

On the allure of noninvasive genetic sampling — putting a face to the name

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Abstract: DNA from remotely-collected samples of hair or feces provides a means of assessing attributes of populations of wild animals, including genetic diversity, spatial distribution, patterns of habitat use, dispersal distances, population fragmentation, and population size. This technique has been called noninvasive genetic sampling, a term in common usage especially in the bear literature. It has taken on the connotation of being more humane than techniques such as radiotelemetry that require capture of animals. The term noninvasive, however, is misapplied: in the biological-genetic sense, it refers only to the invasion of the body (through the skin or an orifice), not to capture or general intrusiveness. If it is construed to mean nonintrusive in a more general sense, then other methods of collecting population data that do not require animal capture, such as camera trapping, sign surveys, sightings, and interviews, should be called noninvasive as well. Moreover, once an animal is radiocollared, the process of collecting telemetry data is also noninvasive. I recommend the use of a more neutral and also more informative and technically correct term, “remote,” to describe genetic and other forms of sampling that do not involve human handling of animals. Remote sampling aids investigators in reducing their effects on the study subjects and also may provide larger samples than can be obtained by trapping. However, many of the important biological questions that can be (and for >30 years have been) studied by capturing animals and tracking them telemetrically cannot be addressed with genetic or other remote sampling techniques.

Key words: bears, camera trapping, genetic tagging, hair snaring, noninvasive sampling, population estimation, radiotelemetry, remote sampling, sign surveys

Ursus 17(2):109–123 (2006)

Every scientific discipline has specific and unique terminology, developed as a shortcut for scientific writing. An oft-encountered problem, however, is that such terminology is poorly defined, inconsistently applied, or the meaning changes over time. In the ecological literature, well trodden terms such as biodiversity (Hamilton 2005), carrying capacity (MacNab 1985), community (Fauth et al. 1996), habitat (Garshelis 2000), home range (Powell 2000), invasive species (Colautti and MacIsaac 2004), keystone species (Mills et al. 1993), population (Wells and Richmond 1995), stability (Grimm and Wissel 1997), and sustainability (Newton and Freyfogle 2005) have acquired multiple and sometimes confusing usages. Meanings of ecological terms also may vary with the intended audience (Adams et al. 1997). Terms may evolve to take on connotations that were unintended or inappropriate.

Here I consider noninvasive genetic sampling. The literature has virtually exploded with reports of studies using DNA from feces, hair or occasionally feathers, urine, and even semen from free-ranging (unrestrained) animals to investigate genetic structure, population size, and geographic distribution (Waits and Paetkau 2005). This new tool is appealing from several respects:

- (1) Such samples may provide more information (larger sample sizes) than could be obtained any other way.
- (2) For rare species, where capture and handling are simply too risky, noninvasively-obtained samples provide a more acceptable method of study.
- (3) For more common species, noninvasive sampling still provides an alternative to capture and handling that may be more suitable for certain circumstances.

These are all valid reasons to employ the technique. However, misconceptions seem to have arisen from the frequent use and misuse of the term noninvasive in the wildlife ecology literature.

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I reviewed the wildlife-related literature using various electronic search engines to find peer-reviewed papers where the term noninvasive genetic sampling (or some derivative thereof: e.g., noninvasive genotyping, noninvasive DNA sampling) was used in the title, abstract, or keywords. Morin and Woodruff (1992) apparently were the first to use the term noninvasive with regard to genotyping material from unrestrained wildlife; however, widespread use of the term and application of the technique in field studies seemed to commence about 5 years later, spurred by their book chapter on the subject (Morin and Woodruff 1996). Of 64 papers published since then (1997–2005) employing the term noninvasive genetic sampling in reference to a study of a distinct mammalian wildlife taxon, 61% ($n = 39$) dealt with the Order Carnivora, of which half ($n = 19$) were about bears. Primates were the second most frequently occurring order ($n = 12$). I divided the 64 papers into those that concerned only the efficacy of a genetic technique ($n = 28$), those that used the technique for a strictly genetic purpose, such as assessment of genetic diversity, paternity, or phylogeny ($n = 8$), and those that applied the technique to address a non-genetic question about free-ranging wildlife, such as population size or distribution ($n = 28$). This paper focuses on studies in this last category. Among those 28 studies, 10 (36%) were about ursids, 6 about mustelids, 7 about other families of Carnivores (canids, felids), and the remainder about diverse other taxa (elephants, lagomorphs, and marsupials).

