

# Masai giraffe population change over 40 years in Arusha National Park

Derek E. Lee<sup>1,2</sup>  | George G. Lohay<sup>1</sup>  | James Madell<sup>2</sup>  | Douglas R. Cavener<sup>1</sup>  |  
Monica L. Bond<sup>1,2,3</sup> 

<sup>1</sup>Department of Biology, Pennsylvania State University, University Park, Pennsylvania, USA

<sup>2</sup>Wild Nature Institute, Concord, New Hampshire, USA

<sup>3</sup>Department of Evolutionary Biology and Environmental Studies, University of Zurich, Zurich, Switzerland

## Correspondence

Derek E. Lee, Department of Biology, Pennsylvania State University, University Park, PA, USA.  
Email: [derek@wildnatureinstitute.org](mailto:derek@wildnatureinstitute.org)

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## Abstract

A population of Masai giraffes (*Giraffa camelopardalis tippelskirchi*) occurs in Arusha National Park (ANP), which is not part of the regular Tanzanian national wildlife monitoring scheme. Urban development of Arusha city and agricultural expansion have contributed to the increasing isolation of ANP from other protected areas in northern Tanzania. The only published data on the Masai giraffe population of ANP were individual-based data collected in 1979 and 1980. Here, we used individual-based data from 2021 to 2022 to provide an update on the current population size, population sex and age structure, movements and genetic connectivity of giraffes in ANP. We documented a 49% population decline and changes in the age distribution, adult sex ratio, reproductive rate and movement patterns relative to the previous study. Mitochondrial DNA analysis revealed genetic connectivity between ANP and other populations east of the Gregory Rift Escarpments in northern Tanzania and southeastern Kenya, evidence that Masai giraffe once moved widely across the landscape.

## KEYWORDS

genetic connectivity, population decline, population monitoring, population structure

## Résumé

Une population de girafes Masai (*Giraffa camelopardalis tippelskirchi*) se trouve dans le parc national d'Arusha (ANP), qui ne fait pas partie du programme national ordinaire de surveillance de la faune sauvage de la Tanzanie. Le développement urbain de la ville d'Arusha et l'expansion agricole ont contribué à l'isolement croissant de l'ANP par rapport aux autres espaces protégés du nord de la Tanzanie. Les seules données publiées sur la population des girafes Masai de l'ANP étaient individuelles-basées sur les données recueillies en 1979 et 1980. Ici, nous avons utilisé des données individuelles de 2021 à 2022 pour fournir une mise à jour sur la taille actuelle de la population, le sexe et la répartition des âges de la population, les mouvements et la connectivité génétique des girafes dans l'ANP. Nous avons noté une baisse de 49% de la population et des changements dans la répartition des âges, le sex-ratio des adultes, le taux de reproduction et les schémas de déplacement par rapport à l'étude

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précédente. L'analyse de l'ADN mitochondrial a révélé la connectivité génétique entre l'ANP et d'autres populations à l'est des escarpements du Gregory Rift dans le nord de la Tanzanie et le sud-est du Kenya, preuve qu'autrefois la girafe Masai se déplaçait largement à travers le paysage.

## 1 | INTRODUCTION

Land conversion, habitat degradation, disease and overhunting have resulted in the extirpation of many African wildlife populations and, consequently, remaining populations are increasingly restricted to protected areas isolated by agriculture and urbanisation (Newmark, 2008). Small, isolated populations are more vulnerable to extinction than larger and connected populations because of stochastic demographic, environmental and genetic threats (Frankham, 2005; Mills et al., 2006; Wilcox & Murphy, 1985). Demographic stochasticity, or variation in realised survival and reproduction rates due to intrinsic differences among individuals, can cause small populations to crash when random outcomes of births and deaths from the low number of individuals deviate from expectations (Legendre, 2020). Environmental stochasticity such as unexpected weather conditions or disease epidemics can devastate small populations (Allendorf et al., 2022; Frankham, 1995). Genetic stochasticity, or genetic drift, in small populations can cause genetic erosion, inbreeding (Allendorf, 2017) and reduced lifespan and fitness (Lohr et al., 2014). Thus, the long-term viability of wildlife species relies on maintaining sufficient population sizes and genetic diversity to counter stochastic threats.

