



Who knows poo? Inaccuracy of scat identifications in the field necessitates genetic confirmation of scat donors

Ryan E. Forbes^{1,2} · Kristoffer T. Everatt^{1,3} · Leah Andresen^{1,3} · Göran Spong^{2,4} · Graham I. H. Kerley¹

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Abstract

Non-invasive sampling using faeces can provide valuable ecological information on rare and elusive species, for example histological diet analyses. However, inaccurate field identifications can prejudice our understanding of carnivore ecology. We assessed the accuracy of field identifications for scats collected (2014–2016) across the Greater Limpopo Transfrontier Conservation Area, in southern Africa, that were putatively identified as African lion (*Panthera leo*) and leopard (*P. pardus*) in the field. 314 and 413 scats were collected and identified in the field as from lion and leopard. These scats were subjected to genetic analyses, producing genotypes from 134, 213 and 58 scats from lions, leopards and cheetah (*Acinonyx jubatus*), respectively. 21% ($n=57$) and 3.7% ($n=10$) of scats identified as leopards in the field were genetically confirmed to be cheetah and lion respectively. 6.7% ($n=9$) and 0.8% ($n=1$) of scats identified as lions in the field were genetically confirmed to be leopards and cheetah scats, respectively. We then compared diet compositions for lions and leopards derived from scats identified in the field, relative to those identified genetically, using a subsample of the scats collected. Lion diets did not differ significantly between the methods of scat identification. Conversely, leopard diet compositions differed slightly between the methods of scat identification, based on the contribution of different prey size classes to leopard diets and leopard prey preferences. We also provide weak evidence that field identifications of scats can underestimate the degree of diet overlap between lions and leopards. We urge those using non-invasive scat sampling to genetically confirm the identity of the scat donor, to ensure unbiased descriptions of carnivore ecology.

Keywords Diet composition · Non-invasive genetic sampling · Lion · Leopard · Cheetah

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✉ Graham I. H. Kerley
graham.kerley@mandela.ac.za

Ryan E. Forbes
rforbes0502@gmail.com

Kristoffer T. Everatt
kteveratt@gmail.com

Leah Andresen
leah.andresen@ecofor.ca

Göran Spong
goran.spong@slu.se

- ¹ Centre for African Conservation Ecology, Nelson Mandela University, P.O. Box 77000, Gqeberha 6031, South Africa
- ² Molecular Ecology Group, Department of Wildlife, Fish and Environmental Studies, Swedish University of Agricultural Sciences, Umeå SE-901 83, Sweden
- ³ Greater Limpopo Carnivore Programme, Limpopo National Park, Mozambique
- ⁴ Luke, Latokartanonkaari 9, Helsinki FI-00790, Finland

Introduction

Effective wildlife conservation and management is strengthened by the availability of robust data on species ecology. Given the difficulty of studying rare and elusive animals such as carnivores (Putman 1984), non-invasive techniques such as scat sampling are used to describe various aspects of their ecology, including diets (Klare et al. 2011), population sizes (Schauster et al. 2002; Spitzer et al. 2016; Forbes et al. 2025b), occupancy (Long et al. 2011; Schooley et al. 2012), stress hormone levels (Van Meter et al. 2009) and population genetics (Waits and Paetkau 2005). However, despite the unquestionable value of information gathered non-invasively from scats, incorrect field identifications of scats can lead to a biased and incorrect assumptions of animal ecology (Lonsinger et al. 2015; Morin et al. 2016; Weiskopf et al. 2016; Akrim et al. 2018).

The issue of scat mis-identification in the field have been well-documented for carnivores in North America (Prugh

and Ritland 2005; Lonsinger et al. 2015; Morin et al. 2016), Europe (Davison et al. 2002; Harrington et al. 2010; Monterroso et al. 2013), and Asia (Anwar et al. 2011; Shehzad et al. 2012; Weiskopf et al. 2016; Akrim et al. 2018; Fatima et al. 2023; Dou et al. 2025) but remains largely unaddressed in Africa (Havmøller et al. 2021). Scats are typically identified in the field based on their morphology (colour, size, segmentation, etc.) and deposition characteristics (e.g., Stuart and Stuart 2019), where identifications are often aided by additional information such as the presence of nearby animal tracks and scat contents (Prugh and Ritland 2005). Although field identifications may result in a high level of accuracy (Prugh and Ritland 2005), a recent meta-analysis of carnivore studies in North America and Europe found that the median percentage of false positive identifications (i.e., scats incorrectly identified as belonging to the target carnivore) was 18% (Monterroso et al. 2019).

The presence of multiple sympatric carnivore species with overlapping body sizes and diets increases challenges for observers tasked with identifying scats in the field. African savannas for example, may have up to six, sympatric (and typically syntopic), large (>21 kg), terrestrial carnivores that overlap in their diets (Caro and Stoner 2003; Hayward and Kerley 2008), in addition to a host of mesocarnivore species (Caro and Stoner 2003). Despite the high levels of inaccurate field identifications of scats in other systems, quantification of these errors in Africa remains rare (but see Havmøller et al. 2021).

We recently collected scats identified as African lion (*Panthera leo*) and leopard (*P. pardus*) in the field, across the Greater Limpopo Transfrontier Conservation Area, and subjected them to molecular analyses. We then investigated their diets for the Kruger and Limpopo national parks within the Greater Limpopo Transfrontier Conservation Area (Forbes et al. 2024). Additionally, the presence of cheetah (*Acinonyx jubatus*) scats (that were misidentified in the field as leopard) allowed us to opportunistically describe the diets of cheetah in Limpopo National Park (Forbes et al. 2025a). This approach enabled us to ensure our diet descriptions were correctly allocated to our three focal carnivores and provided the opportunity to investigate how scat misidentifications in the field can prejudice the diet descriptions of lions, leopards and cheetahs.