The predominance of DNA sampling in studies of bears is striking. Notably, a small bear population was the subject of the first genetics (Höss et al. 1992, Taberlet and Bouvet 1992) and first demographics studies based on remotely-collected hair and fecal samples (Taberlet et al. 1997). It is unclear whether the techniques for remotely collecting hair or feces are particularly suitable for bears, or just that researchers who have been involved in such studies happen use the term noninvasive to describe their sampling method more often than those involved in similar studies of other taxa. I did not undertake a literature review of all studies using this sort of sampling because the number of potential key words is quite large. I did, though, find 13 papers within the bear literature where genetic analysis of remotely collected hair was used in an applied study, but where the term noninvasive sampling was not employed. I also searched not yet published bear studies from the International Conference on Bear Research and Management in 2005 (abstracts at: <http://www.foreste.provincia.tn.it/16IBAconference/>) and

found 12 that referred to noninvasive genetic sampling (or equivalent) and 9 that used such methods but not the term noninvasive.

Not only is noninvasive genetic sampling an increasingly popular technique for bear studies, but the term itself seems to have a certain allure, I suspect because it implies more humaneness and less risk to the study animals (Morin and Woodruff 1992, 1996). With such rapidly increasing use of the term and application of the technique, it seems worthwhile to examine the tradeoffs inherent in this approach (data that cannot be obtained) compared to studies based on capturing and radiotracking, as well as alternative noninvasive methods for studying bears.

Noninvasive defined

Medically, a noninvasive procedure is one in which the animal's body is not invaded, either through the skin or a body orifice (Medical Dictionary 2006). Noninvasive genetic sampling thus refers to collection of DNA from material outside the skin (hair or feathers), or material sloughed, shed (skin), or passed outside the body (feces, urine, semen, saliva, regurgitated pellets). By contrast, invasive genetic sampling generally involves needles (to draw blood) or biopsy probes (to obtain tissue). Shooting a biopsy dart at a free-ranging animal is invasive, whereas shooting a rolled strip of duct tape on the end of a blunt dart to obtain a hair sample is noninvasive (Valderrama et al. 1999). Likewise, using a jagged metal device to pluck hair from the hide of an animal caught in a trap that it could escape from is considered noninvasive (Belant 2003); conversely, a "finger-prick" administered via a jab pole to obtain a few drops of blood from free-ranging animals is invasive (albeit low invasive; Sanvito et al. 2005). More ironically, collection of semen from a captive, unsexed animal is technically noninvasive (VandeVoort et al. 1993), whereas collection of saliva from inside the mouth of an unsexed animal is not (Gómez et al. 2004).

In an attempt to reduce confusion, Taberlet et al. (1999:323) suggested that the term noninvasive be restricted to situations where samples are obtained "without having to capture or disturb the animal." As such, it seems to have taken on the connotation of being a kinder, gentler, noninjurious approach to studying animal populations, and hence, more socially and scientifically acceptable because it has less effect (or potential effect) on research subjects.

In the case of bears, noninvasive genetic sampling is commonly accomplished using barbed wire hair traps,

which are normally set as a corral around a bait or lure (Woods et al. 1999). The bear crouches under the wire to get to the bait, and a chunk of hairs is pulled from its back. This process is certainly less traumatic than capture in a trap, but nonetheless may entail a behavioral effect. Researchers have observed animals becoming either trap happy or trap shy as a consequence of this experience, thus affecting their future probability of visiting a hair trap (Boersen et al. 2003, Boulanger et al. 2004c). Such behavioral modification does not discount the technique as a form of noninvasive sampling in the parlance of geneticists, but seems inconsistent with the evolving view of noninvasive being synonymous with non-intrusive. Analogously, electric fencing, which is used to deter bears from potential food sources (or from doing harm to people), is noninvasive in the medical sense but clearly and purposefully invasive in the behavioral sense. That bears are more apt to avoid repeated exposures to electric fencing than to reenter a trap suggests that the former is more behaviorally invasive than the latter.

The point is not that barbed wire or other sorts of hair snares (Foran et al. 1997, McDaniel et al. 2000, Belant 2003) are particularly invasive, but rather that the term noninvasive has 2 distinct meanings, 1 biological and 1 generic, which have become intertwined in the wildlife literature. As a case in point, Solberg et al. (2006:165) compared what they called “field” versus noninvasive genetic methods to estimate brown bear (*Ursus arctos*) population size in Sweden. They asserted that “traditional field methods involving captures of the animals imply potential dangers of injury or death to the animal,” whereas “animals are not disturbed” with noninvasive genetic sampling. The term noninvasive is clearly not just descriptive of a method that avoids breaking the skin; it creates an image of being more humane and ethical (Solberg et al. 2006) than other field methods. Accordingly, ethical considerations have recently prompted some governmental and non-governmental organizations in the US and Canada to promote noninvasive genetic approaches over traditional telemetry studies for bear research.