In addition to small population size, body size is an important predictor of local extinction because population growth rates and densities decrease with body size while space needs increase (Cardillo et al., 2005). This makes large mammals among the most vulnerable to local extinction (McKinney, 1997). Giraffes (*Giraffa camelopardalis*) are African endemic mega-herbivore ruminants (Dagg, 2014; Shorrocks, 2016) whose numbers have declined significantly over the past 30 years due to habitat loss and illegal poaching (Muller et al., 2018). The Masai giraffe, a subspecies (*G. c. tippelskirchi*) or species (*G. tippelskirchi*) distributed in Tanzania and southern Kenya, has experienced population declines of ca. 50% since the 1980s to an estimated 35,000 individuals, causing the subspecies to be assessed as endangered on the IUCN Red List (Bolger et al., 2019). Similar declines have been documented for overall large mammal abundance across East Africa (Craigie et al., 2010), but reliable long-term direct assessments of wildlife populations are scarce or non-existent for many locations in the region (Stoner et al., 2007).

A population of Masai giraffes occurs in Arusha National Park (ANP), which is not part of the regular Tanzanian national wildlife monitoring scheme. Gazetted in 1960, this park in northern Tanzania receives more than 60,000 visitors a year and provides an important source of income to the nation (Winkle, 2013). Giraffes are an attraction of the park, but the only existing published data on the

Masai giraffe population of ANP were collected from July 1979 to June 1980 by Pratt and Anderson (1982), 20 years after the park was established. That study presented information on the population size, age and sex structure, and spatial distribution and movements of Masai giraffes in ANP from individual-based data. Here, we provide an update on the current population size, population sex and age structure, and genetic connectivity of giraffes in ANP.

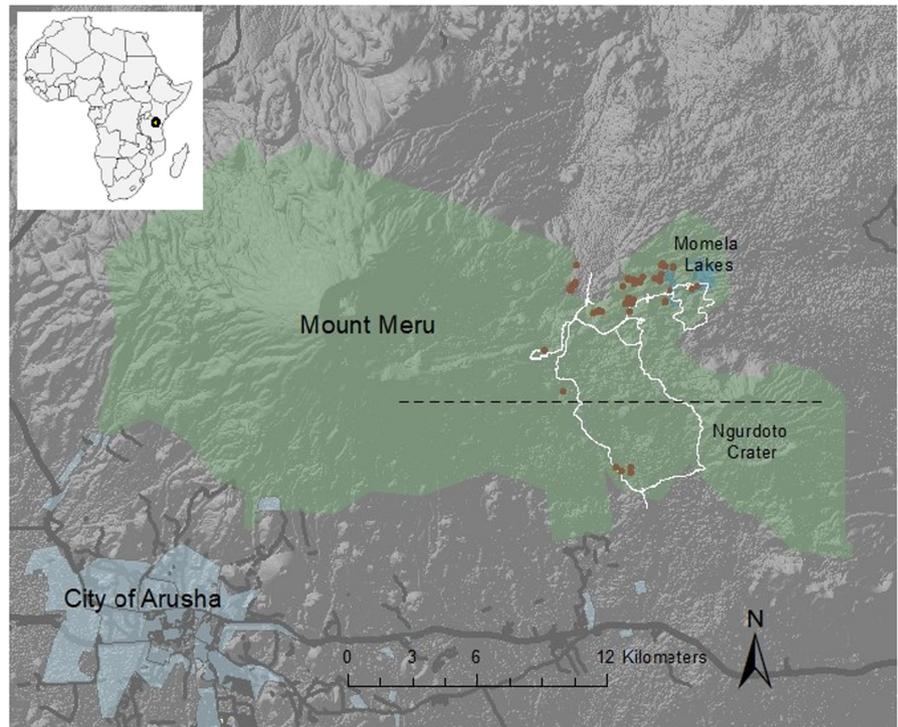
Rapid urbanisation from Arusha city and agricultural expansion has contributed to the increasing isolation of ANP from other protected areas in northern Tanzania. Pratt and Anderson's (1982) assessment of the giraffe population provides a baseline with which to compare the current population and determine whether numbers have increased, decreased or remained stable over the past four decades. We used individual-based methods similar to Pratt and Anderson (1982) to estimate the current population size of giraffe in ANP, quantify population structure (age and sex distribution) and map the spatial distribution and movements of giraffes. We then compared our estimates with the 42-year-old estimates from Pratt and Anderson (1982). Further, given the importance of genetic diversity in maintaining population health, we also used mitochondrial DNA to determine the extent of genetic connectivity between giraffes in ANP and those in other protected areas in northern Tanzania and south-east Kenya from which it was formerly geographically connected. Our results have implications for conservation and management of this iconic mega-herbivore and other large mammals in the region.

