

Do revised giant panda population estimates aid in their conservation?

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Abstract: The small number of giant pandas (*Ailuropoda melanoleuca*) in the world makes this the only species of bear classified as globally endangered on the IUCN red list. The latest rangewide population estimate was derived from scats (feces) found along transects throughout the geographic range of the species. Scats were differentiated into ~1,600 individuals based on their geographical separation and the size of bamboo stem fragments contained within (reflective of bite-sizes). Recently, a team of researchers (Zhan et al. 2006) conducted genetic analysis of scats in a Chinese Nature Reserve (Wanglang). Their estimate of giant panda numbers there was double that obtained using the bite-size technique. Taking this to be representative of the entire range, they speculated that there could be 3,000 pandas in the wild. Many in the international conservation community heralded this as evidence that panda conservation is working well. Moreover, if the revised rangewide estimate is accepted as true, it could mandate the downlisting of pandas on the red list. We believe that such conclusions are unwarranted, or at least premature. First, the DNA-based estimate in the reserve may have been inflated by lack of geographic closure (which seems probable) and genotyping errors (which we found evidence of). Second, it was inappropriate to extrapolate results from this single point to the entire range of the species. The bite-size technique may substantially underestimate panda numbers in dense populations, such as in Wanglang Nature Reserve, where many nearby individuals likely have similar bite characteristics, whereas the technique may be more accurate in differentiating individuals in more sparsely populated areas. Although molecular-based population estimation is more rigorous than the bite-size method, too much uncertainty exists in the revised estimates to surmise either current population size or trend. We recommend (1) quantification of genotyping error rates for panda feces, (2) comparison of population estimates using bite-sizes and DNA derived from the same, short-term collection of scats, and (3) incorporation of both techniques in the next rangewide population estimate.

Key words: *Ailuropoda melanoleuca*, bamboo stem fragment, China, DNA mark–recapture, genotyping error, giant panda, IUCN red-listing, population closure, rangewide population estimate

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There are few species whose total world population is precisely known. Such may be the case for a few rare species with a very limited distribution, but even these are often difficult to enumerate (Marino et al. 2006). Population estimation is especially complex for taxa that occupy environments where they are not readily visible and easily counted. Even single populations of such species are often difficult to estimate, prompting several recent treatises on this subject (Borchers et al. 2002, Williams et al. 2002, Amstrup et al. 2005).

Here we comment on a unique case, that of the giant panda (*Ailuropoda melanoleuca*). Giant pandas occupy a restricted range (portions of 6 mountain ranges within 3 provinces of central China), but counting every individual panda by visual observation is obviously not possible. Nevertheless, 3 rangewide giant panda ‘censuses’ or ‘National Surveys’ (both terms are commonly used) have been conducted. These surveys have been prominently supported by the international conservation community, and have served as a basis for judging not only the conservation status of pandas, but also the effectiveness of measures designed to protect them and their habitat.

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Fig. 1. Scats from giant pandas (photographs are from different individuals), each showing distinct, fairly uniform-sized fragments of bamboo (highlighted by boxes in lower photo). The lengths of these fragments (bite sizes) and the degree to which they were chewed (compare top and bottom photos) have been used to differentiate pandas with overlapping home ranges. (Top photo: Wang Hao; bottom photo: W. McShea)

The latest giant panda National Survey (1998–2002) distinguished individuals based largely on the size of the fragments of bamboo stems in their scats. Pandas digest bamboo poorly, so their scats contain fragments derived mainly from mastication. Pandas insert stems of bamboo into the side of their mouth and bite off pieces in a highly repetitive manner. Researchers have observed, from studies both in the wild and captivity, that pandas exhibit individual differences in the way they bite off and chew bamboo stems, resulting in distinctive ‘bite sizes’ and ‘chew rates’ of bamboo stems in their scats (Schaller et al. 1985, Yin et al. 2005; Fig. 1). In the National Survey, scats were

used only if they met certain criteria for freshness and size (scats assumed to be from cubs <1.5 years old were excluded). Although the bite-size method works best for bamboo stem fragments, it was applied as well to leaf fragments in areas where pandas eat few stems (Qinling Mountains). A 3-step process, originally developed by one of the authors (Wang 2001) and modified slightly for the national survey (State Forestry Administration 2006), was used to determine whether scats were from different pandas:

- (1) The date of defecation of each scat was estimated based on intactness, presence and

sheen of a mucous coating, color, and odor. GPS locations of each scat were used to determine distances between adjacent scats. If 2 scats were defecated within 1 day of each other and were >1.0 km apart, they were considered to be from different pandas. With increasing time lapsed between defecations of scats in the same general area, the distance criteria for distinguishing individuals were incrementally increased, up to 3.5 km. If the distance threshold was not exceeded, step 2 was applied.