How invasive are telemetry studies?

Since the early 1970s, radiotelemetry has served as a primary means of gaining reliable information on many species of animals. In the case of bears, several thousand individuals have been radiocollared (Garshelis and McLaughlin 1998). No doubt many injuries and some deaths have occurred to captured animals due to

physical restraint, stress, or thermoregulatory problems. Moreover, collars may cause neck irritation, especially on bears fattening for hibernation. Efforts to minimize injuries using better trap designs (Johnson and Pelton 1980, Jonkel 1993, Reagan et al. 2002, Lemieux and Czetwertynski 2006), safer drugs and drug delivery systems, and collars with breakaway or expandable mechanisms (Garshelis and McLaughlin 1998, Vashon et al. 2003) are priorities for anyone involved in these sorts of efforts, but no capture-based study could claim to be noninvasive in either the sense of not breaking the skin or not affecting the animal’s behavior (at least in the short term).

After capturing and collaring an animal, however, radiotracking can be very noninvasive, as long as the collar itself does not affect the animal, and if recaptures are not necessary. Indeed, the word telemetry means to measure or monitor from a distance. However, investigators employing telemetry do not typically refer to the technique as being noninvasive, even if the data are gathered by collar-mounted GPS units and transmitted back via ARGOS satellite (Schwartz and Arthur 1999). Ironically, the close observation of human habituated animals (Rogers and Wilker 1990, DeBruyn 1999) is more behaviorally invasive than telemetry because the natural reactions of the study subjects to humans has been altered.

Effects of radiocollars are admittedly difficult to measure, and most investigators (of a variety of species) either assume no effect or test for effects with inadequate samples or study design (Murray and Fuller 2000). In a few contentious cases, claims have been levied about detrimental effects of handling or collars on large mammals (Burrows et al. 1994, Alibhai and Jewell 2001, Alibhai et al. 2001), but researchers involved in these studies have, in my view, made convincing counter-arguments (Ginsberg et al. 1995, Creel et al. 1997, du Toit 2001).

Data obtainable from genetic sampling versus telemetry

Capture and telemetry studies have yielded valuable information on behavior (movements, home range, habitat use, denning, activity patterns, social organization), demographics (survival, reproduction, population growth), morphology (size, weight changes, dentition), and physiology (body condition, hibernation, other adaptations) that would not have been obtainable by other means. This information forms the crux of what

we presently know about many species, including bears. Those species of bears that have not been studied extensively with radiotelemetry are still poorly understood (Garshelis 2004).

Sampling feces or shed or plucked hair may provide valuable information on genetic diversity (Lorenzini et al. 2004, Triant et al. 2004, Belant et al. 2005), population size (Boulanger et al. 2002, Bellemain et al. 2005), spatial distribution relative to landscape variables (Apps et al. 2004, Nams et al. 2006), demographic fragmentation (Proctor et al. 2002, 2005), population connectivity and directional gene flow (Thompson et al. 2005, Dixon et al. 2006), dispersal patterns (Proctor et al. 2004), and even diet (from genetic or isotopic analysis: Höss et al. 1992, Robbins et al. 2004), reproductive attributes, and levels of stress (from hormones: Schwarzenberger et al. 2004, Wasser et al. 2004). These techniques add to but do not supplant radiotelemetry as the cornerstone for gaining reliable knowledge about bears and many other species (Mech and Barber 2002). Below I contrast inferences that can be drawn from telemetry versus genetic sampling studies aimed at 3 distinct objectives: assessment of habitat quality, estimation of population size and trend, and estimation of minimal population size.

Assessment of habitat quality

Telemetry data may yield biased assessments of habitat use due to errors in triangulation (bias against habitats that occur in small patches), poor signal reception in some habitats, or inadequate sampling across hours, seasons, and years (Garshelis 2000). However, generally these biases can be measured and corrected.

