high excess of heterozygotes over the expected ($P<0.0001$). Expected and observed heterozygosities for the remaining 15 microsatellites were 0.59 and 0.49, respectively ($P<0.0001$). Average number of alleles was 4.80 (SE=0.51) and average number of effective alleles was 2.67 (SE=0.21). Pairwise LD tests were significant ($\alpha=0.05$) for 37 pairs before Holm-Bonferroni correction and for only six pairs after Holm-Bonferroni correction.

Census (N_C) and effective size (N_e) estimates

The census estimates were based on a dataset consisting of 151 samples (Table 1) after condensing recaptures within day and location into a single capture event. The classical Lincoln-Peterson estimate of total census was calculated using the 41 individuals identified in spring as marked sample (M), from which 5 were recaptured (m) among the 61 specimens identified in the summer sample (n) (see the Table 1). For males, these values were $M=20$, $n=37$ and $m=4$, and for females, the corresponding values were



M=17, n=21 and m=1. The other 10 estimates were calculated from the individual capture histories presented in Figure 3.

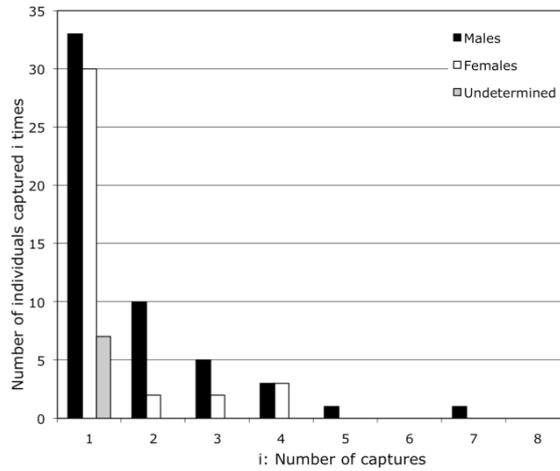


Figure 3. Individual capture histories after discarding resampling in the same day and location.

The different methods and models yield quite different N_C estimates, which ranged between 147 and 557 specimens (Figure 4 and Table 2a). Heterogeneity in the probability of capture was detected using the likelihood ratio test implemented in the program CAPWIRE ($p < 0.0001$). In a similar way, among the models fitted in Rcapture, M0 (which does not include heterogeneity) is the worst possible

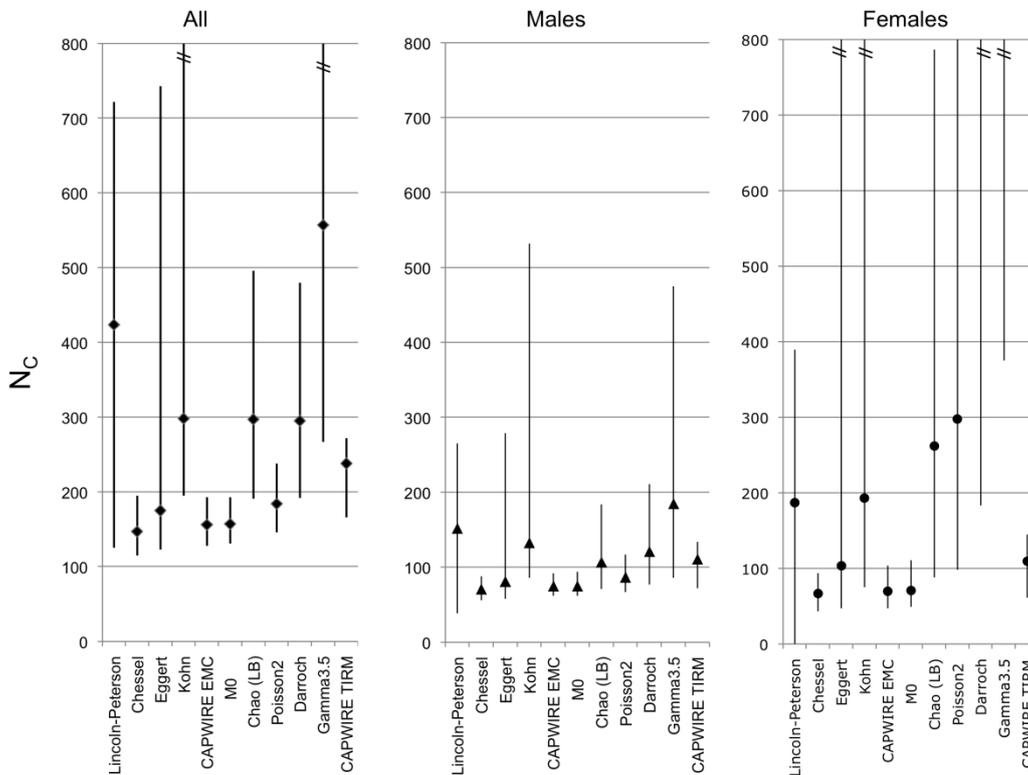


Figure 4. Census size estimates ($N_C \pm 95\% CI$) based on different models.