- (2) If the average length of 100 measured bamboo stem fragments (or leaves) in each of 2 scats (within the distance threshold) differed by >2 mm, the scats were assumed to be from different pandas; otherwise step 3 was applied.
- (3) If the degree to which the bamboo had been chewed differed greatly between 2 scats (i.e., finely chewed versus chewed very little), the scats were assumed to be from different pandas; otherwise the scats were considered to be from the same individual.

Many individual pandas may have similar bite sizes, so, particularly in dense populations (or in mating clusters), this technique is unlikely to be able to differentiate all individuals. Conversely, some variation in bite sizes within individuals could cause scats from the same panda to be tallied as >1 individual. Hence, it is unclear whether the bite-size technique as applied across the range of this species tended to over- or underestimate panda numbers.

The Third National Survey was conducted by >170 people who hiked >11,000 transects systematically spread across the recognized geographic range (nearly 23,000 km²). Loucks and Wang (2004) presented the data form used during this survey and provided information on the selection of survey routes. Nearly 3,800 scats were examined and ultimately separated into 1,596 individuals. This value is about 50% higher than that obtained from the previous (second) National Survey, conducted in the mid-1980s; additionally, the area occupied by pandas seems to have increased (Yan 2005). The purported increasing population trend has been attributed to conservation initiatives implemented in China in the late 1990s to restore more forested lands (Loucks et al. 2001); however, this conclusion is tempered by a lack of methodological consistency between the 2 surveys.

Despite this hopeful sign, giant pandas continue to be listed as endangered in the IUCN red list of threatened animals (<http://www.iucnredlist.org>, 2007); it is the only species of bear so listed. They are listed under a single criteria [C2a(i)] composed of the following elements: (a) less than 2,500 mature individuals exist in the wild; (b) each population has less than 250 mature individuals; and (c) overall numbers are declining (http://www.iucnredlist.org/info/categories_criteria2001, 2007). If numbers are truly increasing, giant pandas should eventually be downlisted. However, the 2 of us who wrote the current red listing account for this species (WD, DG) considered the current level of uncertainty in population trend for this species to be sufficient to maintain their endangered listing.

Recently, genetic techniques were used to re-examine giant panda abundance in Wanglang Nature Reserve, Sichuan Province (Zhan et al. 2006). The resulting estimate of at least 66 pandas, based on DNA-identified feces, was more than double the 1998 estimate (27), based on bite sizes of bamboo. Reactions from the news media, government officials, and conservation groups suggested that giant pandas have been rebounding in response to the unprecedented outpouring of money and attention provided to them in recent decades.

We realize, as did the authors of the DNA study, that the revised estimate did not indicate that panda numbers doubled in this short time (which would have been biologically untenable), or even that pandas increased at all. However, this result was commonly misconstrued, even leading to incorrect quotations attributed to some of us in a prestigious scientific journal (Guo 2007). The difference between the 2 estimates may indeed be due, in part, to an increase in population size, but is also likely a result of differences in methodology. Some confusion may have resulted from one of Zhan et al.'s (2006:R452) concluding remarks, which seems to suggest a continuing increasing trend: "it seems likely that many more individuals are extant in the wild than estimated in the Third National Survey..., which itself showed a substantial increase compared to the Second Survey."

Certainly DNA is a far better tool for distinguishing individuals than the sizes of bamboo stem fragments. Originally, the bite-size technique was used only to differentiate age groups of pandas (Schaller et al. 1985:157). Extending it to separate individuals was probably beyond the rigor of the

technique. That said, we are not convinced that the DNA-based estimate for Wanglang was necessarily more accurate, or even if it was, that the difference between that estimate and the bite-size derived estimate provides meaningful insight into the range-wide status of pandas. In this commentary we address 2 possible sources of error in the DNA estimate. Our comments are not meant to endorse the bite-sized technique or derived estimate, but rather to raise caution about all current estimates posed for this high-profile species.

