Using DNA technology to monitor the movement of wildlife without invasive tracking and tagging systems



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Animal movements – a cental issue in animal ecology

Resource utilization
Territorial defense
Dispersal and migration connectivity and gene flow

 How can these issues be adressed from noninvasive genetic sampling?



1995 – MSc studies on Swayne's hartebeest – pioneering methodological work

Reindeer - MAF 46



Excrement analysis by PCR

Sig — Samples from endangered animals are hard to obtain for genetic analysis. To study a threatened bear population in the Pyreness. Taberlet and Rouver⁴ used hair collected from wire netting attached to trees on which the bears scratch themselves. We have approached the problem by the use of bear droppings, which can be collected without disturbing the animals and can be used to amplify DNA sequences not only from the animals themselves but also from the foods they have ingested. We are studying a torong the form

We are studying a population of European brown bears in the Brenta region of Northern Italy. Like the Pyrenean bears, this population is in decline and today may number less than 10 individuals. The introduction of animals from the large populations in the Balkans is contemplated. To evaluate the extent of genetic variation in the Brenta bears as well as their genetic relationship to Romanian bears, we looked at the sequence variation in mitochondrial DNA from the Italian hears Nucleic acids were extracted from excremental remains, presumed from their morphology to be of bear origin. All extracts contained large amounts of bacterial DNA

Two oligonucleotide primers were designed to span an 88-base-pair-long segment of the mitochondrial control region

a. PCB amplifications of bear mitochoadrail DNA from three droppings. Lane M, size marker (9X174 DNA digested with the resriction enzyme Healti), lanes 1–3. three droppings from the Brenta population: lanes appetchyel. Upper panel, amplification of a 144-base-pair (bp) fragment (including priment (including primers) of the chiooplast display and the Brenta population (Brenta 1, 2 and 3). Sequences are compared with the American brown bear² and a torwn bear from Komania. Droppings (0.5 g) were extract and 3). Sequences are compared with the American brown bear² and a torwn bear from Komania. Droppings (0.5 g) were exact and 3). Sequences are compared with the American brown bear² and a torwn bear from Komania. Droppings (0.5 g) were exact as display and the american brown bear from Komania. Droppings (0.5 g) were exact as display and the american brown bear from Komania. Droppings (0.5 g) were exact as display and the american brown bear from Komania. Droppings (0.5 g) were exact as display and the american brown bear from Komania. Droppings (0.5 g) were exact as display and the american brown bear from Komania. Droppings (0.5 g) were exact as display and the american brown bear from Komania. Droppings (0.5 g) were exact as display and the american brown bear from Komania. Droppings (0.5 g) were exact as display and the american brown bear from Komania. Droppings (0.5 g) were exact as display and the from Komania. Droppings (0.5 g) were exact as display and the from Komania. Droppings (0.5 g) were exact as display and the from Komania. Droppings (0.5 g) were exact as display and the from Komania. Droppings (0.5 g) were exact as display and the from Komania. Droppings (0.5 g) were exact as display and the from Komania. Droppings (0.5 g) were exact as display and the from Komania. Droppings (0.5 g) were exact as display and the from Komania. Droppings (0.5 g) were exact as display and the from Komania. Droppings (0.5 g) were exact as display and the from Komania. Droppings (0.5 g) were exact as disp

Bears

Plants

NATURE · VOL 359 · 17 SEPTEMBER 1992

representative of this genus, P. villosa, is found in the Brenta region. Conse quently, the fruits of this plant seem to which has been sequenced in the Amerbe a dominant component of the bears' ican brown bear2. Using these primers in diet during late summer when the droppings were collected. Thus the feeding the polymerase chain reaction (PCR), we were able to amplify mitochondrial behaviour of animals can be investigated DNA from three droppings (Fig. 1a). after amplification by PCR of DNA Sequences from the Brenta droppings as from their excrement. The collection of well as from a liver sample of a Romadroppings may also be a useful way to

SCIENTIFIC CORRESPONDENCE

screen large areas for the presence of rare animals. Matthias Höss

nian bear are shown in Fig. 1b. The

European bears differ at seven positions

from the American brown bear. The

three Brenta DNA samples are identical

to each other and differ at three posi-

tions from the Romanian bear sample.

Further work will clarify whether this

indicates that the Brenta population is

genetically depauperate compared with

other bear populations. Statistical analy-

sis will have to take into account that the

samples are being drawn with replace-

ment, because individual animals may be

chloroplast rbcL gene to investigate whether nucleic acids of plants ingested

by the bears can pass through the diges-

tive tract. As can be seen in Fig. 1a, all

three bear droppings produced bands.