Table 2. Estimates of animal abundance.

a) All

Models	Estimators	Estimates (N_c)	SE	CI95% lower	CI95% upper	deviance	df	AIC
Classical	Lincoln-Peterson	424	152	125	722			
GIMLET	Chessel	147	9.55	115	195			
	Eggert	175	36.15	123	743			
	Kohn	298	72.31	195	1412			
R-Capture	M0	157	15.5	131	193	27.01	5	52.97
	Mh Chao	297	71.6	191	496	2.30	3	32.19
	Mh Poisson2	184	23.0	146	239	15.23	4	43.12
	Mh Darroch	295	69.1	192	480	9.03	4	36.92
	Mh Gamma	557	221.5	267	1257	6.84	4	34.73
						Lambda	TRV $p(\text{Lambda})$	
CAPWIRE	ECM	156		128	193	44.21		0.000
	TIRM	238		166	272			

b) Males

Models	Estimators	Estimates (N_c)	SE	CI95% lower	CI95% upper	deviance	df	AIC
Classical	Lincoln-Peterson	152	57.83	39	265			
GIMLET	Chessel	71	4.98	56	88			
	Eggert	81	15.84	58	279			
	Kohn	133	32.13	86	532			
R-Capture	M0	75	8.0	62	94	11.77	5	35.76
	Mh Chao	107	26.7	71	184	0.70	2	30.67
	Mh Poisson2	87	12.2	67	117	3.75	4	29.71
	Mh Darroch	121	31.4	77	211	2.93	4	28.43
	Mh Gamma	185	82.3	86	475	2.32	4	28.29
						Lambda	TRV $p(\text{Lambda})$	
CAPWIRE	ECM	75		62	92	24.02		0.002
	TIRM	109		69	132			

c) Females

Models	Estimators	Estimates (N_c)	SE	CI95% lower	CI95% upper	deviance	df	AIC
Classical	Lincoln-Peterson	187	102.94	-	389			
GIMLET	Chessel	67	8.26	44	93			
	Eggert	104	144.02	48	3013			
	Kohn	193	326.75	76	6006			
R-Capture	M0	71	14.5	50	110		2	33.42
	Mh Chao	262	179.7	89	>786		0	21.46
	Mh Poisson2	298	195.1	99	>895		1	20.94
	Mh Darroch	1245	1374.5	184	>3736		1	20.07
	Mh Gamma	5911	9228.8	376	>17734		1	19.79
						Lambda	TRV $p(\text{Lambda})$	
CAPWIRE	ECM	70		48	103	16.14		0.000
	TIRM	110		62	144			



model following AIC. Most census estimates are larger than 100, a situation in which performance of CAPWIRE shorts down (Miller et al. 2005), hence models in Rcapture might be more appropriate for this population. Among the models that include heterogeneity, Mh Chao has the lower AIC and hence seems adequate to fit the data. The abundance estimate yielded by this model is 297 birds (CI95%: 191-496). Population sizes were also estimated for subsets of samples of different sex, 91 male samples and 52 female samples (Figure 4b and c). Again the models including heterogeneity fit the data better (Table 2b and c). Gamma is the model with the lower AIC, both in males and females. However, the estimates from this model largely depart from the other estimates and have extraordinarily large confidence intervals that make them uninformative. In addition, the Gamma model usually yields up-biased population census estimates with small AICs (Baillargeon and Rivest 2007) and was discarded. Among the other models that include heterogeneity in capture probability, we do not have a clearly superior model, therefore we followed the Mh Chao model for congruence with the overall estimate, taking into account its good performance when capture probabilities are low (Chao 1989) and following the recommendation of Rivest and Baillargeon (2007) that the Chao's estimator provides a lower bound when the specific assumptions of the models are untestable. The estimated numbers of males and females were 107 (CI 95%: 71-184) and 262 (CI 95%: 89->786) respectively.

The complete dataset of 253 reliably genotyped samples (including recaptures in the same day and location) was analysed with models that include heterogeneity to evaluate their performance in correcting differences in catchability (see Supplementary Material). In general, the estimates are lower than if resampling is excluded but the Chao estimator yielded a census of 318, quite close to the former estimate.

Estimates of N_e depended largely on the method (Figure 5) and to a much lower extent on the user-defined conditions to run the software. The LD- N_e method yielded an $N_e = 17$ (CI95%: 13-22) when alleles at a frequency <5% are excluded from the analysis, as recommended to avoid estimates biased upwards (Waples and Do 2010). The estimate obtained from ONeSAMP depended to some extent on the priors on N_e . Using an upper limit of 200, which seems appropriate after the N_c obtained before, the software yields a N_e of 80 (CI95%: 60-148).