Lack of geographic closure

Although the new DNA-based estimate of pandas in Wanglang is not biologically implausible, the resulting density is remarkably high: 1 cluster near the eastern boundary of the reserve yields an apparent density of 200–300 pandas/100 km² (in Fig. 1 of Zhan et al. 2006, this cluster of at least 30 points, each purportedly representing the geographic center of a panda home range, falls within an area of 10–15 km²). If true, this may be the densest natural concentration ever measured for any of the world's bears (Taylor 1994), excluding short-term aggregations around temporary rich food sources such as salmon (*Oncorhynchus* spp.) streams, garbage dumps, and large mammal carcasses. The area with a very high apparent density of pandas may have been a temporary mating congregation, as observed by some of us (Pan et al. 2001) and others (Yong et al. 2004b); if so, many of these individuals could have resided elsewhere, even outside the Wanglang Reserve. Wan et al. (2005) observed several pandas in another reserve that traveled ~20 km to breed (calculated from their Fig. 6), and others that dispersed at least this far.

Zhan et al. (2006:R452) dismiss the possibility of long movements, citing home range studies that indicate that pandas have “limited mobility.” Reported home range sizes for giant pandas vary widely among individuals, from 1 to 60 km² (Schaller et al. 1985, Schaller et al. 1989, Pan et al. 2001, Yong et al. 2004a); although most measured ranges were <25 km², none of the studies—all based on ground telemetry—obtained a sufficient number of locations to ascertain the true range (Girard et al. 2002). Some of us, having conducted ground-based telemetry studies of giant pandas, deduced that individuals sometimes ranged beyond our search area and thus could not be located (also noted by

Schaller et al. 1989). In other studies (of bears and wolves [*Canis lupus*]), home range sizes derived from GPS or satellite telemetry were nearly 3x larger than obtained from ground telemetry (Ballard et al. 1998, Arthur and Schwartz 1999). Interestingly, Wan et al. (2005) observed greater panda movements through DNA fingerprinting of scats than Schaller et al. (1989) observed through ground telemetry in the same area.

The underestimation of home range size points to a potentially serious problem with the panda DNA estimate in Wanglang: lack of geographic closure. Much of the land adjacent to Wanglang is forested, protected, and contains pandas. These pandas likely move back and forth among reserves and adjoining lands. This would not be problematic to the estimate if the sampling of feces occurred over a short time, providing in essence a snapshot of each panda's location. However, the fecal collection in Wanglang was conducted over nearly a year. The resulting population estimate thus represents the cumulative total of pandas that ventured into and defecated in the reserve, even if they only resided there for a few weeks.

Lack of closure is a common problem, especially in studies based on remote sampling of hair or scats, which results in overestimation of population size (Boulanger and McLellan 2001, Boulanger et al. 2004, Garshelis 2006). Zhan et al. (2006) sampled reserves adjacent to Wanglang, and the fact that very few scats found in this area were genetically matched to pandas from Wanglang suggested (to them) that lack of closure was not a significant problem. However, they found only a small percentage of the available scats. In order to obtain DNA, they only collected feces that were estimated to be <2 weeks old. Wild giant pandas defecate more than 100x per day (Schaller et al. 1985), resulting in >1,400 feces being deposited in 2 weeks and ~30,000 feces over the collection period. Zhan et al. (2006) collected, on average, only 3.7 feces per genotyped individual. Given this small sample (~0.01% of available), it seems unlikely that the geographic distribution of the collected scats accurately reflected the area utilized by each individual panda (Fig. 2). Analogously, a telemetry study with only 3 or 4 locations per animal could not accurately assess whether animals left a study area. Moreover, if sampling was low outside the study area, one could erroneously conclude that few animals left. The small number of scats found by Zhan et al. (2006) in