Relative use of different habitats also can be assessed from incidence of bear sign (Cuesta et al. 2003, Akhtar et al. 2004, Posillico et al. 2004), assuming that sign is equally detectable by habitat. Hair sampling with barbed wire helps equalize detectability among habitats. Remotely-triggered cameras can be used the same way (Moruzzi et al. 2002). However, hair sampling has the advantage of producing not only data on presence–absence of bears by habitat, but from genetic identities, habitat-specific densities indicative of relative habitat quality (Apps et al. 2004, Nams et al. 2006). A potential weakness of such analyses, though, is that high-density areas may in fact be ecological traps or attractive sinks (Delibes et al. 2001, Battin 2004)—areas with attractive resources but also a high risk of mortality.

Nielsen et al. (2006) combined telemetry data and records of human-caused mortality to identify attractive

sinks for grizzly bears. Naves et al. (2003) performed a similar analysis using bear sightings, sightings of females with cubs (reflective of reproduction), and variables related to human activities linked to human-caused bear mortalities to distinguish potential refuges, sources, and attractive sinks. Nielsen et al. (2006:227) concluded that: “relying on animal occurrence alone for assessment of habitat quality is questionable. One risks promoting habitats that are effectively attractive sinks where occupancy and reproduction may be high, but survival is low.” Because hair sampling readily yields information on spatial distribution but not reproduction or mortality, this technique may be particularly subject to this pitfall.

Estimates of population size and trend

Genetic sampling is often used to produce population estimates, an apt and important application. Common problems are the same as encountered in standard mark–recapture studies. Additionally, genetic tagging entails unique problems associated with misidentification of individuals or unusable samples, leading to biased estimates. Much effort has gone into investigating and attempting to resolve these issues (Taberlet et al. 1996; Mills et al. 2000; Waits and Leberg 2000; Paetkau 2003; Broquet and Petit 2004; McKelvey and Schwartz 2004; Lukacs and Burnham 2005; Roon et al. 2005a,b), including the development of new techniques specifically for analyzing genetic mark–recapture data (Miller et al. 2005, Petit and Valiere 2006). The most problematic issue, though, for large mobile animals like bears, is movement in and out of the study area, making the area pertaining to the population estimate, and hence the density of bears, undefined. In some cases the study area may be sufficiently isolated to assume that the hair-sampled population is geographically closed (Boersen et al. 2003, Belant et al. 2005). More commonly, home ranges of bears straddle study area boundaries, thus necessitating corrections for lack of closure (Boulanger and McLellan 2001, Boulanger et al. 2004a). Such analyses combine losses due to death and emigration (often called apparent survival) and combine gains due to reproduction and immigration (rate of addition).

At the landscape level, immigration and emigration must balance, but at a local level they could be different and varying. For example, salmon (*Oncorhynchus* spp.) streams seasonally attract bears, and differing numbers of bears may be attracted each year, depending on availability of salmon. Estimates of and changes in the superpopulation (*sensu* Kendall 1999) of bears using particular salmon streams have been ascertained from

genetic samples obtained at hair traps along the stream (Boulanger et al. 2004b, Peacock 2004, Haroldson et al. 2005). Bears may be attracted to a stream from a much larger source area, which is typically not sampled. Trends in superpopulation estimates would thus not include all bears in the source area, but just those using the stream each year. Yearly trends in the stream superpopulation would likely be affected mainly by differing numbers of bears moving to and from the stream (immigration and emigration), whereas trends in the population of the larger source area (what might be called the greater-superpopulation) would be driven by reproduction and survival. This is not to say that trends in the stream superpopulation are not informative, only that they may not reflect the larger source area (Fig. 1). This situation may be more problematic in other situations if the goal is to monitor trend in a large area and the sample area has changing rates of immigration and emigration.

In contrast to genetic sampling, lack of geographic closure is directly observable and correctable using radiotelemetry (Garshelis 1992), and rates of mortality and reproduction are estimable without the confounding effects of emigration and immigration. Moreover, and equally important, *sources* of mortality and *sources of variation* in reproduction can be ascertained. Radiotelemetry also provides sex-age specific rates of emigration, and additional information about the areas that emigrating animals traversed though (e.g., corridors) and settled in, as well as their eventual fates (Schwartz and Franzmann 1992). In other words, one achieves an understanding not only of population trend, but also of the specific factors that most influence that trend. For example, from telemetry studies researchers have distinguished the relative importance of varying abundance of different foods as well as changes in the density of bears on the population growth rate (Schwartz et al. 2006a). Telemetry also can be used to determine how often bears were killed on or near roads, and whether that mortality was caused by vehicle collisions or from hunting or poaching. Such information may be obtainable, as well, just from location records of dead bears kept by management authorities (Nielsen et al. 2004), but telemetry data also provide estimates of the percent of dead bears that were recorded by these authorities (McLellan et al. 1999, Cherry et al. 2002, Koehler and Pierce 2005). These data would have direct management applications, both in helping to alleviate sources of mortality as well as in providing a means of monitoring population trend (by monitoring mortality: Benn and Herrero 2002, Garshelis et al. 2005). This sort of