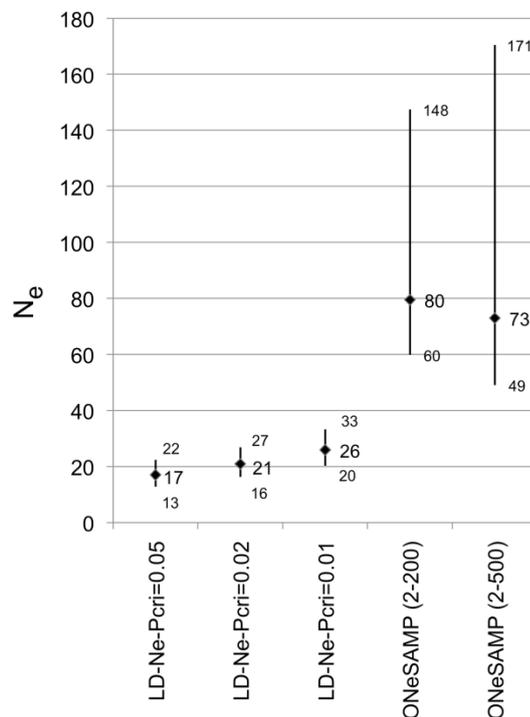


Figure 5. Effective population estimates (N_e) based on the LD- N_e and ONeSAMP methods (estimate \pm 95% CI).



Discussion

Non-invasive sampling provides a reliable method to obtain estimates of N_C and N_e in elusive animals. One of the most important drawbacks of the method comes from its sensitivity to genotyping errors (McKelvey and Schwartz 2004). We have established a strict protocol based on the use of a relatively high number of markers and the comparison of genotype mismatching to get unambiguous identification.

The number of unique multilocus genotypes is 97 and provides the minimum number of specimens in the population. Estimates of the putative number of animals in the population can be obtained from the observed recaptures of individuals. We used different methods to estimate the population size under the assumption of closure of the population, that is, the size of the population remains constant during the experiment. This implies that the population is geographically isolated (no immigration occurs), an assumption that is met in this case, and that there are no demographic changes over the time period of interest. Demographic closure is not totally met since samples were taken from April to September. New-born chicks could be sampled during the summer but this error must be minimal because feathers and faeces of chicks are readily distinguished from adult ones. Some deaths could occur during this period and this would produce a reduction in the probability of capture and hence an upwards bias in the estimate of census. Methods employed included rarefaction (Chessel, Eggert and Kohn), the classical CMR method of Lincoln-Peterson using two sampling sessions, and CMR models based on the histogram of individual capture histories from which the frequency of the class with frequency zero (individuals that haven't been observed) is estimated. Within those CMR methods based on individual capture histories, the models that include capture heterogeneity (Chao, Poisson, Darroch and Gamma in Rcapture and TIRM in CAPWIRE) were superior to the simpler models (M0 in Rcapture and ECM in CAPWIRE), which assume that detection probabilities are uniform. Differences in the estimates from the different methods are remarkable and seem characteristic of each model. Thus, the equation of Chessel, that gives the lower estimate in our data, was shown to give lower estimates than the equation of Kohn in simulated data (Valière 2002), while the Gamma estimator yielded the larger estimate, as it usually does (Baillargeon and Rivest 2007). Capwire estimator does not perform well when N grows substantially above 100; in this case, the Chao estimator was shown to be superior (Miller et al. 2005). From our data, Chao seems to be the more robust model when we consider the congruence between the three estimates, global males and females. In addition, from the analysis of the complete dataset, including resampling in the same day and location, the Chao estimator seems to correct for large differences in probability of capture. The estimate yielded by the classical estimator of Lincoln-Petersen is the largest one apart from Gamma. In fact the two samples used to get the estimate can correspond to different fragments of the population and this would lead to an estimate biased upwards. Therefore, the values obtained with the very different estimators are consistent with one another and provide support to the data.

The reliability of estimates of abundance depends on the capability of models to correct for heterogeneity of capture and for the biases introduced by the sampling strategy. Heterogeneity or differences in the probability of detection can arise from individual variation, kind of sample, spatial and temporal variation or uneven distribution of sampling effort (Agresti 1994; Rivest and Baillargeon 2007). In our study, samples are more or less evenly distributed from west to east of the population but it can be noticed that the southern slope is underrepresented, with only 26 of the 150 or 17.3% of the samples included in the census analysis, while the occupied leks in 2005 represented the 38.6% of the population (Ballesteros et al. 2005). Although differences in sampling effort are corrected by the models, probably this causes our census estimates to be slightly down biased. Following the guidelines presented by Marucco et al. (2011), it is advisable for future estimation of census to homogenize the sampling effort among all the area of distribution and to increase the sampling occasions to increase the number of recaptures.

Abundance estimates based on direct observations of lek occupation showed a dramatic decrease over the last decades (Pollo et al. 2003). The 1981-1982 census estimated 582 males (Del Campo and García-Gaona 1983) while 280-300 males were estimated in 1998 (Pollo et al. 2003). In the present study, all the estimates of male abundance are lower than that figure. This is remarkable bearing in mind that, following a study of capercaillie in the Swiss Alps, field surveys underestimated local abundance (Jacob et al. 2010). Our global estimate of 297 birds for 2006, points to the continued decline of the population since the last traditional census of about 500 birds in 2000-2003 (Pollo et al. 2003; Storch et al. 2006).

