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SPECIES GUIDELINES

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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. The validity of the fifth subspecies/ESU requires priority research.

Management Level

- **Subspecies**

Four subspecies of sable 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)
- *Hippotragus niger kirkii* (Zambian sable)
- *Hippotragus niger variiani* (giant sable)
- *Hippotragus niger niger* (common or southern sable)

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)** (*H. n. roosevelti*)
- **West Tanzanian (WT)** (suggested new subspecies; Rocha et al. 2022)

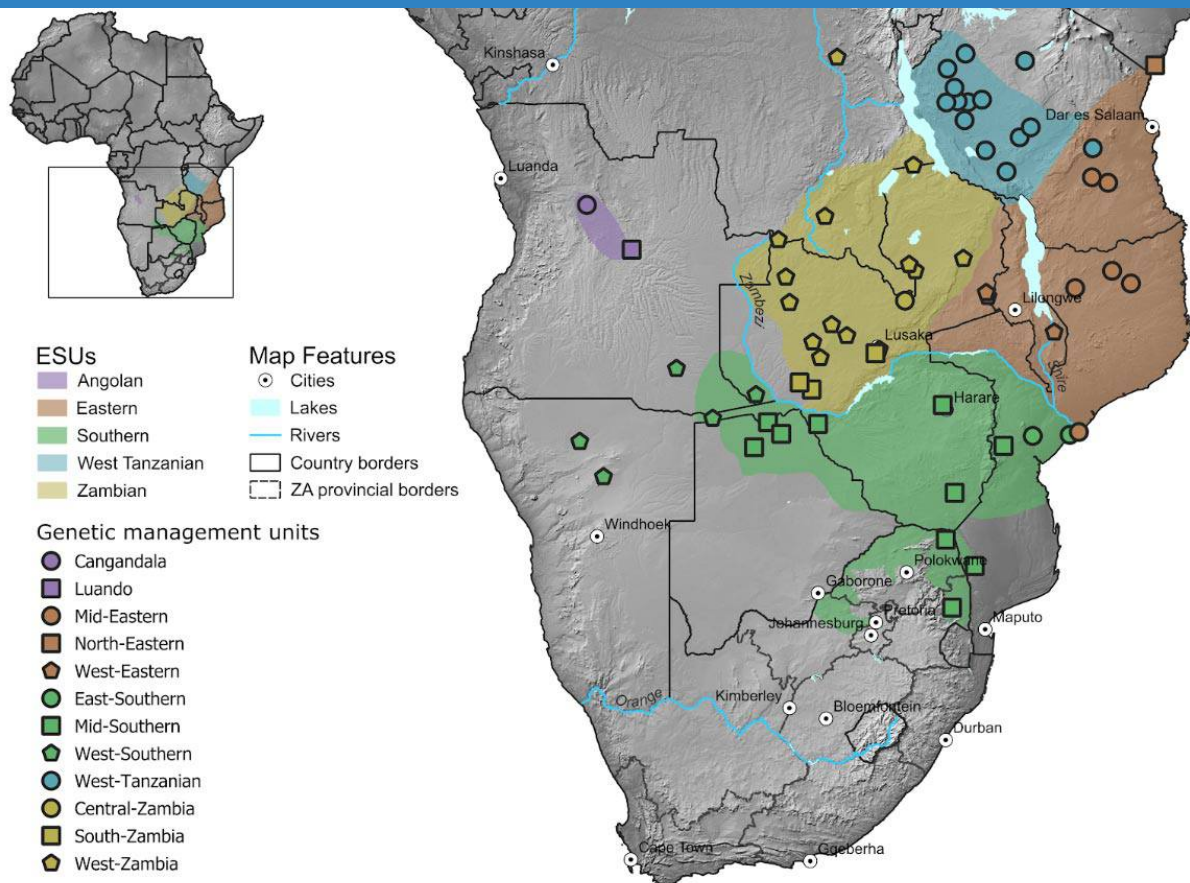


Figure 1: Natural distribution of sable antelope (*Hippotragus niger*) ESUs, indicated by different colours. Genetic Management Units (GMUs) are indicated by different symbols, with the colour corresponding to the ESU to which it belongs. Each point represents a locality which has been sampled for genetic 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 - Continued

- **Zambian (ZM)** (*H. n. kirkii*)
- **Angolan (AO)** (*H. n. variiani*)
- **Southern (SO)** (*H. n. niger*)
- **Genetic Management Units (GMUs)**
 - **Eastern (EE)**
 - West-Eastern (WE)
 - Mid-Eastern (ME)
 - North-Eastern (NE)
 - **Southern (SO)**
 - West-Southern (WS)
 - Mid-Southern (MS)
 - East-Southern (ES)

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. variani*): Angola.
- **Southern (SO)** (*H. n. niger*): south of Zambezi River - Namibia, Botswana, Zimbabwe, south-central Mozambique, South Africa.

