



**Population density and abundance of Lions  
in Yankari Game Reserve, 2008**

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**By**

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**This survey commenced for one year from May 2007 with observational counts and faecal sample collection along predetermined tracks within Yankari Game Reserve in Bauchi, Northern Nigeria. In total 356 faecal samples were collected and from 108 we extracted DNA. Mitochondrial DNA analyses showed that two samples originated from Hyenas. A total of 33 samples contained DNA from lions and microsatellite analyses demonstrated that these involved at least 16 different individuals**

Direct counts through observations are often not a reliable and accurate form to survey mammals due to detectability problem whereby not all individuals may be encountered and counted. DNA-based analysis of faeces (Höss et al. 1992) is potentially a more reliable method of counting individuals in a population (Kohn and Kauner 1997; Kohn and Wayne 1997). This method requires that faeces can be easily found and recovered (Kohn et al. 1999), and suits well for large carnivores such as the Lions (*Panthera leo*) that often defecate along trails to mark territory boundaries (Macdonald 1980). This method has been used intensively, and successfully, in studies on e.g. Mountain Lions (*Puma concolor*; Ernest et al. 2000) and in Sweden to keep track of the Wolf (*Canis lupus*) population (Bensch et al. 2006)

Yankari Game Reserve (The Reserve) is one of the few areas in Nigeria that still harbours Lions. Today Lions are virtually absent in unprotected areas and can mainly be seen in National Parks, Reserves and Zoos.

Yankari Game Reserve (The Reserve), 9°50'N and 10°30'E, is located 100 km south east of Bauchi town in Bauchi state, Nigeria. The Reserve is situated on the border of the Sudan – Guinea Savanna zone and covers an area of 2,244 km<sup>2</sup> (Geerling 1973). The vegetation is made up of swampy flood plains bordered by patches of forest (gallery and riparian), woodland savanna and human occupation zones (farmland and villages; Crick and Marshall 1981, Green 1988). The Reserve records an average rainfall of about 1000 mm a year which occurs between April and October (Crick and Marshall 1981). The variety of mammal species found within the Reserve includes, Lions, e.g. Elephants (*Loxodonta africana*; last estimate 2006 was 358 which make this the largest herd of Savanna Elephants in West Africa, Roan Antelope (*Hippotragus equinus*), Waterbuck (*Kobus ellipsiprymnus*), and Hippopotamus (*Hippopotamus*

*amphibius*).

