

CONGEN
Africa

www.congenafrika.com

SPECIES GUIDELINES

2025



CONTENTS

Sable Antelope.....	1
Leopard.....	4
Common Eland.....	10
Mountain Zebra.....	14

ConGen Africa works with a wide range of species, helping to conserve genetic diversity and implement sustainable translocation practices. Two key examples of our work include sable antelope and leopard, species for which we have developed specific genetic management guidelines.





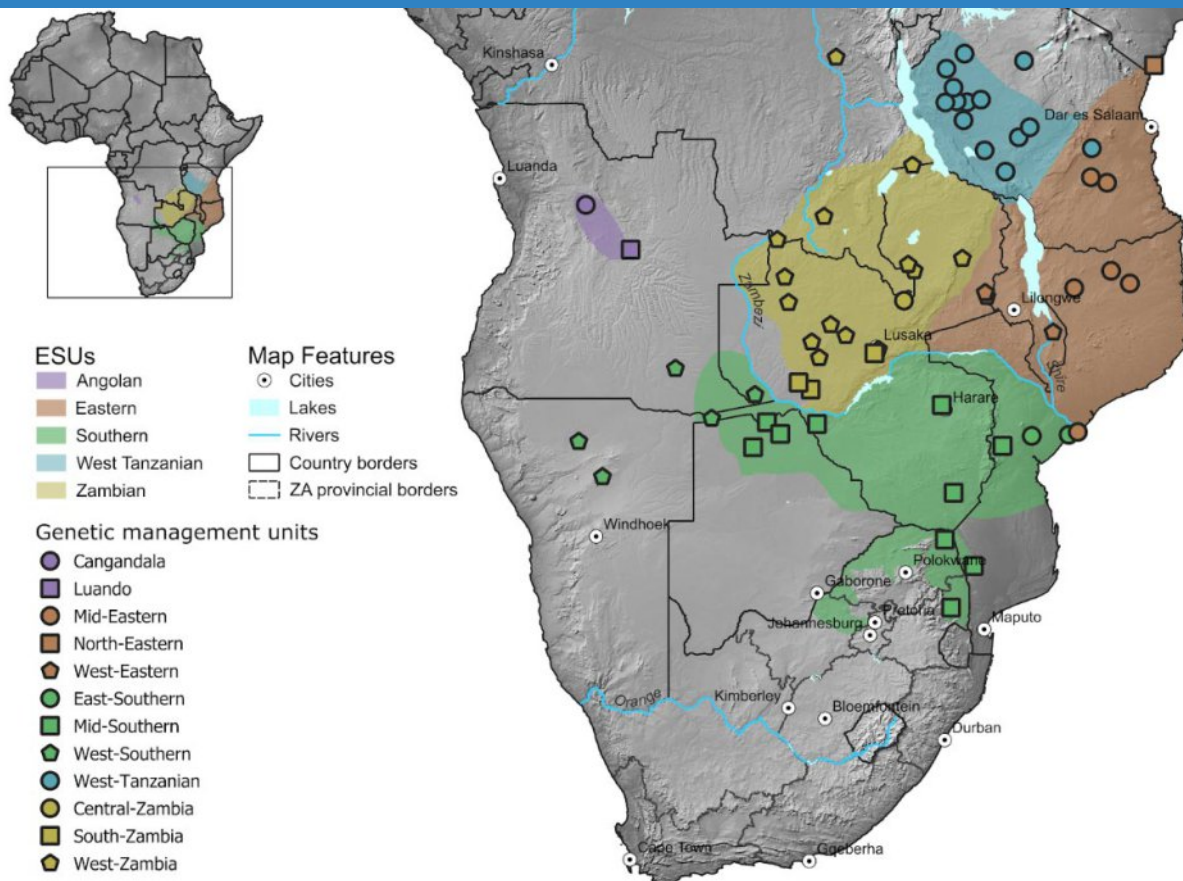
Sable Antelope

(*Hippotragus niger*)

A single species of sable antelope *Hippotragus niger* (Harris 1938) is currently recognised across wooded savanna in southern and East Africa. The species occurs from the south of Kenya to South Africa, with a separated population in Angola. Other species within the *Hippotragus* genus include the extinct bluebuck (*H. leucophaeus*) and roan antelope (*H. equinus*). For permitting purposes in southern Africa, Namibia and South Africa currently utilise *Hippotragus niger niger* (the southern or common sable). There are currently four recognised subspecies and one newly suggested subspecies in western Tanzania (Rocha et al. 2022). This assessment adopted morphological and genetic evidence of four/five subspecies, providing the basis for the recognition of five Evolutionarily Significant Units (ESUs) across the continent and three Genetic Management Units (GMUs) in southern

Africa. Figure 1 illustrates the geographic distribution of these ESUs and GMUs and also indicates localities where natural contact zones appear to exist between them.

Figure 1: Natural distribution of sable antelope (*Hippotragus niger*) ESUs, indicated by different colours. Genetic Management Units (GMUs) are indicated by different symbols, with the colour corresponding to the ESU to which it belongs. Each point represents a locality which has been sampled for genetic data and thus the GMU (symbol) and ESU (colour) designation of each locality is based on genetic data. The inset indicates the part of Africa shown in the main map. Distribution data sources: South Africa – Birss, C., Rushworth, I., Collins, N. B., Peinke, D. & Buijs, D. 2017. Inferred natural distribution ranges of certain large mammals in South Africa. Unpublished GIS coverage. Rest of Africa – IUCN (International Union for Conservation of Nature) 2008. *Hippotragus niger*. The IUCN Red List of Threatened Species. Version 2021-1. <https://www.iucnredlist.org>. Downloaded on 28/04/2021.



Management Level

Subspecies

Four subspecies of sable antelope are recognised based on morphological characteristics (Nowak 1999; Groves 1983) and genetic data (Pitra et al. 2006; Jansen van Vuuren et al. 2010).

- *Hippotragus niger roosevelti* (eastern sable antelope)
- *Hippotragus niger kirkii* (Zambian sable antelope)
- *Hippotragus niger variati* (giant sable antelope)
- *Hippotragus niger niger* (common or southern sable antelope)

However, the guidelines provided in this document are based on genetic data translated into the Evolutionarily Significant Units (ESUs) and Genetic Management Units (GMUs) listed below.