Genetic Management Units (GMUs)

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

Genetic Risk

- Global Nc: 50,000-60,000 (IUCN 2017).
- South African Nc: 664 – 775 (Muller et al. 2025).
- Genetic indicators are calculated at ESU level as there is insufficient data to calculate for GMUs. These calculations are based on a best case scenario where gene flow is maintained.
- Risk levels for GMUs can be assumed based on the Ne500 at ESU level.
- If values are reported as a range, the average is used for subsequent calculations.

Table 1. Effective population size, Ne500 indicator, and confidence in the values calculated per ESU for sable antelope. Colour of the ESU label is linked to the colour used in Figure 1. Colour of Ne500 and confidence text corresponds to positive (green) or negative interpretation (orange/red). Overall Ne500 indicates the proportion of the total ESUs that have an Ne over 500.

ESU	Nc	Ne	Ne500 indicator ¹	Confidence
Eastern (EE) <i>H. n. roosevelti</i>	7,191-8,390	1,558-4,674	> 500	Low
West Tanzanian (WT)	Unknown	Unknown	Unknown	N/A
Zambian (ZM) <i>H. n. kirkii</i>	2,454-2,863	266-798	~ 500	Low
Angolan (AO) <i>H. n. variani</i>	100	10-30	< 500	High
Southern (SO) <i>H. n. niger</i>	22,374-26,103	2,434-7,272	> 500	Low
Overall:	50,000-60,000	N/A	3/5 ESUs have an Ne > 500 = 0.6	Moderate

- **Genetic indicators**

- **Ne500 indicator1:**

- Eastern (EE) individuals: > 11,985 (East 1999). With assumed maturity percentage of 60-70 % (Parrini et al. 2016), Nc: 7,191-8,390. Using an Nc:Ne ratio of 0.1-0.3, Ne = 1,558-4,674.
- **West Tanzanian (WT) Nc:** Unknown.
- **Zambian (ZM)** individuals: 4,090 (East 1999). With assumed maturity percentage of 60-70 % (Parrini et al. 2016), Nc: 2,454-2,863. Using an Nc:Ne ratio of 0.1-0.3, Ne = 266-798.
- **Angolan (AO)** Nc: 100 (IUCN 2017). Using an Nc:Ne ratio of 0.1-0.3, Ne = 10-30.
- **Southern (SO)** individuals: 37,290 (East 1999). With assumed maturity percentage of 60-70 % (Parrini et al. 2016), Nc: 22,374-26,103. Using an Nc:Ne ratio of 0.1-0.3, Ne = 2,434-7,272.

Based on Ne500, the Zambian and Angolan ESUs are most at risk genetically, with the Angolan ESU Ne well under 500 and the Zambian ESU having an Ne only just above 500 on average. ESUs with Ne < 500 are highly susceptible to rapid loss of genetic diversity and are at high risk of extinction due to genetic threats. Figure 2 summarises findings.

- **Proportion of populations maintained (PM2):**

- The global populations of sable antelope make up four subspecies, with a fifth subspecies being proposed by Rocha et al. (2022), relating to the five ESUs. Therefore the proportion of populations maintained globally: $5/5 = 1$.

- **Diversity loss**

- Functional variation: There is risk of functional variation loss due to massive reduction in historical range causing fragmented/isolated populations. Due to this, there has likely been a loss of traits that were adapted to habitats the species formerly occupied.
- Divergent lineages: There is risk of losing divergent lineages as the subspecies, the giant sable (Angolan ESU) is critically endangered (Vaz Pinto et al. 2016).