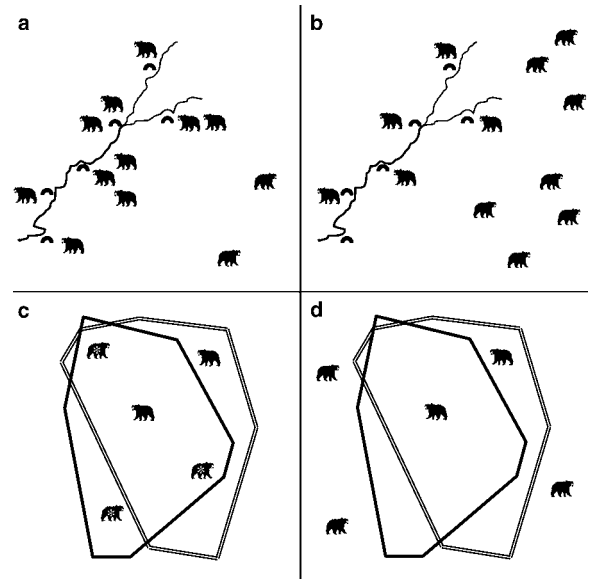


Fig. 1. Lack of geographic closure may affect inferences from remote genetic sampling of bears. Panels a and b show bears around a hypothetical salmon stream with hair snares (semicircles). (a) Ten bears compose the superpopulation of the stream in year 1 (left-facing bears), whereas 2 bears previously visited the stream but not that year (right-facing bears). (b) Only 5 bears visited the stream in year 2, but the number of bears that at some time visited the stream remains at 12. Trend gleaned from hair-snaring along the stream would pertain to the number of bears using the stream during sample periods (here, a decline of 50%), not the number in the source population (greater-superpopulation). This information is useful in terms of defined areas like salmon streams, but removing the stream from this example renders the value of the results questionable. Analogous problems confounded interpretations of immigration and emigration from investigator-defined study areas in bear studies relying principally on eartag mark-recapture data (Sargeant and Ruff 2001). Panels c and d show telemetrically derived home ranges of 2 bears (left-facing symbols), patterned after 2 radiocollared bears in Bolivia (Paisley 2001). These bears were not detectable by ground telemetry a third of the time that radiotracking was attempted, indicating that they were beyond these delineated areas. (c) Three other bears were genetically identified from scats collected from this area over the course of a year (right-facing figures with white asterisks). (d) These other bears likely used areas outside the ranges of the 2 collared bears, and probably spent even less time within the study area. A total of 5 known bears is thus not a minimum estimate, but may well be an overestimate of the number present at any given time. It is an estimate of the minimum number of bears that used the area during 1 year (i.e., a cumulative estimate).

information is not typically obtainable in studies based on collected hair or feces, resulting in greater uncertainty about causes of population decline (Lorenzini et al. 2004).

Minimal population estimates

A commonly posed advantage of noninvasive genetic sampling is that even studies not designed to produce a robust mark–recapture population estimate can nonetheless provide at least a minimal population estimate, which may be useful for conservation and management. That is, the number of distinct, genetically-identified animals sampled from an area should be indicative of the minimum number living there. This information seems particularly attractive in parts of the world where more elaborate studies involving multiple sampling sessions are precluded by difficult access, lack of funding, training, and time (McCarthy 2000).

Consider the following example of such a study: a researcher hikes 100 km of trails and collects 15 scat and hair samples, of which 8 are genetically identified, representing 3 different genotypes. The researcher thus concludes that the area is occupied by a minimum of 3 individuals. Certainly this information, specifically the genetic identities, adds to what would have been known otherwise, but how useful is it?

If fresh sign is present on a survey of an area, then the *minimum* population of that area is 1 animal (unless the animal leaving that sign was a transient visitor). Genetic information helps to determine whether the minimum is >1 . Intuitively this would seem useful, but 2 problems exist. First, if the real number of animals is far above the minimal estimate (e.g., if the real population is 30 and the minimum detected is only 3), then that minimal estimate is not only unhelpful but also possibly misleading. The minimum number of individuals detected is only useful if it reasonably approximates the real population, but there is no way to know if it does. Lorenzini et al. (2004) argued the usefulness of a minimal estimate for an isolated population of brown bears in central Italy based on DNA from opportunistically collected hair samples. However, their tally of 19 different bears identified over the course of a decade did not improve the precision of previous population estimates in this area, which ranged from 38–60 bears.