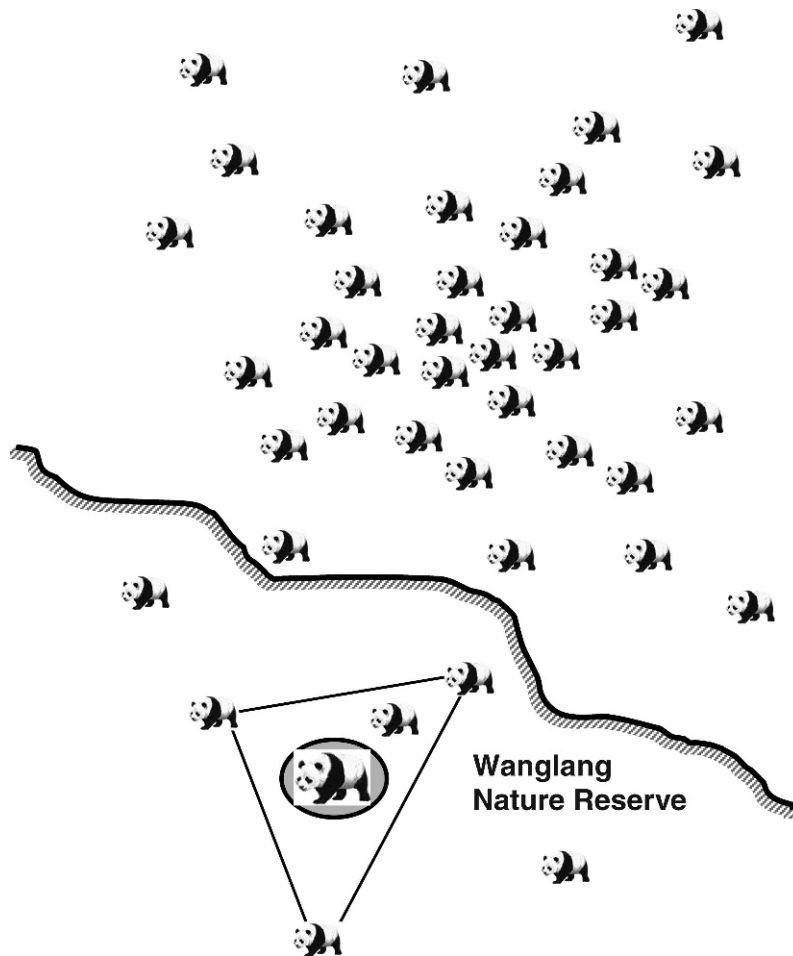


Fig. 2. Panda symbols (www.ace-clipart.com), each representing feces from a single hypothetical individual living near Wanglang National Reserve (reserve boundary shown). Zhan et al. (2006) collected feces over a 10-month period, during which this individual panda would have defecated ~30,000 times. A representative sample of these scats is shown. Zhan et al. (2006) collected, on average, 3.7 feces per genotyped individual, and mapped their locations, and mapped the geographic center. In this hypothetical example, feces in a box were found by the research team, which searched most intensively inside the reserve, yielding the average position highlighted by the larger symbol inside the ellipse. Although this panda lived mainly outside the reserve, more intense sampling within the reserve (study area) created the misperception that this individual was mainly a resident of the reserve. Sampling bias thus creates the illusion of population closure.

adjacent areas suggests that sampling outside Wanglang was inadequate to assess closure.

Conversely, during the National Survey, transects were walked only once, so sampling of each site was more like a snapshot in time, rather than a long-term accumulation. Also each area was sampled with roughly the same intensity (each person surveyed ~2 km²/day; Loucks and Wang 2004). It is not clear from the methods in the DNA study whether all areas were sampled with the same intensity, or if sampling was repeated in some areas.

We used panda feces collected principally by the patrolling staff in Wanglang during 2001–05 to help reveal biases that may arise with varied sampling. We compared bite-size based population estimates (derived by Wang Hao) achieved from a single sampling period to those obtained by pooling scats from samples collected in 2 consecutive years (comparable to Zhan et al.'s 2006 sampling). The combined samples from 2 years yielded estimates that were 30–70% ($\bar{x} = 50\%$) higher than the mean estimate from the 2 years individually (Fig. 3). These