- **Hybridisation/introgression**

- There is strong evidence of hybridisation and introgression within giant sable populations in Angola with roan antelope (Vaz Pinto et al. 2016). Additionally, outdated existing genetic tests may lead to unintended mixing and hybridisation of ESUs.

- **Lower turnover/constraints on adaptive opportunities**

- There has been a noted decrease in sable antelope population densities since the 1970s until the 2010s where these appeared to stabilise (Parrini et al. 2016). This may still have an impact on population turnover, constraining adaptive opportunities.

- **In situ genetic threat level**

- In situ risk (**Moderate**)
Sable antelope exist in small, fragmented populations and can hybridise with roan antelope (*Hippotragus equinus*). Hybridisation presents genetic risks in reduction of functional variation. This issue is especially problematic in Angola for the giant sable subspecies (Vaz Pinto et al. 2016). For more threats, see the IUCN Red List and South African Red List.

- **Confidence in in situ threat level**

- Confidence score (**Moderate**)
Confidence is moderate as the evaluation is based on scientific papers (Vaz Pinto et al. 2019) and IUCN or regional assessment data from within the last decade (IUCN 2017; Muller et al. 2025; Parrini et al. 2016). However, population numbers per ESU to calculate Ne500 were assumed from data provided in East (1999) and the population is assumed to have remained stable (IUCN 2017). This confidence score is based on several assumptions and could potentially misrepresent interpretation and also current population census sizes.

Ex situ representation

- Sable exist in captive populations within southern Africa and North America.
- North American individuals are in private ranches and zoos, similar to wildlife reserves where they are seen in southern African countries.
- Captive individuals are predominantly from Zambian sable or southern sable; hybridisation between these two ESUs in captive populations is widespread (Koepli et al. 2019).

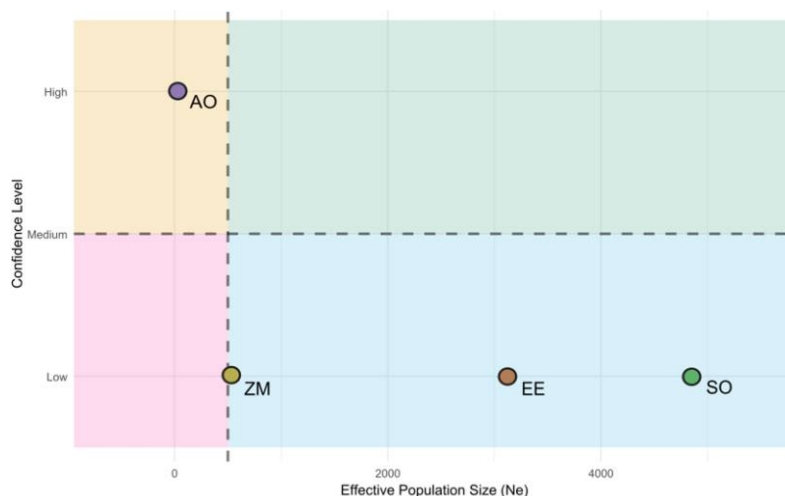


Figure 2. Effective population size compared to confidence in the value. Colour of points and labelling corresponds to the ESU in Figure 1 and Table 1. Dashed lines divide the x axis into above and below Ne500, and the y axis into low and high confidence. ESUs in the low confidence quadrant should be further surveyed to increase confidence in the evaluation. Those with high confidence below Ne500 should have increased genetic management. Note that the WT ESU is not shown due to data deficiency.

1Proportion of populations within species with an effective population size (Ne) greater than 500

(<https://www.gbif-indicators.org/metadata/headline/A-4>)

2Proportion of populations maintained within species

(https://ccgenetics.github.io/guidelines-genetic-diversity-indicators/docs/2_Theoretical_background/PM-indicator.html)

Management Guidelines

- No import of sable from countries containing the other ESUs.
- No translocation between GMUs (based on microsatellite data) within the Southern ESU, however, natural migration should be promoted (Vaz Pinto 2018).
- Efforts must be made to increase the effective population size of the Angolan and Zambian ESUs to over 500.
- Natural gene flow between populations within ESUs should be promoted to increase effective population size (increase Ne > 500).
- Captive bred animals and those on private ranches must be genetically tested before translocation to ensure no admixture between ESUs.
- There has been historical isolation of maternal lineages within the Zambian and Southern ESUs north and south of the Zambezi River (Rocha et al. 2022). As a precautionary principle, these mitochondrial DNA lineages should not be mixed through anthropogenic translocations.