## 2 | METHODS

### 2.1 | Study species

Giraffes are large (830–1000 kg), non-migratory, non-territorial, long-lived (approximately 25–28 years; Dagg, 2014) and slow breeding. Females in the wild bear their first offspring at ~6 years of age, with a mean subsequent interbirth interval of 20 months (Lee & Strauss, 2016). Female giraffes in the tropics reproduce throughout the year with no defined birth pulse (Foster & Dagg, 1972; Leuthold & Leuthold, 1975). Their main natural predators are African lions (*Panthera leo*) and spotted hyaenas (*Crocuta crocuta*), both of which kill mostly calves and rarely adults (Dagg, 2014; Shorrocks, 2016). As is typical for large-bodied, long-lived animals with slow reproduction and delayed maturity, adult female survival makes the greatest theoretical contribution to population growth rates (Lee et al., 2016; Strauss et al., 2015), but calf survival can

**FIGURE 1** Masai giraffe study area in Arusha National Park, northern Tanzania, 2021. White lines are survey tracks. Brown points are giraffe locations from 12 mark-resight surveys conducted from June 2021 to February 2022. Black line is latitude  $-3.27^{\circ}\text{N}$ , the dividing line between the north and south subpopulations from Pratt and Anderson (1982). Circle on inset of Africa shows approximate location of Arusha National Park



also be important to population dynamics (Lee et al., 2016; Suraud et al., 2012).

## 2.2 | Study area

The 137km<sup>2</sup> Arusha National Park (ANP; Figure 1) is located in northern Tanzania ( $36.87^{\circ}\text{E}$ ,  $-3.25^{\circ}\text{N}$ ). Elevation ranges from 1400m to 4565m, with varied habitats including lakes, swamps, grasslands, bush, forests, heath and rock precipices. The park experiences three precipitation seasons per year: short rains = Oct–Jan; long rains = Feb–May; and dry = Jun–Sep (Prins & Loth, 1988). Annual rainfall varies spatially from 600mm to 2400mm, with annual rainfall of approximately 1100mm around Momella Lakes where most giraffes are found (Martinoli et al., 2006). Mean maximum temperature is  $25.4^{\circ}\text{C}$  and mean minimum temperature is  $12.8^{\circ}\text{C}$  (Kahana et al., 2015). According to Pratt and Anderson (1982), the giraffes of ANP are divided into north and south subpopulations with no mixing during their study period, except for a few older males. Arusha National Park is located approximately 30 kilometres from the nearest protected area with known giraffe populations in Tanzania, Enduimet Wildlife Management Area.

## 2.3 | Data collection

### 2.3.1 | Photographic identification

We followed similar methods to Pratt and Anderson (1982), specifically repeated mark-resight surveys with individual identification over the course of all seasons in a year. Each giraffe has a unique coat

pattern that does not change throughout its life (Foster, 1966), and mark-resight methods have been shown to be more accurate and more precise at estimating population sizes than distance sampling methods or aerial surveys (Lee & Bond, 2016). We employed active photographic encounter surveys, collecting data systematically according to a sampling protocol designed to ensure equal sampling effort across time and space. We collected giraffe photographic data during three primary sampling occasions from June 2021 to February 2022 using the robust design, with 3–5 replicated (secondary) surveys during each primary sampling occasion, to improve precision of demographic parameter estimates (Kendall et al., 1995; Kendall & Bjorkland, 2001; Pollock, 1982). In northern Tanzania, there are three Indian Ocean monsoon-driven precipitation seasons per year [short rains, long rains and dry season], so we assigned our primary sampling occasions to occur in each of the three seasons (Jul, Oct, Feb) to capture potential seasonal effects on detectability. Overall, we conducted a total of 12 independent surveys distributed in all three precipitation seasons.