Sex ratio is an important demographic parameter. In spite of the fact that the number of male samples was larger than the number of female samples, the estimated census of females out-exceeded the census of males, even though there was a CI overlap. This result must be taken with caution because the sampling is based on lekking areas of males, which makes it possible that territoriality and the homing behaviour of males (Storch 1997) artifactually increases their capture likelihood. With these limitations in mind, it can be noted that a sex-ratio deviation in favour of females has been reported in a study in



Sweden and was related with increased mortality of the larger sex when breeding success was low (Helle et al. 1999; Homfeldt et al. 2001).

Besides census size, estimating N_e is of prime importance to evaluate the conservation risk of wild populations, because it determines the rate of inbreeding and the strength of genetic drift (Crow and Kimura 1970). The two estimators of N_e gave largely different results, the LD- N_e method yielded a very low estimate of effective size, $N_e = 17$, compared to the value of $N_e = 80$ yielded by ONeSAMP. This difference must be related to the methods resting on different assumptions or being differently affected by them. Both methods assume non-overlapping generations. Violation of this assumption leads to an estimate that is not properly the N_e but is closer to the effective number of breeders that, in general, is lower than N_e (Wang 2009). ONeSAMP has been shown to be quite resistant to violation of the assumption of discrete generations (Skrbinek et al. 2012).

Even more relevant is that the LD- N_e estimates are highly susceptible to bias because of processes other than small N_e , such as a recent bottleneck, substructure and local inbreeding (England et al. 2010; Waples and Do 2010). On this basis, LDNe has been proposed as an indicator of population fragmentation although its utility relies upon the ability to have reasonable expectations that the former population was large and interconnected (England et al. 2010). The same authors pose the question that if highly divergent demes are mistakenly pooled, estimates could be biased down due to excessive mixture LD. Accordingly, the point here can be to ascertain whether the LD arises from fragmentation or from mixing individuals from highly divergent populations. The Cantabrian capercaillie population presented a weak structure (Vázquez et al. 2012) that could bias down the LD- N_e estimate, but the extremely low value we attained can be related to population fragmentation by the following reasons. Although formal census estimates are lacking, the population should have been quite large during the 1960s as the legal chase of more than 200 males during a five year period has been reported (Castroviejo 1975).

The data on population size presented above and the reported fragmentation of the habitat (García et al 2005), and its recent reduction of more than 50% between the early 1980s and 2001 (Quevedo et al. 2006a) all are indicative of population fragmentation. In addition, a recent bottleneck was previously inferred from the comparison of the heterozygosity to the number of alleles (Vázquez et al. 2012). The ONeSAMP estimator has not been evaluated as an indicator of fragmentation (England et al. 2010) but it can be noted that the estimate from LD- N_e relies on the breeders of one generation while Ne-ONeSAMP reflects population events further back (Skrbinek et al 2012), which possibly makes it more robust to recent population fragmentation. Our work suggests that the comparison of these two estimators can provide insight into population fragmentation. The Bayesian approach implemented in ONeSAMP has the greatest potential to provide improved accuracy in N_e estimation because it is based on eight summary statistics (Tallmon et al. 2008). Accordingly, we used the estimate obtained from this software, $N_e = 80$, to calculate the ratio $N_e/N_c = 0.27$. This ratio of effective to actual population size is lower than the average of 0.34 reported by Frankham (1995) and exceeds the estimate of 0.10 for the lekking prairie chicken (Johnson et al. 2004) and the estimate of 0.19 reported for the Gunnison sage-grouse (Stiver et al. 2008). However, comparisons are difficult because of differences among N_e estimators (Luikart et al. 2010).

It was suggested that the minimum effective size for a population to be viable in the short term should be 50 and that number should be between 500 and 5000 when considering the long term protection of adaptive potential (Frankham et al. 2010). Though low, the N_e of the Cantabrian capercaillie population as a whole is not extremely small considering the numbers above. However, the main problem of the population is fragmentation with very low gene flow among patches. This observation relates to the fragmentation of the habitat into patches that are loosely connected (Pollo et al. 2003; García et al. 2005; Bañuelos et al. 2008). Subdivision of the population into small, non-interconnected nuclei would lead to demographic stochasticity, inbreeding and drift at local level which, in turn, contribute to further fragmentation. The evidence of inbreeding depression in the wild is compelling and is a factor of prime importance for the population viability (Frankham 2010). Inbreeding is especially relevant in birds where hatching failure rates were found to increase with genetic similarity of parents (Spottiswoode and Moller 2004; Heber and Briskie 2010). Taking into account the small home range of capercaillie (Storch 1997), the creation of a dense network of suitable patches of habitat is priority to avoid isolation between them.