The direct sequencing of the amplification products showed that they contain

one rbcL sequence. When this sequence

(M. W. Chase, personal communication), it turned out to be identical to

Photinia, a genus in the Rosaceae. A

M 1 2 3 4 5

M 1 2 3 4 5

was compared with 414 rbcL sequences

We also used primers specific for the

sampled several times.

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Evidence for some hot dark matter?

SIR - The recent detection of the large scale microwave background anisotropy by the cosmic background explorer (COBE) satellite is in remarkable agreement with the predictions based on an inflationary scheme in which the dark matter is a mixture of cold and hot 141 bp components. We briefly summarize how the COBE measurements, inflation, and the observed large-scale structure all seem to point to a flat Universe in which a fraction (~20-30 per cent) of the critical energy density resides in massive (~3-9 eV) relic neutrinos. A crucial test of this scheme comes from the aniso tropies expected on smaller (~1°-2°) angular scales, which are estimated to lie within reach of current and planned experiments.

A generic prediction of inflation is that the Universe contains a critical density of matter. Primordial nucleosynthesis arguments imply that <90% of this matter is nonbaryonic, but inflation does not specify what the dark matter should

be. Typically, investigators have assumed the dark matter takes one of two possible forms: cold dark matter (CDM; massive cold particles) or hot dark matter (HDM; relic light neutrinos). Although pure HDM has several well-discussed problems, models with pure CDM provide a basis for structure 199



PhD studies in Uppsala 1999-2002

Development of large-scale DNA-based monitoring of Scandinavian carnivores



(1) Sample collection in the field - scats, hair, urine, blood remains



(2) Laboratory analyses



(3) DNA profiles



DNA-based monitoring Scandinavian carnivores

DNA-profiles from the scat samples provide unique ID-codes (1=6), that can be traced back to certain individuals in the target population(s)

Yearly sample collection allow us to follow the same individuals during a period of several years

mapping⇒



- home range and territories
- reproduction
- dispersal and migration patterns
- population size and dynamics
- genetic structure; levels of isolation



Mapping territorial wolverines





Home ranges and movements





The brown bear – males travel over vast areas





Is it possible to address territorial behaviour from scat samples?



Bischof et al 2016 Ecology and Evolution 6, 1527-1536



Patterns of emigration/immigration in a managed population



2002-2013 3652 samples 619 individuals

DNA samples

+ Culled wolverines

✓ E14 highway

Compared immigration/ emigration of wolverines between Sweden and Norway





Gervasi et al. 2015 (Biological Conservation 191, 632-639)

Compensatory immigration





Inbreeding depression in the Scandinavian wolf popultion



Liberg et al 2005 Biology Letters 1, 17-20



Detection of new immigrants and other genetic important individuals is highly important in the monitoring of the population



Monitoring the reproductive success of offspring to the immigrants









Dispersal and migration patterns



Scandinavian wolves tend to disperse towards the center of the population

Move further on if they do not find a partner and/or vacant territory

Territory dynamics

Aurskog winter 19-20



Aurskog and Svarthus winter 20-21





Metapopulation dynamics in the Scandinavian arctic fox population



Photo: SNO

- Study area: 65,222 km²
- 2,667 faeces and hair samples collected in the field (2008-2015)
- 290 tissue samples fromSweden from marked pups



Patterns of genetic variation





Genetic structure and dispersal patterns

Population	2008/2009			
	Immigration rate	95% CI	Proportion admixed	
Borga	0.046	0.036-0.055	0.139	
Lierne	0.290	0.271-0.309	0.000	
Helags	0.032	0.023-0.040	0.000	
Kjøli				
Snøhetta	0.285	0.271-0.299	0.050	
Population	2014/2015			
Population	2014/2015 Immigration rate	95% CI	Proportio	n admixed
Population Borga	2014/2015 Immigration rate 0.057	95% CI 0.044-0.070	Proportio 0.218	n admixed
Population Borga Lierne	2014/2015 Immigration rate 0.057 0.149	95% CI 0.044-0.070 0.122-0.176	Proportio 0.218 0.143	n admixed
Population Borga Lierne Helags	2014/2015 Immigration rate 0.057 0.149 0.067	95% CI 0.044-0.070 0.122-0.176 0.055-0.080	Proportio 0.218 0.143 0.167	n admixed
Population Borga Lierne Helags Kiøli	2014/2015 Immigration rate 0.057 0.149 0.067 0.219	95% CI 0.044-0.070 0.122-0.176 0.055-0.080 0.196-0.241	Proportio 0.218 0.143 0.167 0.050	n admixed



International projects

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Samarbeid og kunnskap for framtidas miljøløsninger