During surveys, we drove the same network of fixed route road transects throughout our study area (Figure 1). We maintained a driving speed between 15 and 20km/h on all transects. We sampled each road segment only one time per survey, and systematically shifted the order and direction in which we sampled road transects similar to a Latin Square design to reduce sampling biases. Our sampling design has proved to be effective in providing precise estimates of population size, sex-age distributions and demographic rates (Lee et al., 2016, 2022; Lee & Bolger, 2017; Lee & Bond, 2022).

During photographic mark-resight sampling events, when we encountered any giraffes, we ‘marked’ newly observed individuals or resighted previously observed animals by slowly approaching and photographing the giraffe’s right side. We attempted to photograph

every giraffe that we encountered for individual identification from within a distance of approximately 100m at an angle that was as close to perpendicular (90°) as possible. We recorded sex (male, female), GPS location and age class. We categorised giraffes into three age classes following Pratt and Anderson (1982): calf (<1-year-old), juvenile (1–3 years old) or adult (>3 years) using a suite of physical characteristics (Strauss et al., 2015).

### 2.3.2 | Faecal sampling

We collected giraffe faecal samples in August 2020 and July 2022 from Arusha National Park. We searched for giraffes along the same road networks as described above. A razor blade was used to scrape/peel the thin outer layer from each pellet (Austin et al., 2018) and it was placed into a 50ml tube. Queen's College buffer was added immediately into the tube containing the sample (Bourgeois et al., 2019). We recorded GPS coordinates for each sample collected. Two tissue samples were also obtained from Tanzania Wildlife Research Institute's laboratory that were collected from giraffes in the Enduimet Wildlife Management Area, which is to the north-east of ANP, along the western foothills of Kilimanjaro National Park.

## 2.4 | Data analysis

### 2.4.1 | Population size and structure

We cropped photographs of the giraffe torso (Buehler et al., 2019), our area of interest for individual identification and matching. We matched giraffe identification images using WildID ([http://software.dartmouth.edu/Macintosh/Academic/Wild-ID\\_1.0.0.zip](http://software.dartmouth.edu/Macintosh/Academic/Wild-ID_1.0.0.zip)), a freely downloadable computer programme that matches large datasets of giraffe images collected using our protocols with very low misidentification error rates (Bolger et al., 2012). We enumerated individuals and estimated total population size following Pratt and Anderson (1982), so our estimates are directly comparable. We estimated total population using a generalised logistic model with an iterative non-linear least-squares technique (Pratt & Anderson, 1982). For comparison, we also estimated total population size using Pradel Robust Design models in programme MARK (Pradel, 1996; White & Burnham, 1999). We assigned observations to north or south areas using latitude -3.27°N, the dividing line as estimated from Figure 1 in Pratt and Anderson (1982). Animals were assigned to north or south subpopulations according to where the majority of their observations occurred.

### 2.4.2 | DNA extraction, PCR amplification and sequencing of mitochondrial DNA

We extracted DNA at Nelson Mandela African Institution of Science and Technology using the QIAamp Power Faecal DNA kit (QIAGEN) following the manufacturer's protocol. We measured

**TABLE 1** Arusha National Park, Tanzania giraffe population size, percentage of adults (adults/total), adult sex ratio (M/F), reproduction (calves/AF), overall and in the two subpopulations (north and south), as well as movements between subpopulations

	This study	Pratt & Anderson, 1982
<b>Total population</b>		
# identified	184	462
% adults	58	76
Adult sex ratio (M/F)	0.76	1.02
Calves/AF	0.78	0.33
Total population estimate	239	471
<b>North subpopulation</b>		
# identified	168	287
% adults	56	77
Adult sex ratio (M/F)	0.64	1.39
Calves/AF	0.77	0.32
<b>South subpopulation</b>		
# identified	15	175
% adults	80	72
Adult sex ratio (M/F)	3.00	0.59
Calves/AF	1.00	0.33
<b>Movements between subpops</b>		
% of population that moved	10	3
Sex and age classes	AM, AF, C	AM

Note: Data from individual-based photographic data collected during 12 surveys conducted from June 2021 to February 2022.