Conclusions

The results of this study show the effects of habitat loss and fragmentation on the population of Cantabrian capercaillie. The census estimate, 297 birds, confirms the observation based on traditional estimates that the animal abundance is lower than 500 birds, and its decreasing trend. The effective size, the relevant parameter to predict the rate of inbreeding and random loss of genetic variation, is around 80 individuals. The major threat to the population is fragmentation in isolated nuclei, which will produce local inbreeding and local drift, two main factors in the extinction vortex (Brook et al. 2002).



Conservation measures should focus on the protection of local demes and the interconnection of suitable patches to maximize gene flow between them and reduce local inbreeding, drift and demographic stochasticity.

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Supplementary material

Estimates from models correcting heterogeneity of capture based on the complete set of 253 samples

a) Total

Models	Estimators	Estimates (N _c)	SE	CI95% lower	CI95% upper	deviance	df	AIC
R-Capture	Mh Chao	318	93.3	212	611	16.97	16	64.55
	Mh Poisson2	110	4.6	102	120	169.143	19	210.72
	Mh Darroch	138	10.7	119	161	68.78	19	110.35
	Mh Gamma	385	76.3	264	573	5.27	19	74.71
CAPWIRE	TIRM	173		123	179			

b) Males

Models	Estimators	Estimates (N _c)	SE	CI95% lower	CI95% upper	deviance	df	AIC
R-Capture	Mh Chao	128	42.0	75	275	12.19	15	58.17
	Mh Poisson2	57	2.2	53	62	113.43	19	151.42
	Mh Darroch	68	5.9	59	82	38.84	19	76.82
	Mh Gamma	178	44.1	112	294	19.53	19	57.52
CAPWIRE	TIRM	70		56	80			

c) Females

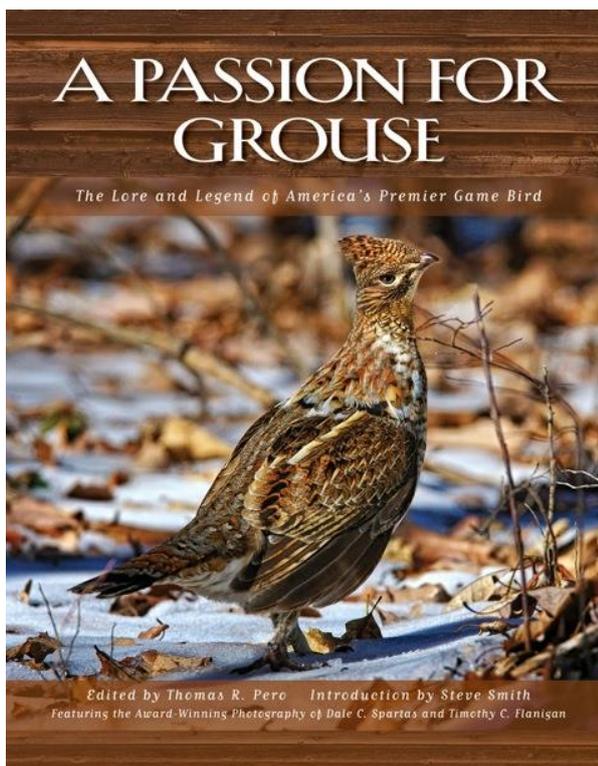
Models	Estimators	Estimates (N _c)	SE	CI95% lower	CI95% upper	deviance	df	AIC
R-Capture	Mh Chao	98	29.7	58	189	7.25	3	33.22
	Mh Poisson2	64	11.6	46	94	19.41	4	43.39
	Mh Darroch	138	54.1	69	320	11.21	4	35.18
	Mh Gamma	438	292.4	130.2	>1315	8.65	4	32.62
CAPWIRE	TIRM	76		47	97			



NEW BOOKS

A passion for grouse. New book on ruffed grouse Ralph. J. Gutiérrez

The ruffed grouse, *Bonasa umbellus*, is the most important grouse for hunting in North America. Thus, ruffed grouse hunting has been the subject of outdoor writers for well over a century because of its elusive nature and the challenge of hunting it. With such popularity, there is always discussion about its biology, the variety and training of grouse dogs, the types of guns to use, different regions to hunt, and different hunting tactics. Wild River Press will publish the largest book on ruffed grouse in recent times on hunting ruffed grouse that covers all these topics. The book, *A Passion For Grouse*, is edited by Thomas Pero (see also www.apassionforgrouse.com) and has 5 principles authors: natural history and management by R. J. Gutiérrez, grouse dogs by Ryan Frame, grouse guns by Larry Brown, and hunting chapters by Mark Parman (Great Lakes Region), Ron Ellis (Appalachian Region), Jerry Allen (New England). The book will also feature an interview with the late George King, who passed away shortly before the publication of the book. He was a legendary grouse hunter who wrote an informative and lively grouse “newsletter” about 30 years ago. Expected publication date is November 2013. Wild River Press is noted for publishing outstanding sport fishing books including the award-winning book by Andy Mill, *A Passion for Tarpon*. This will be its first bird-hunting book. It will be a large-format (approximately 28 x 22 cm) production of over 550 pages filled with hundreds of exquisite photographs and illustrations (price will be \$100 plus \$15 for shipping). Even though this is a book about a North American grouse, European grouse hunters and biologists will find many useful things in the book, especially hunting insight, choices of guns and bird dogs for grouse hunting, and of course biology. There is even a short section on grouse recipes, which will be well suited to the culinary tastes of both European and North American grouse hunters. Contact the editor, Tom Pero (tom@wildriverpress.com), for inquiries or to place an order contact www.wildriverpress.com.