Evolutionarily Significant Units (ESUs)

- **Eastern (EE)** corresponds to eastern sable antelope
- **West Tanzanian (WT)** which corresponds to suggested new subspecies; Rocha et al. 2022
- **Zambian (ZM)** which corresponds to Zambian sable antelope
- **Angolan (AO)** or giant sable antelope
- **Southern (SO)** corresponds to common or southern sable antelope

Genetic Management Units (GMUs)

- **Southern (SO)**
 - East-Southern (ES)
 - Mid-Southern (MS)
 - West-Southern (WS)

Management Boundaries

Evolutionarily Significant Units (ESUs)

- **West Tanzanian (WT)** (suggested new subspecies): western Tanzania.
- **Eastern (EE)** (*H. n. roosevelti*): Kenya, north-east Tanzania, south-east Tanzania, eastern Zambia, Malawi, northern Mozambique.
- **Zambian (ZM)** (*H. n. kirkii*): Zambia (excluding the east) & Democratic Republic of Congo.
- **Angolan (AO)** (*H. n. variati*): Angola.
- **Southern (SO)** (*H. n. niger*): south of Zambezi River - Namibia, Botswana, Zimbabwe, south-central Mozambique, South Africa.

Genetic Management Units (GMUs)

- **Southern (SO)**
 - East-Southern (ES): eastern south-central Mozambique.
 - Mid-Southern (MS): South Africa, Botswana, Zimbabwe, southern Mozambique.
 - West-Southern (WS): north-east Namibia, south-east Angola, south-west Zambia and north-west Botswana.

Management Guidelines

- No import of sable antelope from countries containing the other ESUs.
- No translocation between GMUs (defined by microsatellites) within the Southern ESU, however, natural migration should be promoted (Vaz Pinto 2018).
- Captive bred animals and those on private ranches must be genetically tested before translocation to ensure no admixture between ESUs.
- Individuals within the southern haplogroups S1a + S2a (Zambian ESU, *H. n. kirkii*) and S1b + S2b (Southern ESU, *H. n. niger*) based on mitochondrial DNA (Rocha et al. 2022) should not be mixed.

Threats

Also see the IUCN List:

- Hybridisation between ESUs.
- Outdated existing genetic tests may lead to unintended mixing and hybridisation of ESUs.
- Hybridisation between sable antelope and roan antelope (*H. equinus*).

Limitations & Assumptions

- Private ranches in South Africa, Namibia, Zimbabwe, Botswana and south-central Mozambique (the natural range of the Southern ESU) may have some individuals from the Zambian ESU and/or the Eastern ESU and/or West Tanzanian ESU.

Priority Research

- Existing genetic tests based on mitochondrial DNA must be updated to reflect the latest and most robust (at this point) knowledge from Rocha et al. (2022).
- More samples from the Southern ESU should be genetically analysed, particularly from South Africa, to determine if they qualify as an additional GMU.
- A South African-wide genetic assessment of sable antelope to determine the prevalence of hybrid individuals between ESUs.
- It is recommended that genetic monitoring studies be undertaken every 3-5 generations, if possible, to evaluate whether any changes in the genetic structure and diversity of this species have taken place, possibly warranting an update to these guidelines. Such studies would also contribute to the assessment of genetic indicators under the Kunming-Montreal Global Biodiversity Framework. Note: such studies would not be to assess local pedigree, but rather broad population structure and diversity, and hence the overall genetic health of the species.

Cited References

- Groves, C.P. (1983). A new subspecies of sable antelope, *Hippotragus niger* (Harris 1838). *Revue Zoologique Africaine* **97**, 821-828.
- Jansen van Vuuren, B. et al. (2010). Western Zambian sable: are they a geographic extension of the giant sable antelope? *South African Journal of Wildlife Research* **40**, 35-42. doi.org/10.3957/056.040.0114.
- Nowak, R.M. (1999). *Walker's Mammals of the World*. 6th edition. The Johns Hopkins Press, Baltimore.
- Pitra, C. et al. (2006). DNA-led rediscovery of the giant sable antelope in Angola. *European Journal of Wildlife Research* **52**, 145–152. doi.org/10.1007/s10344-005-0026-y.
- Vaz Pinto, P. (2018). *Evolutionary history of the critically endangered giant sable antelope (Hippotragus niger variati) – insights into its phylogeography, population genetics and conservation*. PhD Thesis. University of Porto. https://sigarra.up.pt/fcup/en/pub_geral.pub_view?pi_pub_base_id=266405.
- Rocha, J.L. et al. (2022). African climate and geomorphology drive evolution and ghost introgression in sable antelope. *Molecular Ecology* **31**, 2968-2984. doi.org/10.1111/mec.16427.
- Pitra, C. et al. (2002). An exceptional case of historical outbreeding in African sable antelope populations. *Molecular Ecology* **11**, 1197–1208. doi.org/10.1046/j.1365-294X.2002.01516.x.

Consultation

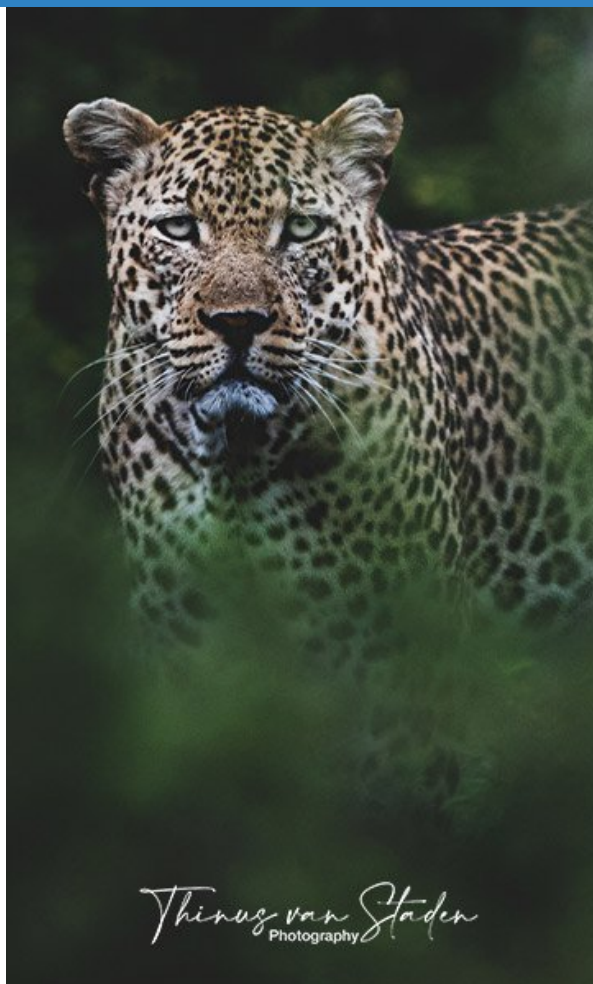
- IUCN SSC Conservation Genetics Specialist Group
- IUCN SSC Antelope Specialist Group

Acknowledgements

We are grateful to Prof Francesca Parrinia and Dr Pedro Vaz Pinto for their valuable comments and for taking the necessary time and effort to critically review the initial guidelines.