Here, we provide an African example of the degree of scat misidentification in the field and provide insight into how scat misidentification can influence carnivore diet descriptions. Since scats are more frequently misidentified in the field among species that overlap in diet and body size (Echegaray and Vilà 2010; Morin et al. 2016), we predicted cheetah scats would be more frequently misidentified in the field with leopards than with lions, given the overlapping body sizes of cheetahs and leopards. We further expected

that inaccurate scat identifications could have a pronounced influence on carnivore diet descriptions and can alter our understanding of diet overlap, diet breadth and prey preferences of the target study species.

Methods

Study area

Samples were collected in the Greater Limpopo Transfrontier Conservation Area, focusing on South Africa's Kruger National Park (19 485 km²; 260–840 m above sea level (a.s.l.); north of the Olifants River), and Mozambique's Limpopo (11 233 km²; 45–521 m a.s.l.) and Banhine (7 250 km²; 69–181 m a.s.l.) national parks, as well as adjacent community lands in Mozambique, namely the Lebombo (1 320 km²; 182–408 m a.s.l.) and Maunge (833 km²; 162–411 m a.s.l.) conservancies (Fig. S1). Climatically, the region is warm, dry tropical, receiving low and variable rainfall (400–530 mm/year; Gandiwa et al. 2016). Vegetation is mixed savanna woodland and scrubland (Gertenbach 1983; Stalmans et al. 2004; Stalmans and Wishart 2005). The region supports the full large, African carnivore assemblage, including lions, leopards, cheetahs, African wild dogs (*Lycaon pictus*), spotted (*Crocuta crocuta*) and brown (*Hyaena brunnea*) hyenas, as well as a host of mesocarnivores.

Scat sampling

Scats were collected in 2014–2015 in Limpopo and Banhine national parks, and in 2015 in Kruger National Park, and Lebombo and Maunge conservancies during systematic scat surveys using a trained detection dog, within a random sampling design (MacKay et al. 2008). Here, the detection dog was walked between 10 and 20 km in road-accessible regions, in the early morning when scenting is optimal, searching for fresh lion, leopard, cheetah and wild dog scats (excluding spotted hyena because their scats are relatively easy to find without a dog). Scats were identified in the field based on their physical features (colour, size, segmentation, etc.) and deposition characteristics, with identifications aided by other nearby carnivore signs (e.g., tracks; Stuart and Stuart 2019). Scats were double wrapped in air-tight plastic bags, with silica in the inner bag. GPS coordinates of the locations of the collected scats were recorded.

In a laboratory, we moistened dried scats with distilled water and sampled the outer surface that contains intestinal cells with Q-tips. Q-tips were then placed in small envelopes and air-dried for 24–48 h, after which they were stored in an airtight container with silica. Samples were then sent

to the Molecular Ecology Group, Swedish University of Agricultural Sciences (Umeå, Sweden) for DNA extraction and genotyping.

DNA extraction and genotyping

DNA were extracted using Zymo's Quick-DNA faecal/soil extraction kit, following the manufacturer's instructions. A total of 314 and 413 scats putatively identified in the field as from lion and leopard, respectively across the Greater Limpopo Transfrontier Conservation Area, were genotyped on a Fluidigm® Biomark™ using panels of 96 Single Nucleotide Polymorphisms (SNPs) identified for lions and leopards (Mamugy et al. 2024 preprint). A specific SNPs panel has yet to be developed for cheetah. However, cheetah samples display a distinct pattern with respects to homozygous alleles when run on the leopard SNP panel, with this observation being derived from running DNA acquired from cheetah tissue samples on the leopard SNP panel (GS pers. obs.). We did not run samples on SNPs panels for the remainder of the larger carnivore guild due to costs. Consequently, we only genetically confirmed the identify from scats of lion, leopard and cheetah.

Physical sorting

Prior to the genetic identification of scat sources, we subjected a random subsample of 164 putative lion scats (82 scats each from Kruger and Limpopo national parks) and 198 putative leopard scats (82 scats from Kruger National Park and 116 from Limpopo National Park) to physical sorting for describing their diets. Following genetic confirmation of scat donors, 58 and 48 genetically confirmed lion samples from Kruger and Limpopo national parks, respectively, and 60 genetically confirmed leopard samples from each site (Forbes et al. 2024), and 42 cheetah scats from Limpopo National Park (Forbes et al. 2025a) were used to provide a description of their diets.

Data analyses

Accuracy of scat identifications in the field

We calculated the percentage of scats incorrectly identified as from lions and leopards in the field by comparing the field identification of the scat with that of the genetic identification. We excluded samples where DNA extraction and carnivore identification was unsuccessful. To test the prediction that cheetah scats would be more frequently confused in the field with leopards than with lions, we compared the percentage of cheetah scats misidentified in the field as leopard scats, with the percentage of cheetah scats

misidentified as lion scats in the field, using two-proportion Z-tests with continuity corrections, in R (v 4.3.1) software (R Core Team 2023).

Diet compositions

See Forbes et al. 2024, 2025a) for full diet descriptions for lions and leopards in Kruger National Park and Limpopo National Park, and for cheetah in Limpopo National Park, respectively. Since we performed the same analyses here as we did in our previous studies (except here we assessed how the outputs from these analyses differed based on diet descriptions derived from scats identified in the field relative to those genetically identified), we briefly describe these analyses and direct readers to our previous studies for detailed descriptions of the analyses below.

Size class consumed

We grouped wild prey into size classes (very small: < 5 kg, small: 5–25 kg, medium: 25–100 kg, and large: > 100 kg), with prey body mass being determined using $\frac{3}{4}$ mean adult female body mass (Hayward and Kerley 2005), using published prey masses (Stuart and Stuart 2015). We determined the percentage biomass consumed in each size class using a generalised biomass model (Chakrabarti et al. 2016). We compared the percentage biomass consumed in each size class for lions and leopards in Limpopo National Park and Kruger National Park, in relation to the method of scat identification (i.e., diets descriptions derived from scats identified in the field, versus those identified genetically), using two-proportion Z-tests, with continuity corrections.