IUCN Status:

- Global: Least concern (indicated below)
- South Africa: Vulnerable



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.
- ESUs with low Ne500 confidence should be surveyed to enable an up to date evaluation of their genetic risk, especially the West Tanzanian ESU which has no population data.
- 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.

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Consultation

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

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Queries

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

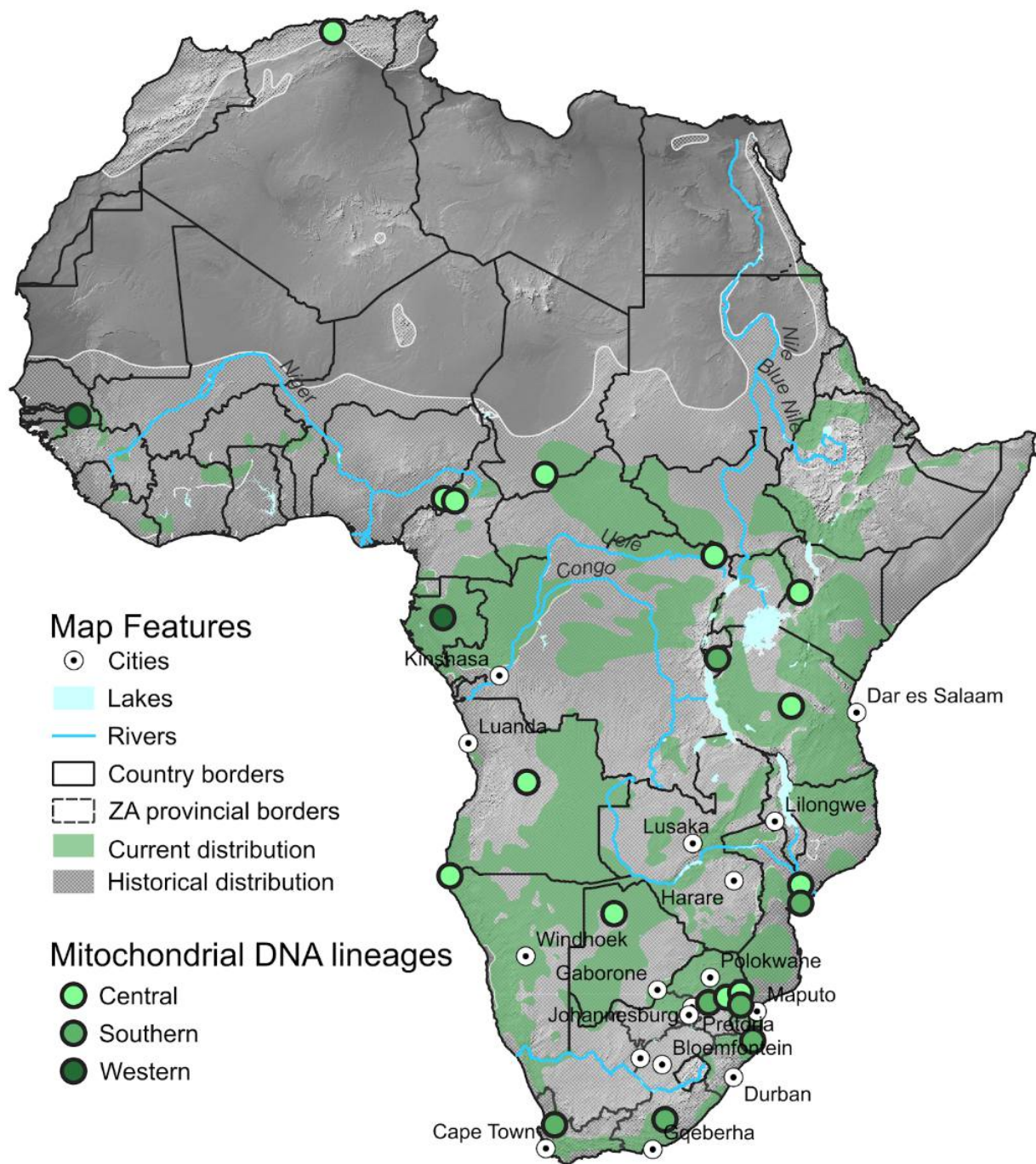


Figure 1: Natural and current distribution of the African leopard (*Panthera pardus pardus*) in southern Africa, illustrated by the hashed white lines and the green shading, respectively. Each point represents a locality which has been sampled for genetic data, with mitochondrial lineages within the 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>.