Queries

For any additional questions related to these guidelines, please contact ConGen Africa at info@congenafrika.com.



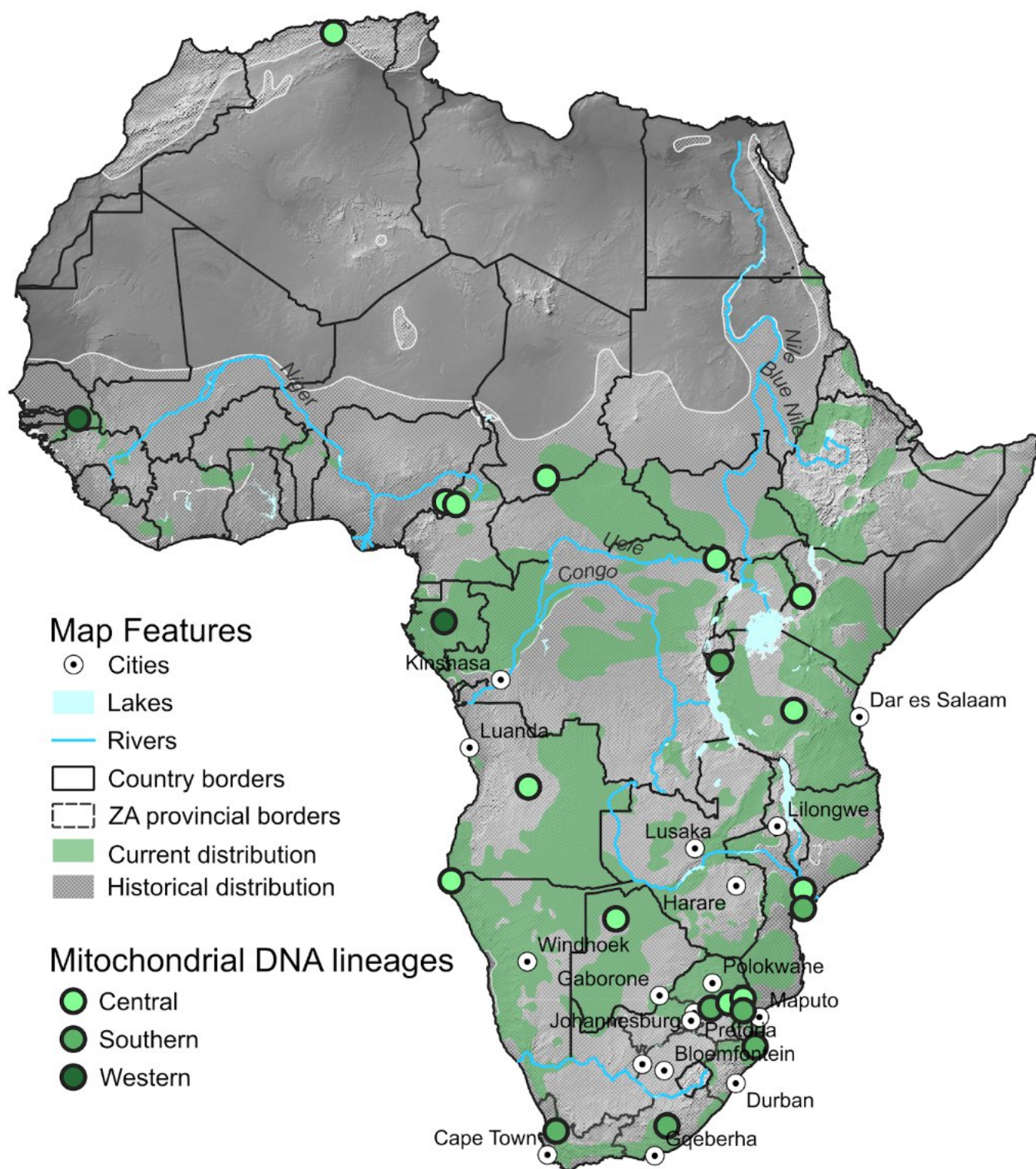
Leopard

(*Panthera pardus*)

The leopard (*Panthera pardus*) is one of five extant cat species which also include lion (*Panthera leo*), snow leopard (*Panthera uncia*), jaguar (*Panthera onca*) and tiger (*Panthera tigris*). African leopard *Panthera pardus pardus* (Linnaeus 1758) is currently recognised as one of the eight subspecies of leopard. It is a widespread subspecies with a mostly sub-Saharan African distribution. The subspecies is now locally extinct in Mauritania, Tunisia, Togo, Morocco, Algeria, Libya and most likely Gambia and Lesotho. For permitting purposes in southern Africa, Namibia and South Africa currently utilise *Panthera pardus pardus*. This assessment adopted morphological and genetic evidence, providing the basis for the recognition of eight Evolutionarily Significant Units (ESUs) which correspond to the eight subspecies of leopard. African leopards form part of one of these ESUs and there are

currently no Genetic Management Units (GMUs) in southern Africa. Figure 1 illustrates the geographic distribution of three mitochondrial DNA lineages across the continent.

Figure 1: Natural and current distribution of the African leopard (*Panthera pardus pardus*) in southern Africa, illustrated by the hashed white lines and the green shading, respectively. Each point represents a locality which has been sampled for genetic data, with mitochondrial lineages within the subspecies indicated by different shades of green of the points. This is to illustrate that there is some genetic variation within the subspecies, but that all the lineages still belong to the same subspecies. Points for locations where both the Central and Southern lineages are found have been separated such that both colours are visible (i.e. in southern Mozambique and the lowveld region of South Africa). Note: The point in Algeria has an unknown location (Pajmans et al. 2018) and was thus placed in the historical range within the country. The range of other subspecies that occur outside Africa are not shown. Distribution data source: Peter Gerngross 2019. *Panthera pardus*. The IUCN Red List of Threatened Species. Version 2021-1. <https://www.iucnredlist.org>. Downloaded on 28/04/2021.



Management Level

Subspecies

Eight subspecies of leopard are recognised based on morphological characteristics (Kitchener et al. 2017) and genetic data (Uphyrkina et al. 2001).