Diet breadth and overlap

We calculated lion, leopard and cheetah diet breadth in Limpopo National Park and for lions and leopards in Kruger National Park, using the standardised Levin's index (Hurlbert 1978). We then assessed the degree of diet overlap between lions, leopards and cheetah in Limpopo National Park, and between lions and leopards in Kruger National Park using the Pianka index (Pianka 1973). We compared diet breadths within each carnivore at each site, and diet overlap between lions and leopards at both sites, based on whether diet descriptions were derived from scats identified in the field versus genetically. We assessed the significance of these differences using *G*-tests, in the R package "AMR" (Berends et al. 2022).

Prey preferences

Prey preferences were estimated as the Jacobs' index (Jacobs 1974) using estimates of the frequency of each prey species consumed in relation to prey availability, with prey availability acquired from Everatt et al. (2023). We assessed lion, leopard and cheetah prey preferences at each site based on whether diet descriptions were derived from scats identified in the field versus genetically.

Diet similarity

To visualise differences in lion, leopard and cheetah diet descriptions derived from scats identified in the field relative to those confirmed genetically, we ran non-metric Multidimensional scaling (nMDS) ordinations, based on Bray-Curtis similarity, in the package "vegan" (Oksanen et al. 2013). We then performed an analysis of similarity (ANOSIM) to assess whether diet descriptions differ (Landman et al. 2013; Cornhill and Kerley 2020) based on the scat identification method. The ANOSIM tests differences using Global R , which ranges from -1 to 1 , with low and high values representing high and low diet similarity, respectively (Clarke 1993). Given that our sample sizes differed, we validated ANOSIM results using permutation tests. Permutation tests produced similar results to the ANOSIM, and we therefore

only report the ANOSIM outputs. Lastly, we ran a SIMPER analysis to assess which species contributed to dissimilarity between diet descriptions (Landman et al. 2013; Cornhill and Kerley 2020).

Results

Of the 314 and 413 scats identified as lion and leopard scats in the field, respectively, genotypes from 134, 213 and 58 scats, respectively, were successfully obtained from lions, leopards and cheetah. Unsuccessful DNA extraction and/or genotyping occurred in 180 (57.3%) and 142 (34.4%) scats identified in the field as from lions and leopards, respectively.

Inaccuracy of scat identifications in the field

Of the scats where the scat donor was successfully determined, 21.03% and 3.69% of scats identified as leopard scats in the field were genetically confirmed to be cheetah and lion, respectively (Fig. 1). 6.72% and 0.75% of scats identified as lion scats in the field were genetically confirmed to be leopard and cheetah scats, respectively (Fig. 1). As predicted, cheetah scats were more frequently mistaken for leopard scats relative to lion scats ($Z_1 = 28.44, p < 0.001$).

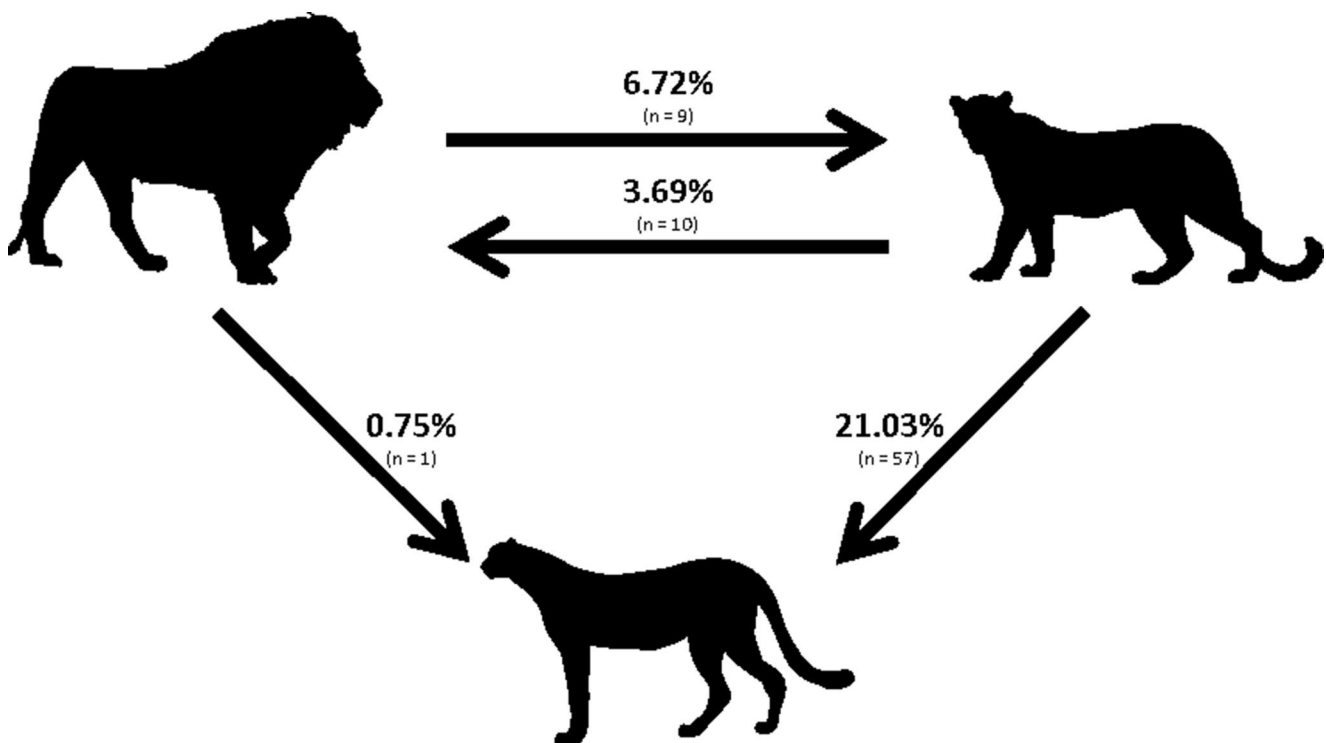


Fig. 1 Accuracy of scat identifications in the field. The direction of arrows shows scats that were identified as a certain species in the field, but genetically confirmed to be the species the arrow points to. No scat

samples identified as cheetah in the field were genetically analysed. Lion - top left, leopard - top right, cheetah - bottom centre. n number of scats misidentified in the field

However, there was no difference in directionality of false positives for lion and leopard scats ($Z_1=1.22, p=0.27$).