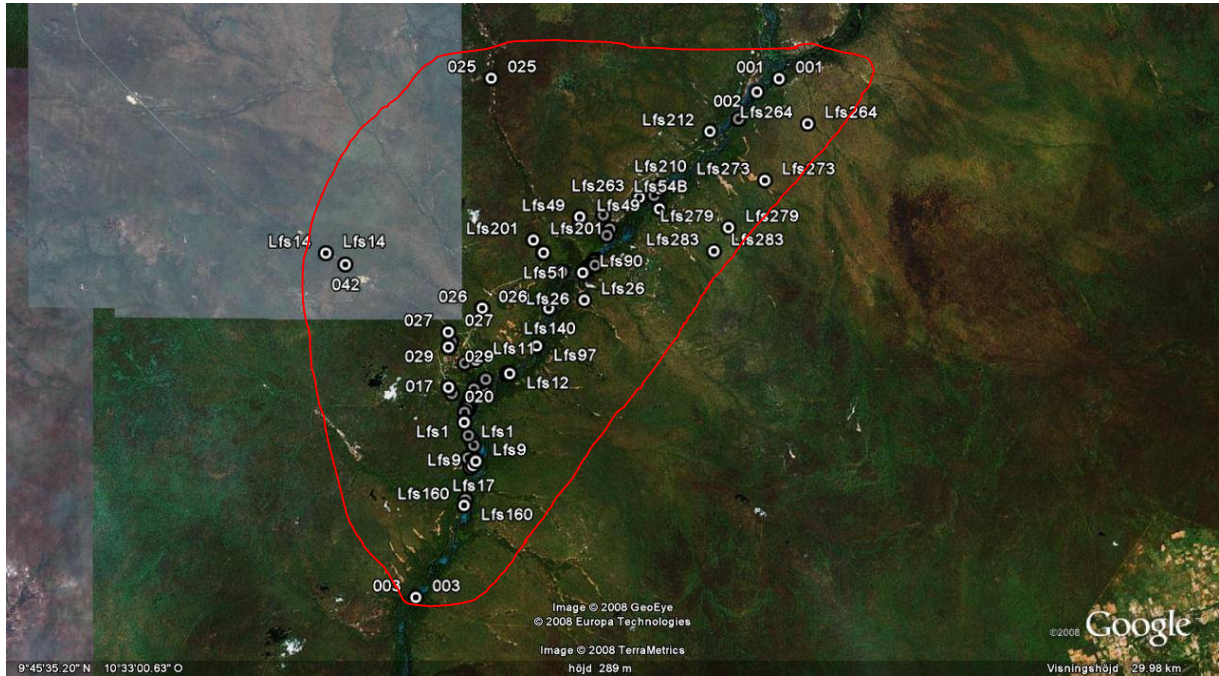


Figure 1. Google Earth image with observations, 001-042, and sites for faecal sampling points marked Lfsxxx. The red line shows the area within which all observations were done and all faeces collected of about 125 km<sup>2</sup>.

The field search for Lions and the faecal sample collection were carried out systematically and exhaustively along predetermined tracks in the reserve. Intensive searches progressed in the core area of the Reserve, along the River Gaji (Fig. 1), where we confined daily searches, often throughout the day, but mainly in the morning and late afternoon-evening periods. The area covered was about 30 km from north to south and extended about 10 km east to west, though observations and faeces were done and found within a smaller area (see Fig. 1). Outside this area, which is most of the Reserve, movement was unfortunately, to large extent impossible due to the bad state of the tracks. Cues such as roars, footprints and alert behaviour of Lion preys were used to locate Lions. We made good efforts to identify individual Lions by their whisker spot pattern using binoculars and close up colour photographs of full face and side views. The pattern formed by the top row of whiskers differs in every Lion and remains the same throughout

its lifetime. Field researchers often use this unique pattern to identify specific animals (c.f. Fig. 2. Pennycuick & Rudnai 1970).



Figure 2. An example of difference in whisker spots in two individual lions (Photo by Talatu Tende).

A total of 75 days and 540 hours were spent in the field during this survey. 356 faecal samples were collected. All faecal samples were stored in 99% ethanol and after arrival to the laboratory stored in a temperature of  $-50^{\circ}\text{C}$  until DNA extraction. DNA was extracted from faeces using Stool DNA extraction protocols in QIAamp® (Qiagen). A polymerase chain reaction and electrophoresis condition as described by Ernest et al. (2000) was used to determine PCR products. Due to time and money constraints, DNA was extracted from 108 samples only.

We used the PCR-technique with locus-specific primers to amplify and sequence a short (206

bp) portion of the mitochondrial cytochrome b gene in both Lions and hyenas. The primers LIHYF (5' - ATGACCAACATTCGAAAATCWC-3') and LIHYR (5' - ATGTGGGTSACTGATGAG-3') were designed to avoid amplification of human and ungulate DNA in general, in order to promote detection of the target species. This resulted in the successful amplification of 43 faecal samples (40%). When tested with BLAST against the GenBank sequence data base, we found that 33 sequences matched with the Lion and two with the Spotted Hyena (*Crocuta crocuta*).

To get individual molecular fingerprints, we scored the 33 Lion samples for allelic variation at two microsatellite genetic markers, locus Ple53 and locus Ple56 (Gaur et al. 2006). From these, 28 samples produced successful results on at least one microsatellite marker. Seven faecal samples showed signs of contamination, i.e. the samples contained genetic material from two or more Lions, and was not used for further analyses, leaving us with 21 samples. Both microsatellite markers showed relatively high genetic variation. Ple53 carried six alleles (among 15 individuals) and had an expected heterozygosity (assuming Hardy-Weinberg equilibrium) of 0.80. Ple56 carried seven alleles (among 14 individuals) and had an expected heterozygosity of 0.77. This indicates that the Lions in The Reserve consisted, at least until rather recently, of a large and/or open population.