- ***Panthera pardus orientalis*** (Amur leopard)
- ***Panthera pardus tulliana*** (Anatolian leopard)
- ***Panthera pardus delacouri*** (Indochinese leopard)
- ***Panthera pardus nimr*** (Arabian leopard)
- ***Panthera pardus pardus*** (African leopard)
- ***Panthera pardus fusca*** (Indian leopard)
- ***Panthera pardus kotiya*** (Sri Lankan leopard)
- ***Panthera pardus melas*** (Javan leopard)

The guidelines provided in this document are based on genetic data, which confirms that the subspecies are equivalent to Evolutionarily Significant Units (ESUs).

Evolutionarily Significant Units (ESUs)

See under subspecies heading above.

Genetic Management Units (GMUs)

No GMUs are recognised at present.

Management Boundaries

Subspecies

- ***Panthera pardus orientalis***: eastern Asia from Russian Far East to China.
- ***Panthera pardus tulliana***: Turkey, Caucasus, Turkmenistan, Uzbekistan, Iran, Iraq, Afghanistan and Pakistan.
- ***Panthera pardus delacouri***: south-east Asia and probably southern China.
- ***Panthera pardus nimr***: Arabian Peninsula.
- ***Panthera pardus pardus***: Africa south of Sahara and northern Africa.
- ***Panthera pardus fusca***: Indian sub-continent, Burma, China.
- ***Panthera pardus kotiya***: Sri Lanka.
- ***Panthera pardus melas***: Java.

Management Guidelines

- No import of other subspecies to Africa.
- While management objectives may vary, translocation guidelines should be grounded in ecological and genetic principles to minimize risks such as disrupting population genetic structures or reducing genetic integrity. In cases where translocations serve critical conservation goals—such as restoring populations, increasing genetic diversity, or mitigating human-wildlife conflict—guidelines should be applied with careful consideration of both risks and benefits.
- Translocation of individuals should be avoided (if possible), unless it serves to recolonise or reinstate previously disrupted gene flow.
- If it is not possible to avoid translocation, then regional variations in the spatial requirements of leopards should be considered. This will inform the translocation distance that is suitable for the specific area/habitat.
- The driving force of genetic differentiation within the African leopard appears to be isolation-by-distance (IBD; Pečnerová et al. 2021), therefore, management of leopard populations in southern Africa (and Africa as a whole) should aim to allow (and promote) natural dispersal as much as possible.

- Ropiquet et al. (2015) recommended translocation distances of no more than 82 km, but this may be overly restrictive.
- Individuals should be moved at least 200 km from the capture site to prevent capture site fidelity and homing instinct (Weise et al. 2015; Briers-Louw et al. 2019).
- Translocation distances of greater than four diameters of the regionally known localised leopard home range should be considered, and this may vary greatly in various locations within the species distribution (Devens et al. 2018; Müller et al. 2022; McManus et al. 2022).
- Therefore, translocation distances between 200-400 km should be considered to preserve the natural processes that led to the IBD pattern (McManus et al. 2022).
- Translocations should occur within the same bioregion where possible to avoid the risk of outbreeding depression.
- Two mitochondrial DNA lineages have been identified in the lowveld region (Morris et al. 2024; Tensen et al. 2024), therefore translocations in this area should be carefully considered until the boundary between these lineages has been established.
- A tissue sample should be collected from all translocated individuals for further genetic analysis. These samples should be stored in the national SANParks or SANBI biobanks.

Threats

Also see the IUCN Red List.

- No current genetic threats, as genetic diversity is high and there is no evidence of inbreeding in southern African populations studied thus far.
- Human-leopard conflict, as a result of real or perceived predation on livestock.
- Habitat loss and fragmentation from land-use change, impacting long-term connectivity and population viability.

Limitations & Assumptions

Previous translocations likely did not take into account the isolation-by-distance (IBD) genetic pattern of leopards.

Priority Research

- Identify natural dispersal corridors at fine scale (local and regional levels), in order to protect, or (re)establish, such corridors, which will in turn preserve the natural processes that create the IBD spatial genetic structure observed in the species.
- Determine the effective gene dispersal distance for additional populations throughout Africa, to guide maximum translocation distance, if translocations must take place.
- For southern Africa, genetic data are required from populations in Angola, Botswana, Zimbabwe and southern Mozambique, as these areas are almost completely absent from genetic studies of the species thus far.
- Understand the distribution of the contact zone between the two mitochondrial lineages identified in the lowveld region.
- Full genome analysis of the southern African population to understand genomic diversity.
- Long-term spatial and genetic monitoring of translocated leopards to evaluate homing tendencies, survival rates, and integration into new populations.
- Determine how land-use affects gene flow and dispersal across fragmented landscapes.

Cited References

- Briers-Louw, W. D. et al. (2019). Big cats return to Majete Wildlife Reserve, Malawi: evaluating reintroduction success. *African Journal of Wildlife Research* **49**(1), 34-50. doi.org/10.3957/056.049.0034.
- Devens, C. et al. (2018). Counting the spots: the use of a spatially explicit capture-recapture technique and GPS data to estimate leopard (*Panthera pardus*) density in the Eastern and Western Cape, South Africa. *African Journal of Ecology* **56**(4), 850-859. doi.org/10.1111/aje.12512.

- Kitchener A.C. et al. (2017). A revised taxonomy of the Felidae. The final report of the Cat Classification Task Force of the IUCN/SSC Cat Specialist Group. Cat News Special Issue 11, 80 pp. <https://repository.si.edu/handle/10088/32616>.
- McManus, J. et al. (2022). Assessment of leopard translocations in South Africa. *Frontiers in Conservation Science* **3**, 943078. doi.org/10.3389/fcosc.2022.943078.
- Morris, D.R. et al. (2024). Unravelling the maternal evolutionary history of the African leopard (*Panthera pardus pardus*). *PeerJ* **12**:e17018. doi.org/10.7717/peerj.17018.
- Müller, L. et al. (2022). Population size, density, and ranging behaviour in a key leopard population in the Western Cape, South Africa. *PloS One* **17**(5), p.e0254507. doi.org/10.1371/journal.pone.0254507.
- Pečnerová, P. et al. (2021). High genetic diversity and low differentiation reflect the ecological versatility of the African leopard. *Current Biology* **31**, 1862-1871.e5. doi.org/10.1016/j.cub.2021.01.064.
- Ropiquet, A. et al. (2015). Implications of spatial genetic patterns for conserving African leopards. *Comptes Rendus Biologies* **338**, 728-737. doi.org/10.1016/j.crvi.2015.06.019.
- Tensen, L. et al. (2024). Mitogenomic characterisation of South African leopards and the effect of past climatic events. *Journal of Zoological Systematics and Evolutionary Research* 2024, 2174469. doi.org/10.1155/2024/2174469.
- Uphyrkina, O. et al. (2001). Phylogenetics, genome diversity and origin of modern leopard, *Panthera pardus*. *Molecular Ecology* **10**(11), 2617-2633. doi.org/10.1046/j.0962-1083.2001.01350.x.
- Weise, F. J. et al. (2015). A home away from home: insights from successful leopard (*Panthera pardus*) translocations. *Biodiversity Conservation* **24**, 1755-1774. doi.org/10.1007/s10531-015-0895-7.