Prejudiced diet descriptions

A total of 58 and 48 genetically-confirmed lion samples from Kruger and Limpopo national parks respectively, 60 genetically confirmed leopard samples from Kruger and Limpopo national parks, and 42 genetically confirmed cheetah samples from Limpopo National Park were used to describe their diets (Forbes et al. 2024, 2025a). Of the 164 scats identified as lion and leopard in the field that were initially used to describe their diets, 3 genetically confirmed lion samples were mistakenly used in leopard diet descriptions, and 6 genetically confirmed leopard samples were mistakenly used in lion diet descriptions. Furthermore, of the 82 samples identified as leopards in the field in Limpopo National Park that were initially used to describe leopard diets, 8 of these samples were genetically confirmed to be cheetah.

Size class consumed

Contrary to predictions, the relative biomass consumed in relation to prey size class for lions did not differ in Limpopo National Park or Kruger National Park, and for leopards in Limpopo National Park, when comparing diet descriptions derived from scats identified in the field relative to those genetically identified (Fig. 2). More pronounced differences were however, recorded for leopards with respect to the method of scat identification in Kruger National Park, particularly in the small- and medium-sized prey classes, that tended to differ, but this was not significant (small: $Z_1=2.80, p=0.094$; medium: $Z_1=3.38, p=0.07$; Fig. 2). Here, leopard diet descriptions based on scats identified in the field suggested that small- and medium-sized prey contributed to 13.9% and 63.5% of the relative biomass consumed. However, leopard diet descriptions based on scats identified genetically suggested that small- and medium-sized prey contributed to 23.7% and 50.1% of the relative biomass consumed in Kruger National Park.

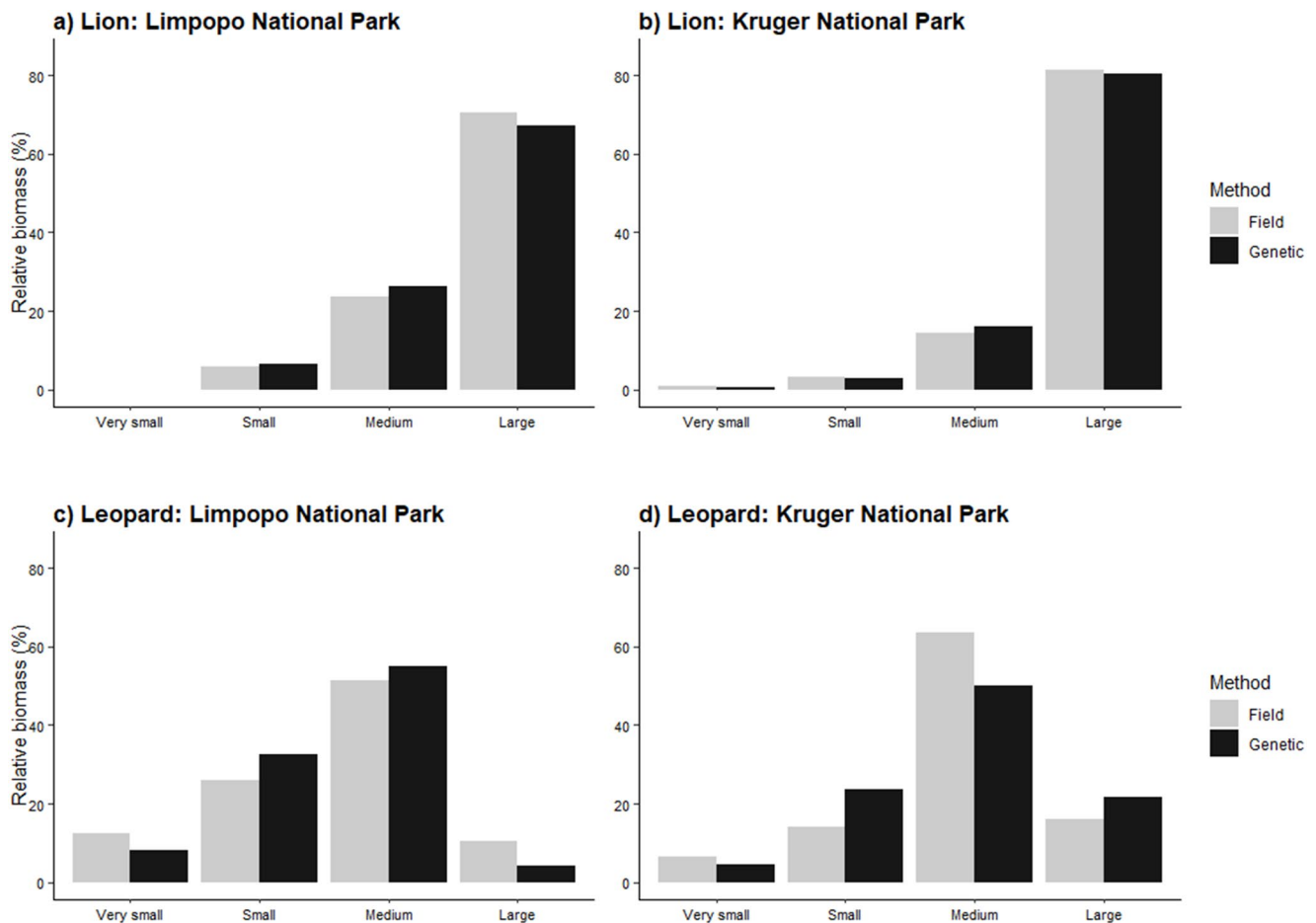


Fig. 2 Relative biomass consumed in relation to prey size class (very small: < 5 kg, small: 5–25 kg, medium: 25–100 kg, large: > 100 kg) for lion in the Limpopo (a) and Kruger (b) national parks, and for leopard

in the Limpopo (c) and Kruger (d) national parks, based on scats identified in the field (grey bars) and genetically (black bars)

Diet breadth and overlap

Contrary to predictions, diet breadth and overlap values were similar when comparing diet descriptions derived from scats identified in the field and those identified genetically and did not differ significantly within carnivores (Fig. 3). However, we note a large increase (albeit non-significant; $G=2.99$, $p=0.08$) in overlap in Kruger National Park between lions and leopards when diets were described using scats genetically confirmed to be lions and leopards (Pianka index=0.40) relative to those identified in the field (Pianka index=0.26; Fig. 3).