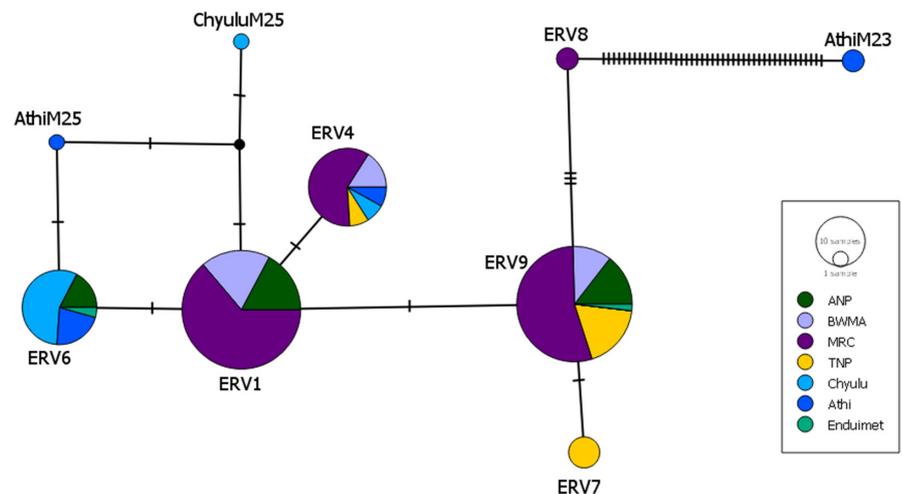
DNA concentration using nanodrop to determine the amount of DNA in each sample. We PCR amplified 1140nt long of cytochrome b gene (Bock et al., 2014). PCR amplification was performed using at least 10 ng of DNA template, 0.5 µl of 10µM of forward and reverse primers, 7.5 µl of 2× GoTaq master mix (Promega) and 3µl of DNA template. The PCR reaction was performed using protocol from the GoTaq mix (Promega). We sequenced PCR products using both forward and reverse primers. We visually inspected sequence results in the trace file format using SnapGene® software 4.2.4 (from GSL Biotech; available at [snapgene.com](http://snapgene.com)). We then aligned sequences using published sequences (GenBank accession: OP442601–OP442932; Table S1) from Tarangire National Park (TNP), Manyara Ranch Conservancy (MRC), and Burunge Wildlife Management Area (BWMA). We also used sequences from Athi and Chyulu reserves in Kenya (Brown et al., 2007), (GenBank accession: EU088317.1–EU088351, Table S1) to determine the extent of genetic connectivity with the ANP population. These sequences were 1709bp long, so we had to trim them to 1140bp to compare with other published sequences. We trimmed sequences and collapsed haplotypes using FaBox (Villesen, 2007). Haplotype diversity ( $H_d$ ) and nucleotide diversity ( $\pi$ ) were calculated from DnaSP whereas pairwise genetic fixation ( $F_{ST}$ ). We constructed median-joining network PopArt 4.8.4 (Leigh & Bryant, 2015) to identify relationship between haplotypes.

**TABLE 2** Genetic diversity of Masai giraffes from northern Tanzania based on 1140bp mitochondrial DNA: Number of samples (N), number of haplotypes (H), haplotype diversity (Hd) and nucleotide diversity ( $\pi$ )

Location	Pop code	GPS coordinates	N	H	Hd	$\pi$ (%)
Arusha National Park	ANP	3.25°S, 36.75°E	22	3	0.658	0.007
Burunge Wildlife Management Area	BWMA	3.96°S, 35.81°E	21	2	0.638	0.066
Tarangire National Park	TNP	4.01°S, 35.98°E	51	5	0.495	0.066
Manyara Ranch Conservancy	MRC	3.58°S, 36.00°E	96	3	0.602	0.061
Enduimet Wildlife Management Area	Enduimet	2°55'S, 37°30'E	2 <sup>a</sup>	2	N/A	0.0017
Athi River Ranch, Kenya	Athi	1°27'S, 36°58'E	10	4	0.733	0.0147
Chyulu Hills, Kenya	Chyulu	2°36'S, 37°51'E	16	3	0.341	0.0007

<sup>a</sup>Small sample size.

**FIGURE 2** A neighbour-joining network of giraffe mitochondrial DNA haplotypes showing the relationship between Arusha National Park and other populations in Tanzania and Kenya. Haplotype data from Athi and Chyulu are from Brown and co-workers (Brown et al., 2007)



**TABLE 3** Pairwise values of genetic differentiation between Masai giraffes sampled in northern Tanzania based on haplotypes derived from 1140 base pairs of mitochondrial DNA sequence FST.