Second, there could actually be fewer animals residing in the area than the number detected genetically; that is, the presumed minimum could be an overestimate. Consider an example from a bear study in Bolivia. After a year of trapping in rugged mountainous terrain, Paisley (2001) captured and radiocollared 2 Andean bears (*Tremarctos ornatus*), which provided data on move-

ments, activity patterns, food habits, and other aspects of their life history (Paisley 2001, Paisley and Garshelis 2006). During the course of the study, scat and hair samples were collected from the general area and preserved for genetic analysis. It was known that at least the 2 collared bears occupied the area, and sightings indicated the occasional presence of 1 other bear. The question that the genetic samples might have answered is whether more bears than these 3 used the area.

Radiotracking data indicated that each of the 2 radiocollared bears were present in the 15-km² study area only about two-thirds of the time (Paisley 2001), so together they could be considered equivalent to 1.3 full-time residents (Garshelis 1992). It was suspected, from the infrequency of sightings of non-collared bears, that they were present much less. Thus, even if genetic information indicated the existence of another 3 bears besides the collared ones, the *minimum* density would still be <10 bears/100 km² (1.3 bear-equivalents/15 km²), because these 3 other genetically-identified bears could have been either transients that just passed through or bears whose home ranges barely overlapped the study area (Fig. 1). Assuming these 3 other bears to be full-time residents would be nonsensical; furthermore, the density estimate so obtained (29 bears/100 km²) would represent neither a minimum nor a maximum, as other bears whose scats or hair were never collected could have been present as well. The only relevant information obtained from the genetic samples would be the documented presence of other bears and their sex. If numerous samples were collected over the course of the study in a carefully designed sampling scheme, more reliable assumptions might be made about the residency of genetically-identified individuals, and from such ‘recapture’ data an estimate might be obtained of the number of other, undetected individuals also present.

The Bolivia situation exemplifies 2 key points. First, density estimates can be extremely biased if the study area is not geographically isolated (closed) or if the size of the area is not much larger than the size of home ranges (Garshelis 1992). Second, although only 2 individuals were caught and radiocollared, the data that these bears provided made evident the fallacies of estimating density from genetic material without corresponding information on use of the area. Had the Bolivia study been totally noninvasive, the results would have more likely been misinterpreted, unless sufficient samples were obtained to infer how much time bears spent on the study area, or alternately, how large the sampled area really was (Karanth and Nichols 1998, Boulanger and McLellan 2001). This was the first

radiotelemetry study of this species. It required obstinate persistence to overcome inordinate difficulties to catch and collar just 2 animals. Others faced with similar challenges might opt for the simpler and less intrusive DNA sampling approach, which could yield an estimate that might naively be considered minimum but could well be an overestimate.

An example of a presumed minimal estimate possibly being too high occurred in a study of giant pandas (*Ailuropoda melanoleuca*), where researchers genetically identified feces collected within a Nature Reserve in China (Zhan et al. 2006). Because the scat sampling was focused within the reserve, it yielded the perception of a very high panda density; however, some of the animals may have spent a large proportion of their time beyond the reserve boundary.

Cost

Inasmuch as financial support for conservation is inadequate, it seems only prudent to ensure that reliable results are achieved most efficiently. Analyzing DNA in scat and hair samples is expensive, especially when rechecked for genetic errors (McKelvey and Schwartz 2004), so should be considered carefully, particularly in developing countries where research funds are limited. Telemetry studies can be even more expensive, especially those involving satellite radiocollars, or the need for aerial locations of VHF (very high frequency) collars. Dividing cost by the sample size would be misleading if the full sample did not actually contribute to the study goals (e.g., many radiolocations clustered together, many genetic samples from the same individuals). Expense should be weighed against the reliability and applicability of results. Sometimes, very cheap methods, such as sign surveys and local interviews, are satisfactory.

Also relevant to the issue of cost is the ability of the study to attract support. Although the choice of field methodology should rarely be dictated by fundraising potential, that consideration is real. For example, whereas researchers would likely not choose expensive satellite collars just because they offer the ability to post near-real time animal movements on the internet (unless educational benefits were the prime motivation for the study), this sort of expensive but highly useful technology might attract more potential funders than less engaging research techniques. Likewise, the poaching-related death of a named or numbered collared animal would draw more attention than the detection of poaching derived indirectly from a mark–recapture model. Oftentimes it is

the study itself, and a few high-profile incidents, that generate the funds, attention, teaching moments, and initiatives that ultimately lead to successful accomplishment of both research and management goals.