Prey preferences

Broadly, lion prey preferences based on diet estimates derived from scats identified in the field and those genetically identified were similar in Kruger National Park and Limpopo National Park (Fig. 4). However, noteworthy differences were recorded. For example, in Limpopo National Park, lions showed a strong preference (>0.5) for kudu (*Tragelaphus strepsiceros*) based on scats identified in the field (Jacobs' index=0.54), whereas preference for kudu was only slight (Jacobs' index=0.27) based on scats genetically identified (Fig. 4). Additionally, in Kruger National Park, lions showed a slight preference for zebra (*Equus quagga*) based on scats identified in the field (Jacobs' index=0.10), and a slight avoidance for zebra based on genetically identified scats (Jacobs' index = -0.15; Fig. 4).

Differences between prey preferences for scats identified in the field relative to those genetically identified were more

pronounced for leopards, particularly in Limpopo National Park (Fig. 4). Based on scats identified in the field, leopards showed preferences for kudu (Jacobs' index=0.13) and wildebeest (*Connochaetes taurinus*; Jacobs' index=0.45) but avoided these species (Jacobs' index = -0.42 and Jacobs' index = -1 for kudu and wildebeest, respectively) based on scats identified genetically (Fig. 4). Additionally, leopards avoided zebra (Jacobs' index = -0.31) and completely avoided waterbuck (*Kobus ellipsiprymnus*; Jacobs' index = -1), based on scats identified in the field. However, zebra and waterbuck were completely (Jacobs' index = -1) and slightly (Jacobs' index = -0.40) avoided, based on scats genetically identified. Furthermore, in Kruger National Park, leopards consumed zebra relative to their abundance (Jacobs' index=0.05) based on scats identified in the field but showed a slight avoidance for zebra (Jacobs' index = -0.34) based on scats identified genetically (Fig. 4).

Analysis of similarity

Contrary to predictions, diet descriptions did not differ significantly for both lions (Limpopo National Park: Global $R = -0.01$; $p=0.89$; Kruger National Park: Global $R = -0.01$; $p=0.86$) and leopards (Limpopo National Park: Global $R = -0.01$; $p=0.71$; Kruger National Park: Global $R = -0.01$; $p=0.68$) in Limpopo National Park and Kruger National Park, based on whether scats were identified in the field or genetically (Fig. 5). In Limpopo National Park, buffalo (*Syncerus caffer*; 20%) and impala (*Aepyceros melampus*; 11%), and impala (23%) and duiker (*Sylvicapra grimmia*; 10.6%) accounted for the majority of dissimilarity between

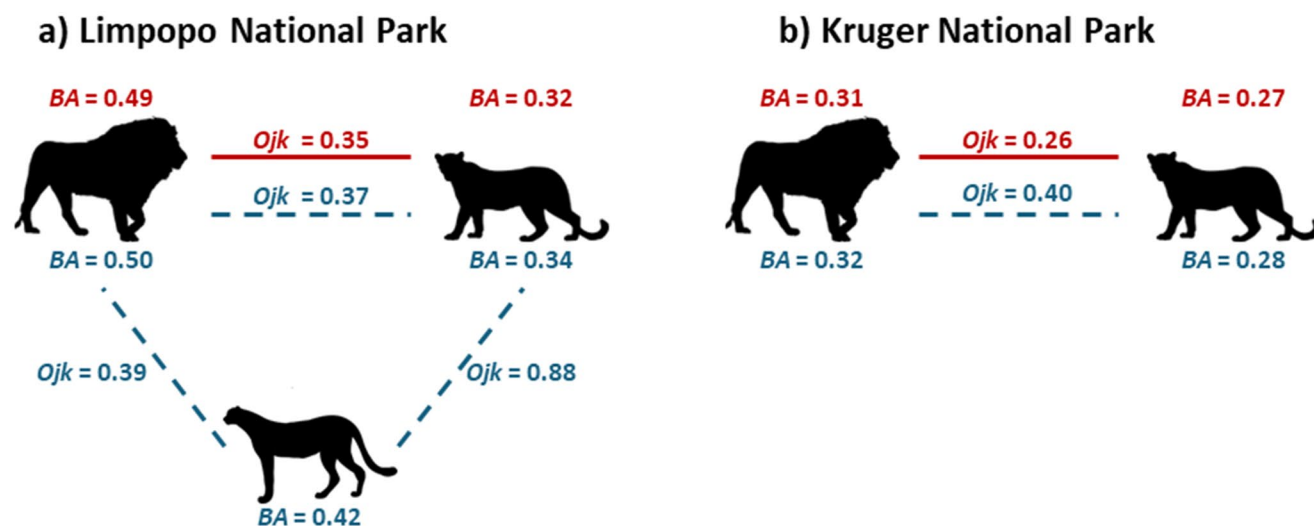


Fig. 3 Diet breadth (Levin's index; BA) and overlap (Pianka index; O_{jk}) for lion, leopard and cheetah in Limpopo National Park (a), and for lion and leopard in Kruger National Park (b), based on the method of scat identification. Text in red and blue refer to BA and O_{jk} values for diet descriptions based on scats identified in the field and genetically,

respectively. Solid, red lines between silhouettes refer to O_{jk} for those carnivores based on scats identified in the field, whereas dotted, blue lines between silhouettes refer to O_{jk} for those carnivores based on scats identified genetically