	Chyulu	Athi	ANP	MRC	TNP	BWMA
Chyulu	-					
Athi	0.172*	-				
ANP	0.603*	0.250*	-			
MRC	0.638*	0.513*	0.052*	-		
TNP	0.639*	0.270*	0.019	-0.007	-	
BWMA	0.698*	0.245*	0.048*	-0.027	-0.021	-

\*Significance level  $p \leq 0.05$ .

### 3 | RESULTS

#### 3.1 | Population size and structure

Our 12 independent surveys identified 184 individuals (Table 1). Our individual giraffe accumulation curve was similar to that of Pratt and Anderson (1982), with few (<10) new individuals identified in each survey after the fourth survey. Using Pratt and Anderson's (1982) methods, we estimated a total population size of 239 giraffes (95% confidence interval 212–266), a 49% decline from Pratt and Anderson (1982). We observed 168 giraffes in the north subpopulation area, and only 15 in the south (Table 1). Overall, in ANP as whole, the population age and sex structure now versus 1980 had: fewer

adults relative to immatures, fewer adult males relative to adult females and more calves per adult female (Table 1). We observed 10% of the population moved between the two subpopulations, with five adult females and four calves observed moving in addition to 10 adult males. Movement rates were higher and included a greater diversity of sex and age classes than were observed by Pratt and Anderson (1982). Pradel robust design models estimated a current total population of 208 (95% confidence interval 177–254). The two population estimates (239 and 208) are similar, with broadly overlapping confidence intervals (212–266 and 177–254), so the true population size is likely within the range of 177–266. We have more confidence in the Pradel robust design model estimate as the most accurate total population estimate (208) because this method

accounts for detection probabilities and is a more generally accepted current method.

### 3.2 | Genetic connectivity with other populations across northern Tanzania and Kenya

We used a total 218 DNA sequences which included 22 samples from ANP (Table 2). We identified three haplotypes in ANP (ERV1, ERV9 and ERV6). Our results show high genetic relatedness between ANP and TNP, MRC and BWMA. Haplotype ERV1 and ERV9 were shared between ANP and giraffes from the Tarangire Ecosystem (Figure 2). One haplotype (ERV6) was shared between ANP and the Masai giraffe from Athi and Chyulu and Enduimet WMA (Figure 2). Low  $F_{ST}$  values were observed between ANP and TNP, MRC and BWMA suggesting historical female-mediated gene flow between them (Table 2). Pairwise  $F_{ST}$  value between ANP and Athi was the lowest of all pairwise comparisons between the giraffes from Tanzania and Kenya (Table 3). Haplotype diversity ranged from 0.341 in Chyulu Hills to 0.658 in ANP (Table 2). Apart from one haplotype from Athi (AthiM23, Figure 2) that significantly diverged from other haplotypes found east of the Gregory Rift (ERV), all other haplotypes from Athi and Chyulu in Kenya were similar or had one nucleotide difference with ERV haplotypes (Figure 2).

## 4 | DISCUSSION

The population of Masai giraffes in Arusha National Park (ANP) has declined by ca. 49% in the 42 years since it was last enumerated by individual-based data, with the south subpopulation nearly extirpated. This magnitude of decline for ANP is in accordance with the subspecies-wide estimate of 49–51% decline during a similar time period, reportedly mainly due to poaching and habitat loss (Bolger et al., 2019). ANP is a protected area with high levels of law enforcement, but ANP is unfenced and the giraffes seen within its boundaries can travel outside the park where they are exposed to land use changes, poaching and livestock-carried diseases. Human population and land use changes outside protected areas can have significant impacts deep within nearby protected areas (Veldhuis et al., 2019), so isolated protected areas like ANP are limited in their ability to maintain biodiversity and ecological functions (Belote et al., 2017; Craigie et al., 2010). In addition to population decline, we documented changes in the age distribution, adult sex ratio and reproductive rate. The current proportion of adults and adult sex ratio in ANP is in line with observations from other populations (Dagg, 2014; Lee & Bond, 2022).