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Handbook of technical considerations for management of Pyrenean capercaillie habitats

Emmanuel Ménoni

The Pyrenees are the range of less than 1/1000 of the capercaillie in the world, and about 7% of this species in Europe outside Scandinavia, but in this mountain range a subspecies (*Tetrao urogallus aquitanicus*) of this grouse very different from any other in the world is living. Also, the Pyrenees hold 90% of an Evolutionary Significant Unit of capercaillie situated in the Pyrenees and in the cordillera Cantabrique (n-w Spain). Because these mountains are at the extreme south of the world range of the species, and transformed by man since Neolithic age, the ecological conditions are quite different than in northern latitude. Finally, without Black grouse in sympatry for thousands of years, the capercaillie



enlarged his ecological nest, using both typical habitats, but also habitats looking very suitable for Black grouse.

The Pyrenees are situated in 3 countries-(France-Spain-Andorra), and the Spanish side is divided in 3 autonomic regions-(Catalonia-Aragon-Navarra), with quite different cultures and land uses. Typically there is a south side very dry, under Mediterranean influence, and a north side very wet, under oceanic climate.

For all these reasons, the existing guidelines for eastern French population of capercaillie and for other countries in central Europe are far not sufficient, and unable to face at all the diversity of ecological situations encountered in the Pyrenees, and we needed a specific tool, recognized by the managers and foresters of any Pyrenean country or regions.

It's the reason why writing this handbook was an important part of the "Gallipyr" project, supported by European Union from 2009 to 2012, gathering French, Spanish and Andorran biologists and managers in order to improve the conservation of mountain galliforms in the Pyrenees.

The introduction recalls the high Pyrenean responsibility regarding the conservation of the Pyrenean subspecies of capercaillie. It evaluates the proportion of the forests concerned by this major issue, and indicates in what state of mind it has been written. Namely, amongst usual forestry practices, we are looking for those supposed to be the best appropriate to maintain or improve the habitats suitability of that species. The handbook offers solutions for concrete situations mostly faced by foresters, and other managers, and suggests processes to reach the goal of maintaining or improving capercaillie habitats.

The first chapter is dedicated to the biology and ecology of the capercaillie. This chapter focuses on relationships between species and its habitats, and on the Pyrenean particularities of these relationships. The most typical situations of capercaillie habitats layout along the slopes of the valleys are showed as diagrams, according to the different bioclimatic zones existing in the Pyrenees.

The second chapter shows a method of diagnostic of habitat suitability for capercaillie at three different scales: landscape, forest and stand, in order to give tools for management at each level of Pyrenean natural habitats. Thus, the needs of this species could be considered both in regional decisions and forest planning, but also during tree marking, forestry works, and other land uses as farming. This method of diagnostic is based on biotic and abiotic local conditions, and takes into account the present and past status (10-30 years) of the capercaillie at different spatial scales.

The third chapter shows the good practices regarding forest management favourable for capercaillie according to three different potential levels belonging whether to the plot or to the forest (first: unsuitable forest for permanent life, but with possible crossing, second: area situated in the current recent range but outside vital areas (leks, wintering zones, nest and brood habitats), and third: vital areas.) According to these levels, a work schedule is set up.

Then, after establishing a list of the essential principles in forestry practices for conservation of good life conditions, the handbook offers:

- technical solutions for capercaillie conservation in current Pyrenean situations;
- silvicultural processes for most of the forest types we can find in the Pyrenees, both in north and south side of this mountain;
- practical/technical proposals for delicate and very concrete situations foresters use to face.

These technical solutions are shown as commented diagrams, and are both based on foresters' experiences on the field, or forest experiments old enough to be able to give a good understanding on silvigenetic processes.

Ménoni, E., Favre-Ayala, V., Cantegrel, R., Revenga, J., Camprodon, J., Garcia, D., Campion, D. Afonso, I. et Riba, L. 2012. Réflexion technique pour la prise en compte du Grand tétras dans la gestion forestière pyrénéenne. - FORESPIR, Union Européenne, DREAL-Midi-Pyrénées. Pau.