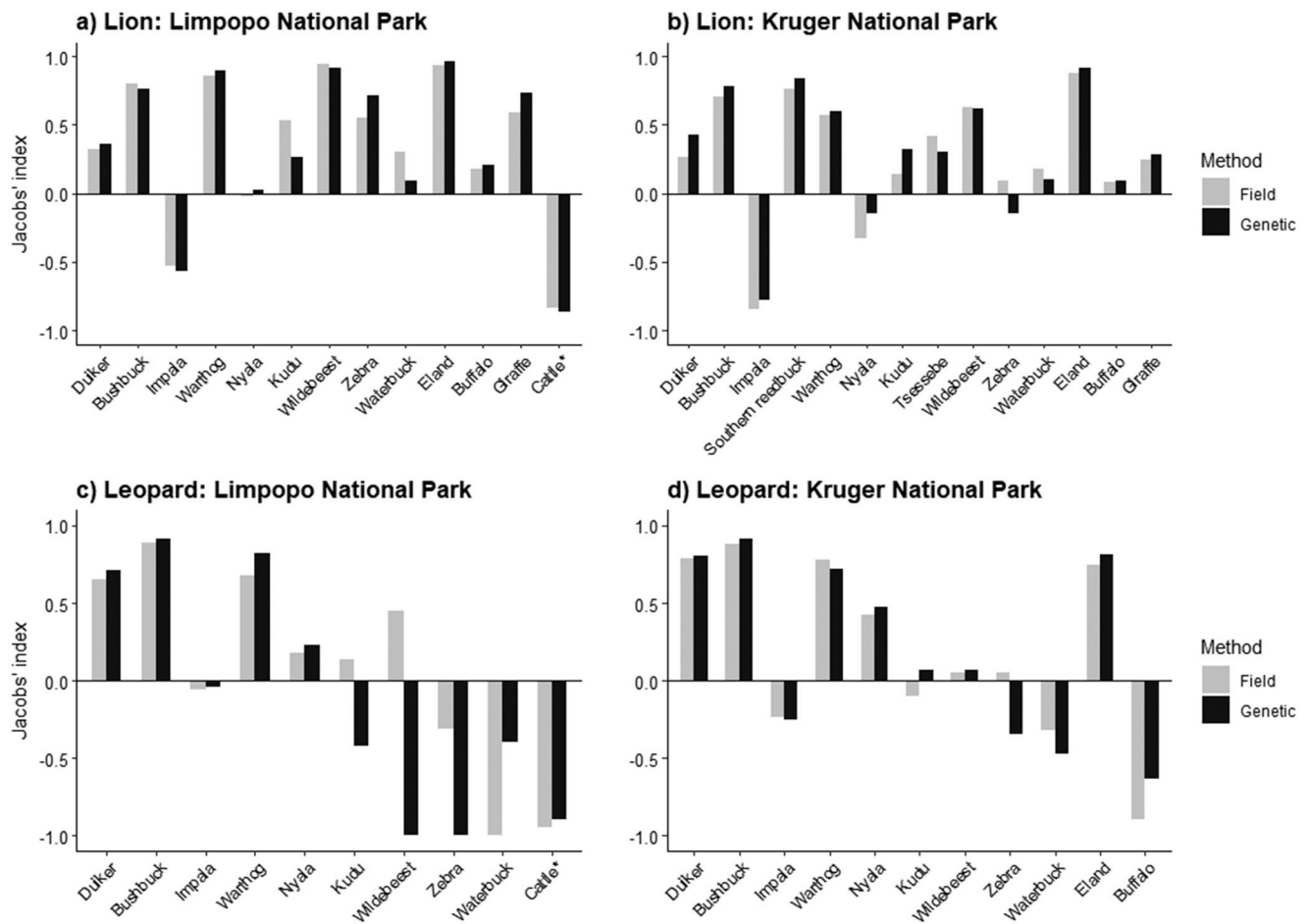


Fig. 4 Prey preferences (Jacobs' index) for lions in Limpopo (a) and Kruger (b) national parks, and for leopards in Limpopo (c) and Kruger (d) national parks, based on scats identified in the field (grey bars) and

genetically (black bars). Prey ordered in ascending body mass from left to right, and cattle (*) placed at the end of each plot (in Limpopo National Park only)

lion and leopard diet descriptions based on scats identified in the field versus genetically (Fig. 5). Diet descriptions based on genetically-confirmed leopard and cheetah scats in Limpopo National Park differed, albeit non-significantly (Global $R=0.004$, $p=0.27$), with most of the dissimilarity being attributed to impala (22%) and duiker (9%; Fig. 5). In Kruger National Park, buffalo (26%) and blue wildebeest (15%), and impala (24%) and warthog (*Phacochoerus africanus*; 10%) accounted for the majority of dissimilarity between lion and leopard diet descriptions, respectively, based on scats identified in the field versus those identified genetically (Fig. 5).

Discussion

We investigated the accuracy of scat identifications in the field and assessed how inaccurate scat identifications in the field can prejudice carnivore diet descriptions. Given that inaccurate scat identification in the field can prejudice

understanding of carnivore ecology (Lonsinger et al. 2015; Morin et al. 2016; Weiskopf et al. 2016; Akrim et al. 2018), quantifying the degree of this inaccuracy is vital for using scats as a source of information on carnivore ecology. Our work fills a key knowledge gap, serving as one of the first descriptions of the degree of scat misidentifications in Africa (Havmøller et al. 2021), and the first African example of how inaccurate scat identifications can prejudice diet descriptions.