Additional references:

- Anco, C. et al. (2018). Historical mitochondrial diversity in African leopards (*Panthera pardus*) revealed by archival museum specimens. *Mitochondrial DNA Part A* 29, 455-473. doi.org/10.1080/24701394.2017.1307973.
- Mamugy, F. et al. (2024). SNP panel for non-invasive genotyping of leopard (*Panthera pardus*). bioRxiv 11.01.621452. doi.org/10.1101/2024.11.01.621452.

Consultation

- IUCN SSC Conservation Genetics Specialist Group
- IUCN SSC Cat Specialist Group

Acknowledgements

We are grateful to Drs Bool Smuts, Jeannine McManus, Anne Ropiquet and Prof Michael Somers for their valuable comments and for taking the necessary time and effort to critically review the initial guidelines.

Queries

For any additional questions related to these guidelines, please contact ConGen Africa at info@congenafrika.com.



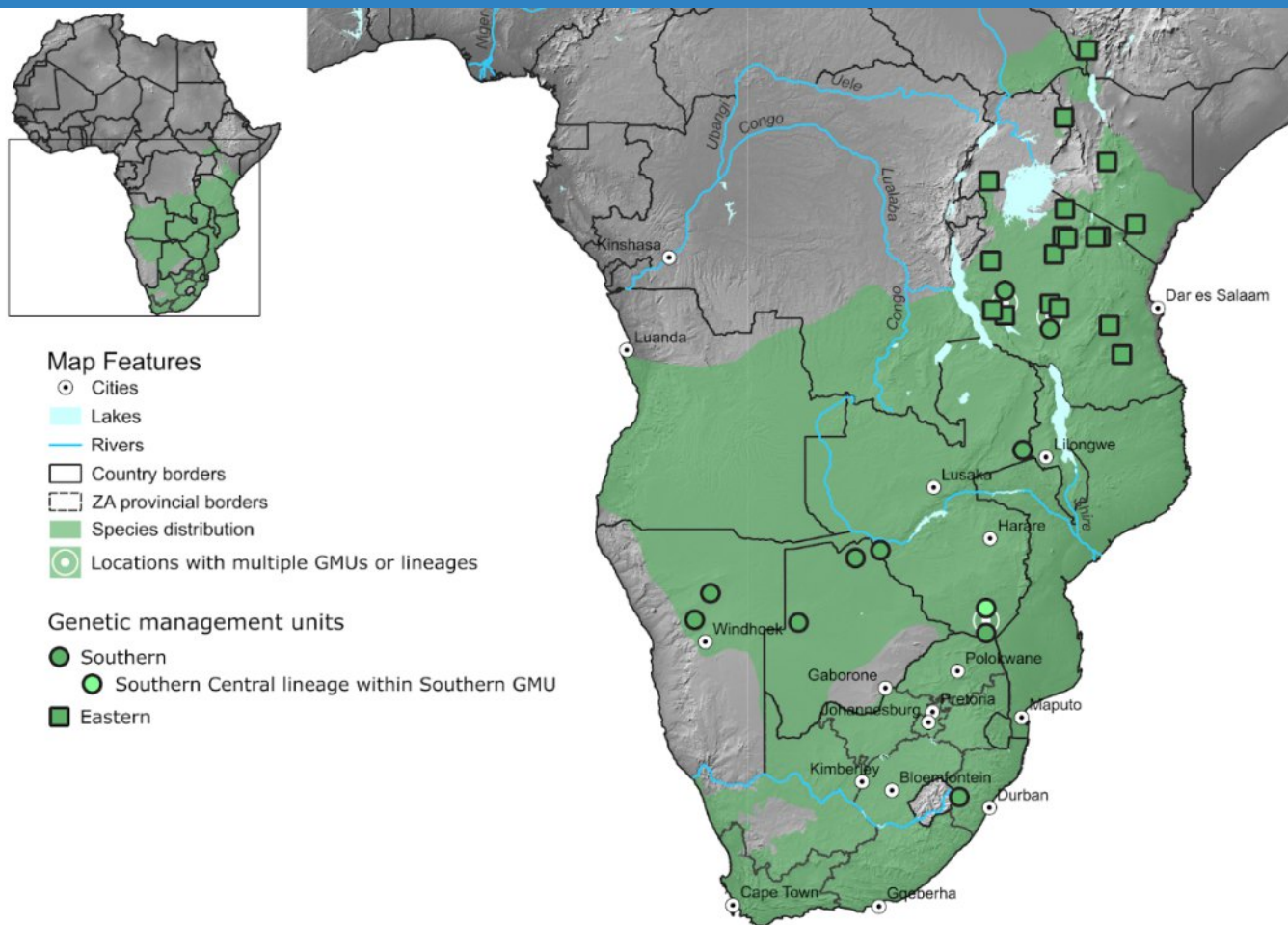


Common Eland

(*Tragelaphus oryx*)

A single species of the common eland *Tragelaphus oryx* (Pallas 1766) is currently recognised across the southern and East African parts of the geographic range. This species name is synonymous with the former *Taurotragus oryx*. For permitting purposes in southern Africa, Namibia and South Africa currently utilise *Tragelaphus oryx*. There is dispute about the number of subspecies; this assessment adopted morphological and genetic evidence of distinction between two forms, providing the basis for the recognition of two Genetic Management Units (GMUs). Figure 1 illustrates the geographic distribution of these GMUs and also indicates localities where natural contact zones appear to exist between them. The validity of the third lineage requires priority research.