We can conclude that the 21 successful samples consisted of at least eleven individuals, which is likely to be an underestimate, considering the few markers analyzed, and 16 individuals is probable (Fig. 3). Moreover, the effort curve shows low tendency to level off, which would be expected if the number of individuals genetically identified approach the population size or if the population were highly inbred.

When we compared the observed and expected heterozygosity we found that both markers had a lower observed heterozygosity than expected at random mating (0.61 and 0.57 in Ple53 and Ple56, respectively). This indicates that the population is partially inbred. Alternatively, it may

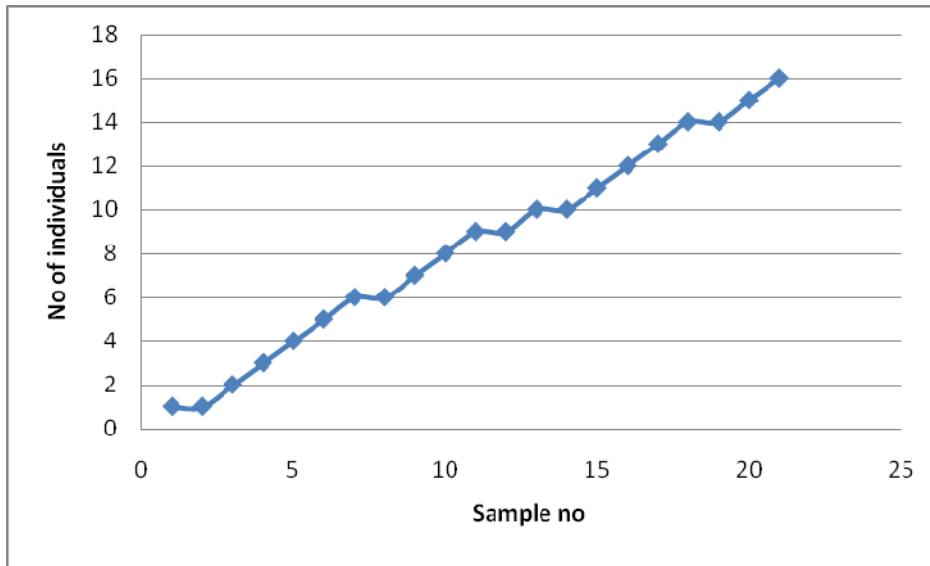


Figure 3. Effort curve showing the cumulative number of new individual encountered in comparison with the number of successful samples.

result from an underestimation of the observed heterozygosity and more samples and markers need to be run to draw stronger conclusions about the frequency of inbreeding in the population.

During the study, Lions were observed by us or reported by rangers at 43 different occasions all in all including 95 different individual sightings. A more detailed analysis of the observational data, considering the sex, age and the number and locations, suggests that a minimum of 35 individuals were observed comprising about 22 females (probably involving some juveniles/immature), 8 males and 5 juveniles. The largest pride we encountered hunting and feeding after a catch was made up of six individuals comprising of 2 males and 4 females and this pride was seen in the same area for several days.

From whisker spots we have identified more than 10 different individuals but for this part of the project we need more and better photographs.

From the molecular part of this study we can conclude that there are definitely at least 16 lions in Yankari, and if we continue to encounter new individuals at the same rate as shown in Figure 3,

the 356 samples we have will yield 52 individuals. However, it is also likely that the encounter rate of new individuals will level off and eventually reach an asymptote at a level lower than 52.

Putting the molecular data, 16-50 lions, and observational data, approx 35 lions, together we can make an educated guess that within the studied area we have lion population of 30-40 individuals. The population of Lions in the remaining part of the Reserve which we did not cover is probably small or non-existing, though further investigation is needed to prove this.

### *Acknowledgement*

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