Other noninvasive study techniques

Many scientific naturalists (*sensu* Futuyma 1998) rely on observations of animals or their sign, without traps or attractants, to gain information about natural history, ecology, and relative abundance. Spencer (1955) used a statewide sign survey to generate a crude population estimate for American black bears (*Ursus americanus*) in Maine. Sign surveys are still used in many areas to assess bear distribution, population size (Pulliainen 1986, Chestin 1994, Camarra and Dubarry 1997), habitat use (Cuesta et al. 2003, Posillico et al. 2004, Akhtar et al. 2004), relative abundance (Garshelis et al. 1999, Laidlaw 2000), and population trend (Kendall et al. 1992, Clevenger and Purroy 1996, Rice et al. 2001; Fig. 2). Sign surveys can be enhanced with the use of remote cameras to determine species presence, habitat use, activity patterns, physical condition, relative abundance, and for species with distinguishing marks, population estimates (Karanth and Nichols 1998, Moruzzi et al. 2002, Sanderson and Trolle 2005, Wong et al. 2005). Techniques are still emerging for estimating population size and density from photos, sightings, or sign when animals are not individually recognizable (Barnes et al. 1997, Stander 1998, O'Brien et al. 2003, Royle and Nichols 2003, Kawanishi and Sunquist 2004, Tosh et al. 2004).

Sign and camera-based surveys are becoming more common and more sophisticated. These techniques have become popular because they are logistically easy, efficient in terms of data gained per effort, inexpensive, and noninvasive. Curiously, though, they are rarely referred to as being noninvasive (but see Jewell et al. 2001, Moruzzi et al. 2002, Dixon 2003). In fact, remote photography is commonly referred to as camera trapping (Lu et al. 2005), a term that implies a behavioral (invasive) effect, even when no bait is used.

Animal sightings are another noninvasive source of information. Bears are often difficult to see; nonetheless, visual observations and counts have been used to document changes in distribution, assess habitat use, monitor population trend, and estimate population size (Keating et al. 2002; Schwartz et al. 2002, 2006b; Evans et al. 2003; Naves et al. 2003).

Interviews, questionnaires, and workshops are additional noninvasive means of obtaining information on animal populations. Data on bears obtained by such



Fig. 2. Examples of sign useful for noninvasive sampling of bear populations. (a) Scat of giant panda: measurements of the length of fragments of bamboo stems in panda scats are used to distinguish neighboring individuals and thereby estimate population size (China; photo: W. McShea, Conservation and Research Center, National Zoological Park, USA); (b) Claw mark of sun bear (*Helarctos malayanus*): incidence of climbed trees relates to the density of bears, use of habitat, and use of specific types of fruit-producing

means regard distribution (Sathyakumar 2001, Can and Togan 2004), diet (Hwang et al. 2002), and bear-human interactions (Zimmerman et al. 2003, Bargali et al. 2005, Fredriksson 2005, Jorgenson and Sandoval-A 2005). For other species, local knowledge has been helpful in interpreting population estimates and complex ecosystem interactions (Huntington 2000, Pierotti and Wildcat 2000). Ironically, most of the above-mentioned techniques tend to be less intrusive toward the study animals than commonly-used methods of noninvasive genetic sampling (Fig. 3).

Terminology matters

Noninvasive sampling of any kind has obvious appeal, both scientifically and to the non-scientific public (including governmental and non-governmental agencies, and potential funders). There are 2 potential downsides, however, to the persistent use of this term specifically in reference to the collection of hair and scat samples. First, such emphasis suggests that other methods, notably telemetry, are invasive, not just in the technical sense of penetrating the skin (to drug the animal), but also in terms of altering the health or behavior of the animals studied. Second, the tight connection between the term noninvasive and genetic sampling yields the misimpression that other non-invasive research methods do not exist. Other non-invasive approaches are gaining in popularity, not because they are noninvasive per se, but because they are most fitting of the circumstances (objectives, access, budget, etc.). For example, Vilà et al. (2004:147) attempted to locate remnant populations of a highly endangered fox (*Pseudalopex fulvipes*) in Chile using “live traps, non-invasive techniques and interviews.” Interviews (while obviously noninvasive, but not considered so by these authors) provided the only evidence of the species.