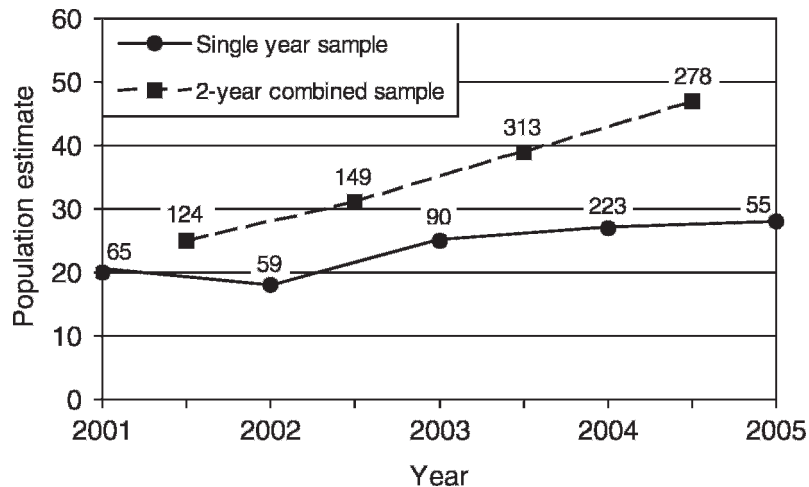


Fig. 3. Giant panda population estimates for Wanglang Nature Reserve derived by differentiating individuals from bite sizes of bamboo fragments in feces. Data were collected during each of 5 years (number of feces collected indicated above each point). Upper curve shows inflated effect of combining data from 2 consecutive years (analogous to procedure used by Zhan et al. 2006). Increasing trend may reflect true increase in panda numbers, but was partially confounded by increased search effort in later years.

estimates appeared to increase through time, although that result may have been confounded, as the search effort did not remain constant: students working on thesis projects significantly increased the number of scats collected in the later years. These data (Fig. 3) thus demonstrate that search effort and the length of the sampling period can affect the estimate of population size: the pooled data for 2004–05 produced an estimate of 47 pandas, substantially higher than the estimate of 27 obtained during the National Survey in 1998.

Genotyping errors

Genotyping errors may be another potential source of population overestimation (Waits and Leberg 2000, Roon et al. 2005). In 1 case (with wolves), fecal DNA produced a population estimate that was more than 5x the known number of animals in the population (Creel et al. 2003). The panda DNA study followed the well-accepted multi-tubes approach for detecting genetic errors, but did not report an error rate. Schwartz et al. (2006) showed that with hair samples from American black bears (*Ursus americanus*), and using, like the panda study, 9 microsatellite markers, genotyping errors would have led to a 28% inflation in the number of distinct individuals detected. They concluded that the multi-tubes approach reduced, but did not eliminate, all errors.

It has come to our attention that an error did exist with at least 1 of the genetic markers in the panda study. Another recent panda genetics study, based on known individuals, found that Ame- μ 19 resides on the X chromosome (David et al. 2006), but in the Wanglang data, 13 of 31 individuals assigned as males were scored as a heterozygote for this marker (our analysis of their Supplemental Data); this indicates that either Ame- μ 19 or sex was scored incorrectly.

Others have stressed the importance of error checking and reporting of error rates in genotyping studies, especially those involving small quantities of potentially degraded DNA (Bonin et al. 2004, McKelvey and Schwartz 2004). Pompanon et al. (2005:857) gave examples of the consequences of neglecting such errors. Some fields “suffered a crisis of confidence,” they observed, when misled by “erroneous papers published in leading journals.” We are concerned that Zhan et al. (2006) did not quantitatively estimate their genotyping error rate, and that such errors in their panda study may mislead the evaluation of the conservation of this species.

Conservation implications

It is possible that giant pandas have increased at Wanglang—even the bite-size estimates seem to show this (Fig. 3)—but whether there are presently

more or less than 66 individuals in this reserve is not a critical concern for the conservation of pandas. We find it troubling, however, that Zhan et al. (2006:R452) used their results from this reserve to suggest that other areas covered in the Third National Survey might also have twice the number of pandas, “leading to the possibility that there may be as many as 2,500–3,000 giant pandas in the wild.” This assumes that the proportional difference between the DNA and the bite-size based estimates at Wanglang holds for all other portions of the range. This is a poor assumption. Wanglang is one of China’s premier panda reserves, with a high density of pandas, especially (apparently) in one small area near the eastern edge of the reserve (Zhan et al. 2006:Fig. 1). Under these conditions, many nearby individuals are likely to have similar bite sizes, so the bamboo stem fragment technique is apt to produce an underestimate of population size. Thus, the difference between this estimate and an estimate derived from DNA identification of scats would tend to be large. Conversely, in less dense panda populations, bite size and distance-between-scat criteria are more likely to correctly distinguish individuals. Both Durnin (2005) and Wan et al. (2005) found close agreement between population estimates derived from bite sizes and DNA in scats in portions of 2 other panda reserves where the density was substantially less than in eastern Wanglang. That does not necessarily mean that any of these population estimates were accurate, but indicates that the difference between the DNA and bite-size derived estimates at Wanglang are not universal through the panda range.