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CONFERENCES

International wildlife professionals meet at Brussels' 2013 IUGB Congress

Yves Lecocq

The 31st biennial Congress of the *International Union of Game Biologists* (IUGB), which took place during 28-30 August 2013 under the headline '*Diversity in Wildlife Management – Objectives & Tools*', brought together more than 300 participants from 34 countries and four Continents in the European capital of Brussels, Belgium. Set up in Germany in 1954, IUGB has positioned itself as a key international player promoting rational wildlife conservation and management. Operating as a flexible structure, IUGB provides a unique platform for discussion and the exchange of ideas for biologists, foresters, veterinarians, game managers, sociologists, rural economists, hunters and others, all sharing a professional or academic interest in the biology, management and sustainable use of game, other wild species and their habitats.

The 2013 Congress headline was addressed in a wide range of quality presentations including 6 Keynote speeches, 84 oral papers and 118 posters given during 5 Plenary, 17 Parallel and 7 Thematic Sessions. This breadth reflects the diversity in which world-wide, professionals and volunteers are managing wildlife species and habitats, for a wide range of objectives and using a variety of tools and techniques.

From these presentations and perhaps even more from the related discussions and exchanges of views (also the informal ones during the breaks, side-events and excursions), a number of issues stood out.

As far as applied methodologies are concerned, consensus developed among participants that straightforward counting and monitoring of wildlife may no longer be sufficient. Clear management aims and objectives need to be set at the start, with the emphasis not only on the game species and habitats, but also the whole ecosystem and wider environment.

Following on from this concept of adaptive management, increasing attention was devoted to molecular biology techniques and genetic research for wildlife management and conservation programmes.

Other aspects covered more extensively at the 2013 IUGB Congress included the human and socio-economic dimensions of wildlife management, which is indeed not only about wild species, but increasingly about people and their interactions. Stakeholder involvement and participatory management were identified as key themes for future research.

The need for more research is also apparent for the issue of *Invasive Alien Species*, their impact on wildlife management and many other aspects of society. It is likely that this topic will receive even greater attention at future IUGB Congresses.

The new topical issue of research into wildlife welfare and its practical applications in the management of wild species was addressed for the first time at an IUGB Congress, both in a Plenary session and in a Thematic workshop.

Other Thematic workshops included the management of large carnivores in the EU, the environmental impact of the Common Agriculture Policy, the role of sustainable trapping in wildlife management and how to deal with "urban" wild boar; also the use of GPS technology in wildlife research and the management of migratory waterbirds (the latter with the reconstitution of the *Waterbird Harvest Specialist Group* within *Wetlands International*).

A number of other topical environmental issues, such as climate change and ecosystem services were less prominent at this Congress – perhaps because they are underestimated by wildlife professionals, or on the contrary considered as already integral to their work? The future will tell.

Download the Congress Programme and Abstract Book at:

http://www.iugb2013.org/docs/AbstractBookIUGB2013_Full%20Final.pdf.

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The 32nd Congress of the International Union of Game Biologists 2015

The next IUGB Congress will take place in August 2015 in Puebla, Mexico, the new Presidency being conferred on Professor Daniel Jimenez-Garcia who took over from outgoing IUGB President Dr Yves Lecocq. Historically and culturally, IUGB has focused primarily on Europe, but there was a good North American participation in Brussels, with two out of six keynote presentations, including that of Dr Wini Kessler, President of *The Wildlife Society* (TWS) at the Opening session. It became obvious that there are indeed many similarities between Europe and North America in the domains of wildlife management and research, and closer cooperation between IUGB and TWS can only be beneficial. Therefore the geographical shift for the 2015 Congress to the Americas can only serve to foster future cooperation on a more global scale, including participation from countries in the southern hemisphere; this will certainly be the case for the 2017 Congress which the French ONCFS wildlife agency has offered to host.

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The 7th International Black Grouse Conference

The 7th International Black Grouse Conference will be organized in Pechoro-Ilychskiy Nature Biosphere Reserve, Komi Republic, Russia, at 24-28.05.2014. We hope that the conference will be a great opportunity to discuss the present situation of the black grouse in Europe, and further initiatives concerning the protection of this fine species and its habitats. Organizers: Pechoro-Ylych reserve, Institute of Biology, Komi Science Centre, Russian Academy of Sciences and Helsinki University. The first circular will be sent before 01.12.2013.

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RECENT GROUSE LITERATURE

For a complete bibliography on grouse, go to: <http://www.suttoncenter.org/pages/publications> (please note that the link in previous editions may not be current).

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SNIPPETS

Old Cantabrian Capercaillie film saved from extinction...

In the early 80's of the last century the University of León (Spain) was in charge of the first radio-tracking study to inquire into the unknown Cantabrian Capercaillie ecology. At that time the team research led by Dr. Vicente Ena trapped and radio-tracked the first Cantabrian capercaillie male in the eastern distribution of the subspecies. Dr. Ena took advantage of the project and prosperous situation (University support and a healthy Capercaillie nucleus) in order to film wild Cantabrian Capercaillie during the display season. He recorded images both in beech *Fagus sylvatica* forests of the eastern part of the Cantabrian range (Picos de Europa National Park) but also in the birch *Betula pubescens* forests of the western distribution of the range (Omaña county). These images were recorded in Super 8 film and never published although they are even now the only long live recording of wild Cantabrian Capercaillie.