Figure 1: Natural distribution of common eland (*Tragelaphus oryx*) in green shading. Genetic Management Units (GMUs) are indicated by different symbols. Each point represents a locality which has been sampled for genetic data and thus the GMU (symbol) designation of each locality is based on genetic data. Note two localities in eastern Africa with both the Eastern and Southern GMUs present (Lungwa and Mlele, Tanzania). The Eastern I lineage (= "Intermediate" lineage from Lorenzen et al. 2010) within the Eastern GMU is shown in light green and is presently known to occur at Nuanetsi, Zimbabwe together with individuals that fall within the Southern GMU lineage. The inset indicates the part of Africa shown in the main map. Distribution data sources: South Africa – Birss, C., Rushworth, I., Collins, N. B., Peinke, D. & Buijs, D. 2017. Inferred natural distribution ranges of certain large mammals in South Africa. Unpublished GIS coverage. Rest of Africa – IUCN (International Union for Conservation of Nature) 2008. *Tragelaphus oryx*. The IUCN Red List of Threatened Species. Version 2021-1. <https://www.iucnredlist.org>. Downloaded on 23/04/2021.



Management Level

Subspecies

Three subspecies have been suggested, based on morphological characteristics (Ansell 1972; Lydekker 1906; Pallas 1766; Sclater 1864), although their exact characteristics and distribution are unclear and their classification is disputed (Thouless 2013; Buys et al. 2016; IUCN 2016).

- *Tragelaphus oryx pattersonianus* (Patterson's or East African eland)
- *Tragelaphus oryx livingstonii* (Livingstone's eland)
- *Tragelaphus oryx oryx* (Cape eland)

However, the guidelines provided in this document are based on genetic data translated into the Evolutionarily Significant Units (ESUs) and Genetic Management Units (GMUs) listed below.

Evolutionarily Significant Units (ESUs)

No ESUs are recognised at present (but see Priority Research).

Genetic Management Units (GMUs)

- **Eastern (EE)**
- **Southern (SO)**

Management Boundaries

Genetic Management Units (GMUs, based on genetic data from Lorenzen et al. (2010))

- **Southern (SO):** Zambia, Zimbabwe, Botswana, Namibia, Angola, South Africa, Mozambique.

Management Guidelines

- Allow migration between GMUs at natural “contact zones”. For example, between Zambian and Tanzanian populations.
- No translocations of individuals from countries containing the Eastern GMU into countries containing the Southern GMU, and vice-versa.
- As far as possible, manage “Cape” and “Livingstone’s” phenotypes within the Southern GMU separately. See Priority research for short descriptions of these phenotypes.
- The “Livingstone’s” eland phenotype in the Southern GMU is challenging to distinguish from the “East African” eland phenotype in the Eastern GMU (number of stripes and coat colour). Therefore, captive bred animals, and those on private ranches, must be genetically tested before release to ensure no inadvertent introductions of the Eastern GMU into the range of the Southern GMU occurs.

Threats

Also see the IUCN Red List and the South African Red List.

- It is critical to limit introductions of out-of-range individuals from each GMU, based on the guidelines given above. Once introduced, hybridisation is highly likely to occur. Eland can jump over game fences (>2 m high) with relative ease and are highly mobile and nomadic. This increases the probability of escape and consequent hybridisation of out-of-range animals with local, natural populations (e.g. Eastern GMU on southern African farms, or “Livingstone’s” phenotype in the range of the “Cape” phenotype).

Limitations & Assumptions

- It is assumed that the phenotypic differences between “Cape” and “Livingstone’s” have an ecological function, and potentially an underlying genetic cause. Hence, the recommendation to manage them separately.
- Only mitochondrial data are currently available (Lorenzen et al. 2010), which may not show the full picture. Recommendations may change when new data are generated. At least two studies using nuclear data are currently underway in this species.
- Eland on private ranches may be a mix of GMUs and/or phenotypes.
- There is some evidence that eland in the Eastern GMU are 50% grazers, while eland in the Southern GMU are predominantly browsers (Gagnon & Chew 2000).

Priority Research

- Further studies are required to investigate the cause/s and function/s of phenotypic variation within the Southern GMU. Two distinct phenotypes exist, which were originally used as support to classify and distinguish two subspecies (not currently supported by genetic data, see Frost 2014):
 - “Cape” eland (*T. o. oryx*): Dull fawn in colour, with no white stripes, typically found from the southern tip of Africa, extending northwards to the southern parts of Botswana and northern Namibia and south-western Zimbabwe.

Priority Research - continued

- “Livingstone’s” eland (*T. o. livingstonii*): Rufous-fawn in colour, with thin white stripes down their flanks and a dark brown mark on the back of the forelegs just above the knee. Typically found in north-eastern Namibia, Angola, northern Botswana, Zimbabwe, Zambia, Mozambique, Malawi, and the southern Democratic Republic of the Congo.
- The distribution and origin of the Southern Central lineage (equivalent to the “intermediate” lineage from Lorenzen et al. 2010) within the Southern GMU, but overlapping with the range of the Eastern GMU, should be investigated to further elucidate its relationship to the Southern and Eastern GMUs.
- Range-wide genetic studies using nuclear data are required for each GMU to investigate genetic structure.
- Kruger National Park (South Africa), Mozambique, Zambia and Malawi must be sampled more extensively to obtain a clearer picture of the phylogeography within the species. There may be additional “contact zones” between the two GMUs in Malawi, Zambia and the north of Mozambique.

Cited References

- Meester, J. A. J. & Setzer, H. W. (1971). *The Mammals of Africa: an identification manual*. Smithsonian Institution Washington, 1-15.
- Buys, D. et al. (2016) A conservation assessment of *Tragelaphus oryx*. In: M.F., Child, L. Roxburgh, E. Do Linh San, D. Raimondo D & H.T. Davies-Mostert (eds). *The Red List of Mammals of South Africa, Swaziland and Lesotho*. South African National Biodiversity Institute and Endangered Wildlife Trust, South Africa. <https://speciesstatus.sanbi.org/assessment/last-assessment/2254/>.
- Gagnon, M. & Chew, A.E. (2000). Dietary preferences in extant African Bovidae. *Journal of Mammalogy* **81**(2), 490-511. [doi.org/10.1644/1545-1542\(2000\)081<0490:DPIEAB>2.0.CO;2](https://doi.org/10.1644/1545-1542(2000)081<0490:DPIEAB>2.0.CO;2).
- Frost, W. (2014). *The Antelope of Africa*. Jacana Media, Auckland Park, South Africa. 78-81.
- IUCN SSC Antelope Specialist Group 2016. *Tragelaphus oryx* (errata version published in 2017). The IUCN Red List of Threatened Species 2016: e.T22055A115166135. doi.org/10.2305/IUCN.UK.2016-3.RLTS.T22055A50196938.en.
- Lorenzen, E. D. et al. (2010). A long-standing Pleistocene refugium in southern Africa and a mosaic of refugia in East Africa: Insights from mtDNA and the common eland antelope. *Journal of Biogeography* **37**(3), 571-581. doi.org/10.1111/j.13652699.2009.02207.x.
- Thouless, C. R. (2013). *Tragelaphus oryx*. In: J. S. Kingdon and M. Hoffmann (eds), *The Mammals of Africa*. Academic Press, Amsterdam, The Netherlands.