Applying a correction factor derived from Wanglang to adjust population estimates elsewhere may thus lead to significant over-estimation of total numbers, especially if the DNA estimate at Wanglang is itself too high due to lack of closure. Even if DNA estimates were conducted in a number of different reserves, summing them, or applying a correction factor derived from comparison with bite-size estimates, would still yield an overestimate if each were inflated due to the closure issue.

Over-estimation of panda numbers would not just be an academic error. As their red-listing status is based entirely on estimated population size and trend, revised estimates, if generally accepted, would mandate that this species be downlisted. For example, Zhan et al.’s (2006) estimates suggest that some panda populations may have more than 250

mature individuals, which would mean that the species would no longer fit the criteria for endangered. Certainly, their listed status should be changed if they have indeed recovered to the extent that they no longer fit the criteria for this category. This would be indicative of the success of current panda conservation efforts, and offer support for continuation of the types and level of conservation initiatives instituted by the Chinese government, with help from the international conservation community. We believe, however, that there is a strong possibility that Zhan et al.’s (2006) estimate for Wanglang was biased high, and furthermore that it is inappropriate, both scientifically and in terms of panda conservation, to extrapolate results from this single point to the rangewide population. Indeed, it was this extrapolation, and not the specific situation in Wanglang, that attracted and continues to attract international attention.

A follow-up paper by some of the same authors cites the Zhan et al. (2006) article as showing that the “molecular census found that the national survey may have substantially underestimated the population, implying that the population may not have gone down to the tiny numbers previously thought,” supporting their contention that “the species has a much better chance of long-term viability” (Zhang et al. 2007:1808). They add the caveat that this optimistic prediction assumes continued habitat protection, but this misses the point: if panda numbers are indeed this high and increasing, the current level of habitat protection may be sufficient; if not, then more protection may be needed.

Recommendations

Our observations, experience, and evaluation of the present evidence indicate the need for more scrutiny of the data as well as expanded monitoring before concluding that there are now far more pandas than anyone imagined, or that the new population number “augers well for giant panda conservation” (Zhan et al. 2006:R452). For a politically-sensitive, conservation flagship species such as this, where the success or failure of conservation initiatives is gauged largely by periodic assessments of total numbers, scientists should exercise great caution and critical analysis when producing population estimates.

We do not defend either the bite-size methodology or the resulting population estimates. Moreover, we applaud the molecular advances made by Zhan et al.

(2006), and view these as a potentially significant improvement in population estimation and monitoring. Our comments here are meant as a warning to the conservation community that there is still substantial uncertainty related to panda populations. In this regard we make the following specific suggestions for future work:

- (1) Testing and reporting of error rates in molecular analysis of panda feces, combined with an analysis of the effects of such errors on population estimates.
- (2) Comparison of molecular and bite-size derived estimates in other reserves, applied to the same, short-term collection of feces.
- (3) Incorporation of molecular methods for differentiating feces in the next National Panda Survey. However, to compare results and thereby ascertain population trend, the bite-size technique should also be continued (with the same criteria as used in the Third National Survey) in the next survey.

Currently, many reserves in China are monitoring changes in panda numbers using scat surveys conducted every few months. Such frequent trend monitoring is preferable to rangewide surveys spaced at intervals of more than a decade. However, because of the extraordinary attention directed toward the giant panda, there will continue to be a desire to obtain estimates not only of population trend, but of total numbers—and unlike all other bear species, the range of the giant panda is sufficiently small to make such an estimate logistically feasible. It is important to note, though, that the National Surveys serve not only to obtain a population estimate for pandas, but also to detect changes their geographic range, to acquire information on habitat use, and to build capacity among the many individuals involved in the fieldwork. These are greater aids to conservation than point estimates of total numbers.

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