After 30 years these images have been recovered, digitalized and published thanks to a documentary and eco-tourism company (www.morethanbirds.es). In its web you can watch the film split into two parts. The images in a beech lek involve a high documentary value as that lek held the highest number of Cantabrian capercaillie displaying ever registered (up to 20 males). Although eco-tourism with Cantabrian capercaillie is not feasible due to its critical situation, with these images grouse researchers and nature enthusiasts will enjoy of this fascinating species in the Cantabrian Mountains. Link: http://www.morethanbirds.es/?page_id=44

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Jan Van Haaften Wildlife Management Award, a new honour bestowed by IUGB

A highlight in the Closing session of the Congress was the launch of the *Jan Van Haaften Wildlife Management Award*, a new honour bestowed by IUGB for distinguished service to applied wildlife research in Europe. It commemorates Professor Jan L. Van Haaften (1928 – 2012) from the Netherlands, a longstanding IUGB supporter who advocated the wise use of wildlife resources and scientific research to improve understanding of wild species and their management.

It was Professor Ilse Storch (University of Freiburg), who, on behalf of the judging panel, presented the Award – a superb bronze sculpture of a roebuck, created by Dutch wildlife artist Pieter Verstappen – to Professor Harto Lindén from Finland. With an impressive professional career of almost four decades at the *Finnish Game and Fisheries Research Institute*, Harto Lindén has performed research on a wide range of species, from voles to large carnivores, and in particular on grouse. He also developed the Finnish “wildlife triangle census” scheme, often described as the best game monitoring scheme in Europe. Professor Lindén has been teaching in several Nordic countries, organised and chaired the 8th International Grouse Symposium (Rovaniemi, 1999) and was inter alia founding Editor-in-chief of the leading “*Wildlife Biology*” magazine as well as President of the *Finnish Ornithological Society*. Last but not least, he was IUGB Liaison Officer for Finland from 1987 until 2007.



Bronze sculpture made by Pieter Verstappen, Wildlife Art, Kanaaldijk 3, 5768 Re Meijel, Netherlands. info@pieterverstappen.com.

Yves Lecocq, Past President 2011-2013, International Union of Game Biologists (IUGB), c/o FACE, Rue F Pelletier, 82, B1030 Brussels, ylecocq@face.eu.



Wildlife Professor Honored for Lifetime Achievement

MOSCOW, Idaho – Nov. 1, 2013 – Kerry Paul Reese, longtime professor of wildlife sciences in the College of Natural Resources, was honored this month for his lifetime achievement in wildlife management and his leadership in research. Reese was named a Fellow of The Wildlife Society (TWS) at its annual conference in Milwaukee, Wisconsin. Internationally, 10 professionals were inducted as fellows.

Reese's work on sage and sharp-tailed grouse has had many implications for wildlife managers and has guided management efforts on these species in four states. His work on grouse habitat has provided vital information on what constitutes quality habitat for these species. Reese has supervised more than 40 graduate students — including five doctoral candidates — that conducted fieldwork on prairie grouse and other wildlife species. He serves as department head of fish and wildlife sciences.

He has served as a consultant on several sage grouse issues/projects and on state and national expert panels to assess risks of extinction for greater sage-grouse. Reese has also been extremely effective at placing research into a management context, both with publications and leadership on specific management issues.

A TWS member for 39 years, he has been active on many committees at all levels and served as president of the Idaho chapter. He has received many TWS awards and co-chaired a very successful symposium on grouse conservation and management at the 2012 TWS Annual Conference.

Jodi Walker, Communications and Marketing, College of Natural Resources, jwalker@uidaho.edu

Prairie Grouse Technical Council

The 30th Biennial Prairie Grouse Technical Council meeting was held in Crookston, Minnesota, USA, 10-12 October. A huge thanks to Dan Svedarsky for organizing a wonderful and successful conference. At each meeting since 1991, one or more individual or organization that has made substantial contributions to prairie grouse conservation or research is honored with the Hamerstrom Award, named after Frederick and Fran Hamerstrom. The current recipients of the honor were Mike Schroeder, Terry Wolfe, and the G. M. Sutton Avian Research Center. Below is a list of all past Hamerstrom Award recipients:

1991 – Fran Hamerstrom

1993 – Ron Westemeier

1995 – Dan Svedarsky, and Jerry Kobriger

1998 – Robert Robel

1999 – Bill Berg

2001 – Len McDaniel

2003 – John Toepfer

2005 – Nova Silvy, and The Society of Tympanuchus Cupido Pinnatus, Ltd.

2007 – Rick Baydack, and Kerry Reese

2009 – Randy Rogers, and Bill Vodehnal

2011 – Mike Morrow, Jack Connelly, and The Minnesota Prairie Chicken Society

2013 – Mike Schroeder, Terry Wolfe, and the G. M. Sutton Avian Research Center