Consultation

- IUCN SSC Conservation Genetics Specialist Group
- IUCN SSC Antelope Specialist Group

Acknowledgements

We are grateful to Prof Eline Lorenzen and Dr Frans Radloff for their valuable comments and for taking the necessary time and effort to critically review the initial guidelines.

Queries

For any additional questions related to these guidelines, please contact ConGen Africa at info@congenafrika.com.



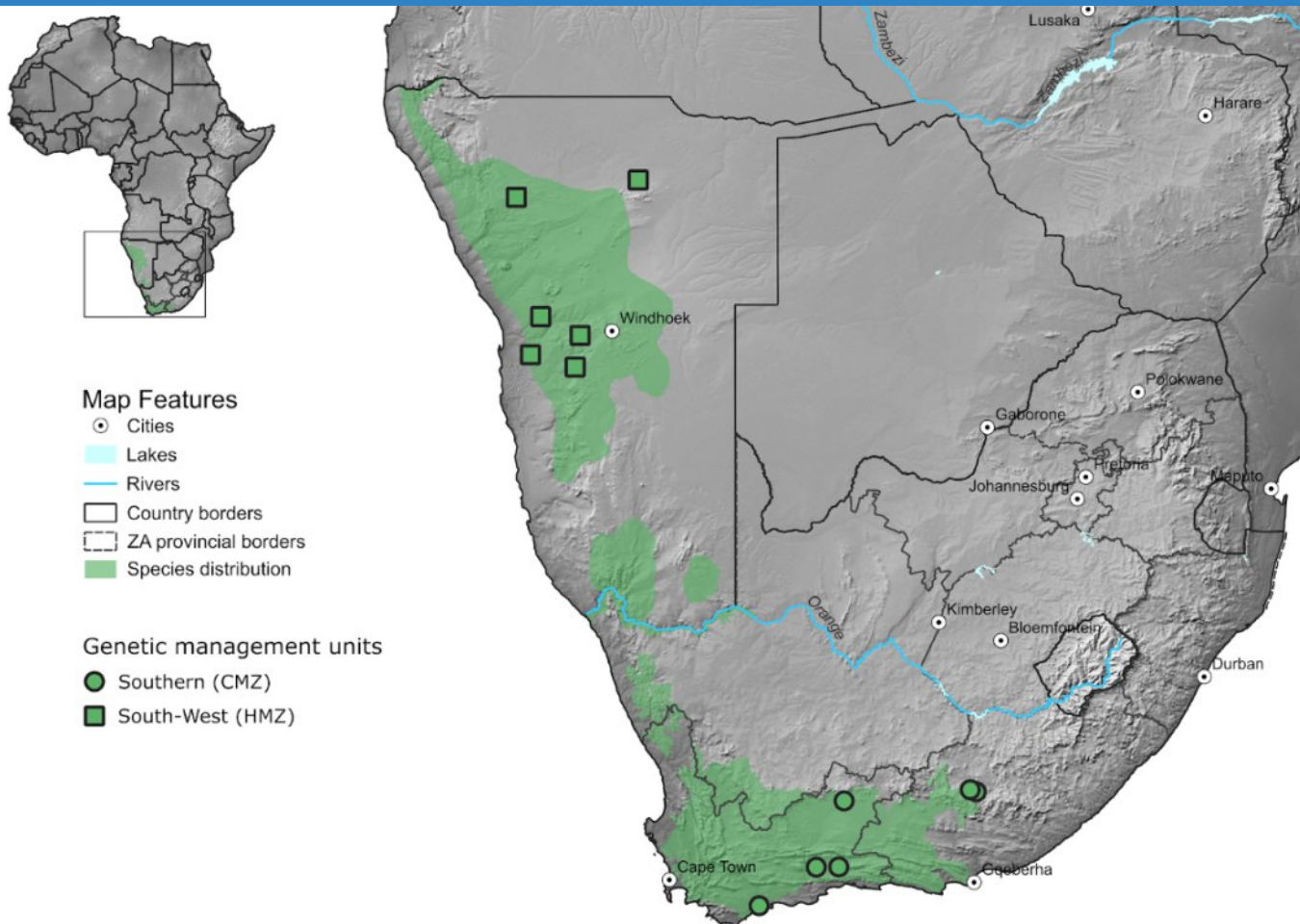
Mountain Zebra

(*Equus zebra*)

Within *Equus zebra* two subspecies are currently recognised (*Equus zebra hartmannae*: Hartmann's mountain zebra, HMZ, and *Equus zebra zebra*: Cape mountain zebra, CMZ). They are primarily differentiated by their habitat and size, with CMZ being slightly smaller (Wilson & Reeder 2005). For permitting purposes in southern Africa, Namibia and South Africa currently utilise *Equus zebra hartmannae* and *Equus zebra zebra*, respectively. Early molecular investigations based on mitochondrial DNA was unable to detect any subspecific genetic structure, however, subspecies-level differentiation was detected based on microsatellite data. These subspecies are therefore not considered Evolutionarily Significant Units (ESUs) but rather Genetic Management Units (GMUs). Figure 1 illustrates the geographic distribution of these GMUs. Within *E. z. zebra*, additional genetic structure has been identified

corresponding to the individual reserves in which these animals are found (Mountain Zebra National Park, De Hoop Nature Reserve, Kammanassie Nature Reserve; e.g. Kotze et al. 2019), however, this differentiation is the result of recent anthropogenic (human-mediated) fragmentation and isolation before the 1950s from hunting and reduced habitat (converted to pasture for livestock; Millar, 1970).

Figure 1: Natural distribution of mountain zebra (*Equus zebra*) in green shading. Genetic Management Units (GMUs) are indicated by different symbols. Each point represents a locality which has been sampled for genetic data and thus the GMU (symbol) designation of each locality is based on genetic data. The inset indicates the part of Africa shown in the main map. Distribution data sources: South Africa – Birss, C., Rushworth, I., Collins, N. B., Peinke, D. & Buijs, D. 2017. Inferred natural distribution ranges of certain large mammals in South Africa. Unpublished GIS coverage. Namibia – Brown, C. J. (2005). Historic distribution of mammals in Namibia. Unpublished GIS coverage.