One alternative would be for all studies that did not involve animal capture to employ the term noninvasive:

noninvasive camera trapping, noninvasive sign surveys, noninvasive interviews, etc. Not only is this language redundant and cumbersome, but it bolsters the illusion that animal handling should be avoided. Biologists thus might be tempted to design studies around noninvasive methodology, rather than around the questions they are attempting to address. In that sense, the recurrent use of the term noninvasive and the “growing wave of enthusiasm” over this “conceptual revolution” (Mills et al. 2000:283) could steer us away from obtaining the sort of information actually needed to conserve and monitor populations.

A better alternative would be to use more appropriate terminology for genetic sampling. More descriptive terms include “shed hair sampling”, “plucked hair sampling”, or “scat sampling.” Notably, papers written by wildlife biologists often use these kinds of terms, or phrases like “genetic tagging,” whereas those written by geneticists seem inclined toward the use of noninvasive genetic sampling, which was recently reduced to the acronym NGS (Roon et al. 2005*a,b*; Waits and Paetkau 2005). In fairness, this distinction arises because geneticists must deal with the special problems related to the low quantity and quality of such samples, which are markedly different than invasively-obtained genetic samples, such as blood or tissue.

To be consistent with other ecological literature, where samples are obtained without human presence (from a satellite, from a motion-detecting camera, or in the case of genetic samples, from a strand of barbed wire, on a rub tree, or defecated on a trail), I suggest substituting the term noninvasive with “remote” (Sloane et al. 2000, Piggott and Taylor 2003, Frantz et al. 2004) — hence, RGS for short. Indeed, this term is more fitting than noninvasive to describe “sampling techniques in which direct contact (visual or otherwise) between researchers and animals is avoided” (definition of noninvasive posed by Schwartz et al. 1998:294).

This alternative terminology seems particularly well suited for studies aimed at population estimation.

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trees (Thailand; photo: D. Garshelis); (c) Hole in termite mound dug by sloth bear (*Melursus ursinus*): incidence of digging relates to abundance of bears and abundance of termite mounds, so both holes/mound as well as holes/area are important considerations (Nepal; photo: D. Garshelis); (d) Remnants of *Puya* sp., a terrestrial bromeliad growing in high-altitude South American grasslands, left after consumption by an Andean bear: prevalence of sign gives an indication of bear numbers and seasonal use of this habitat (Bolivia; photo: D. Garshelis); (e) Tree nest formed by branches broken by an Asiatic black bear (*Ursus thibetanus*) feeding in the canopy of an oak tree: this easily visible sign is useful for quickly ascertaining the presence of bears and their use of a patch of forest in a particular year (China; photo: D. Garshelis); (f) Track of Tien Shan brown bear documenting their presence in Chatkal nature reserve in 2005 (Uzbekistan; photo: A. Esipov, Institute of Zoology, Uzbek Academy of Sciences).



Fig. 3. Methods of remote sampling of bear populations, other than sign surveys, ordered from most to least behaviorally invasive: (a) baited, barbed-wire hair snare used to obtain genetically-identifiable samples (*U. americanus*, Minnesota, USA; photo: D. Garshelis); (b) camera trap with scent lure (here documenting presence of *U. thibetanus* in Laohegou, a previously logged area, China; photo: Li Sheng, Beijing University); (c) interview of local people (here informing researchers of the presence of *M. ursinus*, including females with cubs, in a highly fragmented forest, and providing descriptions of a recent hunt by foreigners, Nepal; photo: D. Garshelis).

Indeed, few population estimates have been obtained by *invasive* genetic sampling. The first may have been that of Palsbøll et al. (1997), who shot biopsy darts at whales (but also collected sloughed skin noninvasively) to obtain genetic samples (in the case of whales, non-invasive sampling typically involves photographic identification). For most wild animals, invasive genetic sampling requires capture, and if animals are to be captured, then other forms of marking for mark-recapture are usually more appropriate than genetic tagging. For population estimation, where sampling bias is an important consideration, the relevant distinction is thus not between invasive and noninvasive, but between sampling based on animal capture versus remote

sampling. Furthermore, these can be subdivided into techniques involving baits or lures, versus sampling without artificial attractants. Geneticists should be aware that their categories of sampling do not correspond well with the wildlife applications for which genetic samples are increasingly being used.

Acknowledgments

I thank the Minnesota Department of Natural Resources for support, and A. Esipov, W. McShea, and S. Li for use of their photos. L. Waits provided helpful comments on an earlier draft.

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Received: 17 January 2006

Accepted: 24 May 2006

Associate Editor: R. Harris