Inaccuracy of scat identifications in the field

As predicted, the directionality of scat misidentifications in the field differed between our focal carnivores, where false positives were higher between cheetah and leopard than cheetah and lion. Cheetah and leopard are typically solitary, similarly-sized and are far smaller than gregarious lions (Stuart and Stuart 2015), which possibly explains the higher rate of confusion between cheetah and leopard scats, than between cheetah and lion, and between leopard and lion

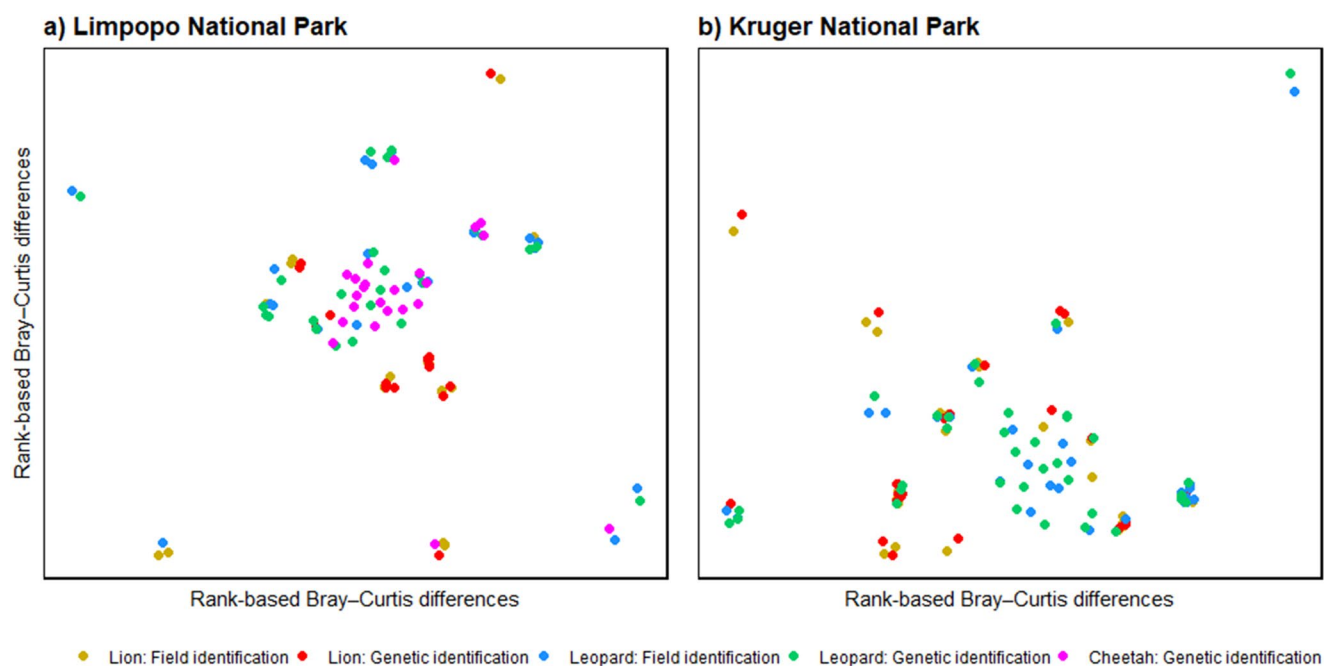


Fig. 5 Non-metric multidimensional scaling plot (based on Bray-Curtis similarity) for carnivore diet composition estimates in the Limpopo (a; 2D stress < 0.01) and Kruger (b; 2D stress < 0.01) national parks, with respects to the method of scat donor identification (in the field vs.

genetic). Scats genetically confirmed to be lion, leopard and cheetah are represented by red, green and purple points respectively, and scats identified as lion and leopard in the field are represented by orange and blue points, respectively

scats. This finding supports previous studies on both carnivores and ungulates, where faeces from species of similar body size and within the same taxonomic family are more prone to confusion than those with differing body sizes and in different families (Echegaray and Vilà 2010; Morin et al. 2016; Spitzer et al. 2019).

In the only other study conducted in Africa that reported on the inaccuracy of field identifications of scats (Havmøller et al. 2021), 12% and 6% of scats identified as leopards in the field were genetically confirmed as spotted hyena and serval (*Leptailurus serval*). The false positive percentages recorded here (ranging between 1 and 21%) are largely consistent with Havmøller et al. (2021) findings, and with the 18% median false positive percentage recorded in a meta-analysis across North America and Europe (Monterroso et al. 2019), with some studies recording false-positive rates of >75% (Davison et al. 2002; Monterroso et al. 2013; Lonsinger et al. 2015). However, all these previous studies reporting on scat misidentifications in the field (including Havmøller et al. 2021) lack the carnivore diversity present in our study area.

We believe our results are an underestimate of the full extent of the inaccuracy of field identifications, since we were only able to identify three of the carnivore species present in our study area. Indeed, this may explain the large proportion of scats subjected to molecular analysis that we were unable to successfully genotype/extract DNA from. Since scats were collected ~9 years prior to molecular

analysis, we suspect that the large proportion of scats that did not produce genotypes is partly due to DNA degradation. However, the difference between the genotyping/DNA extraction success rates between scats identified as lions and leopards in the field suggests that lion scats may be more prone to confusion with other carnivores such as spotted hyena and wild dogs, that we were unable to identify. Additionally, although scats are typically confused more frequently between closely-related species, and those with similar body sizes, scats from mesocarnivores are frequently confused with large carnivores elsewhere. For example, in Tajikistan, ~40% of scats identified as snow leopard (*P. uncia*) in the field, were genetically confirmed to be red fox (*Vulpes vulpes*) scats, even though these species differ in size and are not closely related (Weiskopf et al. 2016). Indeed, scat diameter and deposition traits overlap between and within meso- and large- carnivore species (Lonsinger et al. 2015; Stuart and Stuart 2019), and confusion may therefore be prevalent between carnivores of differing sizes. Furthermore, we encourage researchers to be cognisant for the potential of over-marking by mesocarnivores (Wikenros et al. 2017), which may contaminate the scats of the larger, target carnivores (see Groen et al. 2023 for example of how over-marking may have influenced the description of lion diets).