Management Level

Subspecies

Two subspecies of mountain zebra are recognised based on morphological characteristics (Wilson & Reeder 2005).

- ***Equus zebra hartmannae*** (Hartmann's mountain zebra, HMZ)
- ***Equus zebra zebra*** (Cape mountain zebra, CMZ)

The guidelines provided in this document are based on genetic data translated into the Evolutionarily Significant Units (ESUs) and Genetic Management Units (GMUs) listed below. However, the name that is used for permits in southern Africa reflect the subspecies designations.

Evolutionarily Significant Units (ESUs)

No ESUs are recognised at present.

Genetic Management Units (GMUs)

- **South-West (SW)** which corresponds with HMZ
- **Southern (SO)** which corresponds with CMZ

Management Boundaries

Genetic Management Units (GMUs)

- **South-West (SW)**: along the entire escarpment of Namibia with a small number of individuals in south-west Angola.
- **Southern (SO)**: southern South Africa.

Management Guidelines

General management guidelines

- Translocations between the GMUs should be prevented to maintain genetic differentiation.
- However, if the species or GMUs are in imminent risk of extinction (poor to low diversity metrics and heavy sex-biased populations resulting in increased inbreeding) then translocations between the GMUs should be permitted.

South-West (SW)

- Natural gene flow within this GMU should be encouraged to maintain genetic diversity and ensure continued population growth.

Southern (SO)

- Plains zebra (*Equus quagga burchelli*) should be removed from areas containing Cape mountain zebra (*E. z. zebra*) to prevent hybridisation.
- To prevent the further loss of genetic diversity, more effort should be made to encourage translocations and breeding between sites (farms, reserves, etc.) of *E. z. zebra*, primarily between members of natural populations not derived from common relic populations (Mountain Zebra National Park, Gamkaberg Nature Reserve, Kammanassie Nature Reserve).
- Maintaining differentiation between Mountain Zebra National Park, De Hoop Nature Reserve, Kammanassie Nature Reserve is ill advised (see background).

Threats

Also see the IUCN Red List.

- *Equus zebra zebra* is particularly threatened by further loss of genetic diversity through genetic drift and inbreeding due to small subpopulation sizes.
- *Equus zebra zebra* is highly fragmented with little potential for natural gene flow.
- Genetic divergence among the relic subpopulations of *E. z. zebra* was primarily due to the high degree of anthropogenic isolation.
- Low levels of genetic diversity have made many populations increasingly vulnerable to disease, with outbreaks of sarcoid tumours becoming more common within inbred populations (e.g., Marais et.al. 2007).
- Commercial trade of *E. z. hartmannae* needs to be carefully monitored to prevent adverse effects on population viability.

Limitations & Assumptions

- Some level of hybridisation between *E. z. zebra* and *E. q. burchelli* (Burchell's zebra) has already occurred within small populations in proximity to plains zebra.
- The bulk of newly established *E. z. zebra* subpopulations originate from only Mountain Zebra National Park. However, individuals from Gamkaberg Nature Reserve and Kammanassie Nature Reserve have rarely been used in establishing new subpopulations, as both have fewer than 50 individuals.
- Translocation of individuals between the GMUs has already occurred, as well as from species outside of these GMUs.

Priority Research

- Collect more genetic data from the isolated subpopulations of *E. z. zebra* within South Africa to develop a better understanding of the rate of loss of genetic diversity and causes for the decline in population growth.
- Genetic data are also needed from gaps in the genetic sampling such as the north-western Cape, southern Namibia, Sperrgebiet, Fish River area and south-west Angola.
- Genome research is needed to better understand the evolutionary history and possible unique adaptations of the two mountain zebra GMUs.
- More research is needed to evaluate the extent and effect of hybridisation within the different zebra species.
- It is recommended that genetic monitoring studies be undertaken every 3-5 generations, if possible, to evaluate whether any changes in the genetic structure and diversity of this species have taken place, possibly warranting an update to these guidelines. Such studies would also contribute to the assessment of genetic indicators under the Kunming-Montreal Global Biodiversity Framework. Note: such studies would not be to assess local pedigree, but rather broad population structure and diversity, and hence the overall genetic health of the species.
- Encourage authorities to collect genetic samples opportunistically for downstream genetic monitoring. This is essential for tracking the introduction or mixing of alleles when members of different relic stocks are used to seed new populations.

Cited References

- Hrabar, H. & Kerley, G. I. H. (2013). Conservation goals for the Cape mountain zebra *Equus zebra zebra* – security in numbers? *Oryx* **47**(3), 403-409. doi.org/10.1017/S0030605311002018.
- Kotzé, A. et al. (2019). Lessons for conservation management: monitoring temporal changes in genetic diversity of Cape mountain zebra (*Equus zebra zebra*). *PLoS ONE* **14**(7). doi.org/10.1371/journal.pone.0220331.
- Moodley, Y. & Harley, E. H. (2005). Population structuring in mountain zebras (*Equus zebra*): the molecular consequences of divergent demographic histories, *Conservation Genetics* **6**(6), 953-968. doi.org/10.1007/s10592-005-9083-8.
- Smith, R. K. et al. (2008). Monitoring and management of the endangered Cape mountain zebra *Equus zebra zebra* in the Western Cape, South Africa. *African Journal of Ecology* **46**(2), 207-213. doi.org/10.1111/j.1365-2028.2007.00893.x.
- Solari, S. & Baker, R.J. (2007). Mammal species of the world: a taxonomic and geographic reference by D. E. Wilson and D. M. Reeder. *Journal of Mammalogy* **88**(3), 824-830. doi.org/10.1644/06-MAMM-R-422.1.

Additional references:

- Marais, H. J. et al. (2007). Prevalence and body distribution of sarcoids in South African Cape mountain zebra (*Equus zebra zebra*). *Journal of the South African Veterinary Association* **78**(3), 145-148. doi.org/10.4102/jsava.v78i3.306.

Consultation

- IUCN SSC Conservation Genetics Specialist Group
- IUCN SSC Equid Specialist Group

Acknowledgements

We are grateful to Drs Rae Smith and Peter Novellie for their valuable comments and for taking the necessary time and effort to critically review the initial guidelines.

Queries

For any additional questions related to these guidelines, please contact ConGen Africa at info@congenafrica.com.



Thinus van Staden
Photography

CONGEN
Africa

www.congenafrika.com