The south subpopulation appears to have undergone a more drastic decline than the north subpopulation. Pratt and Anderson (1982) reported much lower calf survival in the south subpopulation, perhaps indicating lower habitat quality or lower subpopulation growth rate even 40 years ago. The ultimate

reasons for the disparity of population declines between subpopulations within ANP are not known, but we also observed considerably more movements between the subpopulations and movements of a more diverse sex and age of animals relative to Pratt and Anderson (1982). These observations indicate that giraffe social communities, which are quite modular and stable over at least 7 years (Bond et al., 2021; Lavista Ferres et al., 2021), may be more dynamic over decadal time scales. One explanation for the greater rates of population decline in the southern part of the park might be differential external impacts in the south where more intensive agriculture is present relative to areas north of ANP. Another explanation could be poaching of giraffes for bushmeat (Rentsch & Damon, 2013; Rentsch & Packer, 2015) due to proximity of the park to Arusha town. Despite conservation efforts, illegal hunting of giraffes is common, for example, about 7 years ago, in Serengeti National Park illegal hunting was estimated to remove 2–10% of the population annually (Rentsch & Packer, 2015; Strauss et al., 2015).

Mitochondrial DNA analysis reveals genetic connectivity between ANP and other populations east of the Great Rift Valley (or Gregory Rift) escarpments in northern Tanzania and south-eastern Kenya, providing evidence that the Masai giraffe once moved widely across this landscape. It was also interesting that giraffes from Arusha share the same haplotypes with giraffes from Athi and Chyulu in Kenya. Although our results only reflect female-mediated gene flow, they provide insight into the extent of genetic diversity and the level of genetic differentiation among sampled areas. Analysis of habitat connectivity between ANP and other protected areas in Tanzania shows that the relevant wildlife corridors are degraded due to land use conversion to agriculture and human settlement (Riggio & Caro, 2017).

This study updates the 40-year-old population estimate for ANP with a second datapoint. Longer term monitoring is necessary to determine whether this population has stabilised following the decline, or whether population declines are ongoing. Further genetic studies that use nuclear genetic markers will uncover whether the population is experiencing signs of inbreeding.

### 4.1 | Implications for conservation

Community conservation efforts that incorporated anti-poaching patrols and provided tangible economic benefits to local villagers from wildlife and habitat protection have proven successful in improving adult survival and sustaining giraffe populations in the nearby Tarangire Ecosystem (Lee, 2018; Lee & Bond, 2018, 2022). We are hopeful that such measures would be equally effective in communities surrounding Arusha National Park. However, effective conservation of wildlife populations entails not only safeguarding individual animals and their habitats by preventing incursions into protected areas, but also preserving connectivity between protected areas to maintain gene flow (Nabe-Nielsen et al., 2010;

Rudnick et al., 2012). Reversing the isolation of ANP by restoring linkages to the Tarangire Ecosystem's and Enduimet protected areas where giraffes are genetically similar will be another important step towards sustaining ANP's wildlife and the associated ecological and economical benefits.

Studies of giraffes can serve as useful proxies for understanding savannah ecosystem processes, because giraffes interact with and respond to many of the factors that have been hypothesised to drive population dynamics in other tropical and subtropical ungulate species, such as changes in vegetation, predation risk and poaching (Lee et al., 2016; Muller et al., 2018; Strauss et al., 2015). The giraffes' large body size and large space use needs make them particularly vulnerable to extinction and as such they require targeted conservation actions, but such actions should also benefit smaller sympatric species, such as dik-diks (*Madoqua kirkii*), impalas (*Aepyceros melampus*) and other browsers and mixed feeders.

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## CONFLICT OF INTEREST

The authors declare no conflict of interest.

## DATA AVAILABILITY STATEMENT

Lee et al. (2022), Masai giraffe population change over 40 years in Arusha National Park, Dryad, Dataset, <https://doi.org/10.5061/dryad.pg4f4qrtg>. GenBank accession numbers for all sequences used in the manuscript are listed in Table S1.

## ORCID

Derek E. Lee  <https://orcid.org/0000-0002-1042-9543>

George G. Lohay  <https://orcid.org/0000-0003-1129-8933>

James Madeli  <https://orcid.org/0000-0003-3657-7242>

Douglas R. Cavener  <https://orcid.org/0000-0002-1558-7137>

Monica L. Bond  <https://orcid.org/0000-0001-8500-6564>

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