Scat detection dogs can be trained to detect and indicate scat samples from a single species with high accuracy (Mackay et al. 2008). However, for this study we chose not

to have the dog trained for a single species but rather to detect any sample from a group of species, namely lion, leopard, cheetah and wild dog to study the entire large carnivore guild. If, however, we chose to have the dog trained to detect a single species only then presumably the inaccuracy in field identification of scats of that one species found by this study would be significantly lower. For example, in a controlled laboratory experiment, Grimm-Seyfarth et al. (2019) showed that detection dogs were able to correctly discriminate scats Eurasian otter (*Lutra lutra*) and the American mink (*Neovison vison*) scats with an accuracy of 95%. However, since various factors influence the accuracy of detection dogs in identifying scats of target species (Long et al. 2007; DeMatteo et al. 2018), genetic confirmation of these identifications is still advised.

Diet descriptions

Leopard diet descriptions derived from scats identified in the field relative to those genetically identified differed based on relative biomass consumed, prey preferences, and diet overlap. For example, diet descriptions based on scats identified in the field overestimated the importance of medium-sized prey (likely by including lion scats) and underestimated the importance of small- and large prey (likely by mistaking leopard for cheetah scats) in Kruger National Park, based on relative biomass consumed. Prey preferences for leopards also differed based on diet descriptions derived from scats identified in the field relative to those identified genetically in Limpopo National Park, particularly for kudu, wildebeest, zebra and waterbuck. Additionally, diet descriptions based on scats identified in the field relative to those genetically identified underestimated the degree of diet overlap between lions and leopards in Kruger National Park.

Our findings support previous studies that investigated prejudiced diet descriptions due to inaccurate scat identification. For example, in Pakistan the inclusion of scats in snow leopard diet descriptions that were incorrectly identified in the field resulted in the underestimation of ungulates in snow leopard diet (Weiskopf et al. 2016). Additionally, in North America, although the contribution of prey species to the diets of coyote (*C. latrans*), bobcat (*Lynx rufus*) and black bear (*Ursus americanus*) did not change by any order of magnitude based on whether scats were identified in the field or genetically (similar to our study), misidentification resulted in biased estimates of diet breadths and overlap (Morin et al. 2016). Additionally, had we solely relied on field identifications of scats, we would have been unable to describe cheetah diets in Limpopo National Park, since they would have mistakenly been included in our leopard diet descriptions.

Although we recorded dissimilarity in lion and leopard diets based on whether scats were identified in the field relative to those identified genetically, these differences were not significant, contrary to predictions. Indeed, diet descriptions for lion displayed no apparent differences with respect to the relative biomass consumed of different prey size classes, diet breadths, or prey preferences. In North America, Morin et al. (2016) highlighted that biases in diet descriptions may be low when carnivores display a high degree of overlap, which may explain why our diet descriptions did not differ significantly when comparing those derived from scats identified in the field versus those genetically identified. Leopards and cheetah for example, displayed a high degree of overlap in Limpopo National Park, with both carnivores experiencing moderate degrees of diet overlap with lions. Additionally, the broad diet breadth of lions in our study area, in conjunction with the moderate overlap with cheetah and leopards, may mask differences in methods for identifying scats. In regions where lion diet breadths are narrower than in our study, differences between methods for identifying scats and the diet descriptions that result, may be more pronounced. Additional testing in other regions, as well as assessing the diets of the remainder of the larger carnivore guild in our study area may provide clarity.

Implications

Despite the high levels of inaccurate scat identification in the field recorded across the world, and the pervasive influence this can have on carnivore diet descriptions, less than 16% of carnivore diet studies based on scat analyses in North America and Europe (2004–2017), genetically confirmed the identity of the scat donor (Monterroso et al. 2019). The low proportion of genetic confirmation in dietary studies is somewhat alarming considering that it has been possible for DNA to be extracted from faeces since the early 1990s (Höss et al. 1992). Our work, in conjunction with previous studies, highlights that morphological identification of scats in the field is inherently inaccurate and can have a pronounced effect on our understanding of carnivore ecology. Although we recognise the logistical constraints associated with molecular analyses (particularly cost), we believe the use of these methods will ensure accurate descriptions of carnivore ecology. The use of molecular techniques can also allow researchers to investigate other aspects of carnivore ecology. For example, from the scats we collected in the Greater Limpopo Transfrontier Conservation Area, we have described the diets of lions, leopards (Forbes et al. 2024) and cheetah (Forbes et al. 2025a), provided population size estimates for lions (Forbes 2024) and leopards (Forbes et al. 2025b) in the Mozambique portion of the Greater Limpopo Transfrontier Conservation Area, and have investigated lion

and leopard dispersal and connectivity across the region (Forbes 2024). Indeed, from a single scat sampling event, multiple valuable questions can be addressed. However, should the ability for genetic confirmation of the scat donor not be a viable option for researchers, necessary precautions (e.g., witness defaecation, no other carnivore present at study site, etc.) should be followed to ensure that scats are collected from the target species (see Monterroso et al. 2019 for a comprehensive review).

Conclusion

Our study highlights that identifying carnivore scats in the field, based solely on scat morphology is unreliable, particularly in systems with a high diversity of large carnivores such as African savannas. Additionally, the inaccuracy of scat identifications in the field can prejudice our understanding of carnivore ecology, as we have illustrated here using diet descriptions. These prejudices can, extend beyond diet descriptions into, for example, modelling occupancy. Self-evidently, misidentifications of scats in the field can have serious and potentially adverse conservation and management implications. We strongly advocate for the use of non-invasive sampling techniques in studying carnivore ecology but urge future studies examining carnivore ecology using scat analyses to take necessary precautions to ensure that the scat samples are of the target species.

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Data availability The data are at <https://mandela.figshare.com/account/articles/30610109file=59537939>.

Declarations

Compliance with ethical standards The authors declare there are no conflicts of interest. This work is based on non-invasive sampling of excreta; hence no animal ethics approval is required as per institutional policy.

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