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

See Figure 1 for visual representation of African management boundaries (Arabian and Asiatic distribution excluded). Text descriptions follow.

- **Subspecies**

- ***Panthera pardus pardus***: Africa south of Sahara and northern Africa.

Genetic Risk

- **Global Nc**: 78,780 (Slovikovsky et al. 2025; Swanepoel et al. 2016)
- **South African Nc**: 1,688–6,979 (Mann et al. 2025)
- To keep the scope of guidelines consistent, the Ne500 indicator will focus on the **African leopard** only.
- Genetic indicators are calculated at **ESU level** which correlates to subspecies for leopards. These calculations are based on a best case scenario where gene flow is maintained.
- If values are reported as a range, the average is used for subsequent calculations.

Table 1. Effective population size, Ne500 indicator, and confidence in the values calculated per ESU for sable antelope. Colour of the ESU label is linked to the colour used in Figure 2. Colour of Ne500 and confidence text corresponds to positive (**green**) or negative interpretation (**orange/red**). Overall Ne500 indicates the proportion of the total ESUs that have an Ne over 500.

ESU	Nc	Ne	Ne500 indicator ¹	Confidence
<i>Panthera pardus pardus</i> (PP)	64,421	6,442-19,326	> 500	Moderate
Overall:	64,421	N/A	1/1 ESUs have an Ne > 500 = 1	Moderate

Genetic indicators

• Ne500 indicator1:

- ***Pardus pardus pardus*** individuals: 107,369 (Slovikosky et al. 2025). With assumed maturity percentage of 60% (Swanepoel et al. 2016), Nc: 64,421. Using an Nc:Ne ratio of 0.1-0.3, Ne = 6,442-19,326.

The African ESU has an Ne above 500 which indicates the ESU will maintain genetic diversity, assuming gene flow is maintained, thus indicating lower genetic risk. For comparison, the Ne of other leopard subspecies ranges from 12-1,542 (Calculated using Nc data from IUCN subspecies Red Lists).

• Proportion of populations maintained (PM2):

- The global populations of leopards make up eight subspecies, considered ESUs. Therefore the proportion of populations maintained globally: $8/8 = 1$.

• Diversity loss

- **Functional variation:** There is risk of functional variation loss due to massive reduction in distribution, with leopards now only occupying 25-37% of their historical range causing fragmented/isolated populations (Jacobson et al. 2016). Due to this, there has likely been a loss of traits that were adapted to habitats the species formerly occupied.
- **Divergent lineages:** There is risk of losing divergent lineages due to small remaining population sizes in several areas of its range as well as human-leopard conflict, as a result of real or perceived predation on livestock.

• Hybridisation/introgression

- There is no evidence of persistent hybridisation between leopard subspecies and no detectable introgression. There is also no evidence of hybridisation with other *Panthera* species in the wild.

• Lower turnover/constraints on adaptive opportunities

- African leopards have the highest genetic diversity of big cats, therefore less constraints on adaptive potential than other subspecies of leopards (Pečnerová et al. 2021).

• In situ genetic threat level

- In situ risk (**Low**)

Leopards exist in small populations, however no current genetic threats exist for *P. p. pardus* as genetic diversity is high and there is no evidence of inbreeding in southern African populations studied thus far. For more threats, see the IUCN Red List and South African Red List.

• Confidence in in situ threat level

- Confidence score (**Moderate**)

Confidence is moderate as the evaluation is based on scientific papers (Slovikosky et al. 2025; Pečnerová et al. 2021) and IUCN or regional assessment data from within the last decade (Stein 2025; Swanepoel et al. 2016; Mann et al. 2025). However, population numbers for the African ESU to calculate Ne500 were taken from estimates provided in Slovikosky et al. (2025), meaning they may be inaccurate.

• Ex situ representation

- Leopards exist in captive populations within southern Africa, North and Central America, Europe, and Asia totalling to 741 individuals in 230 institutions across 58 countries.

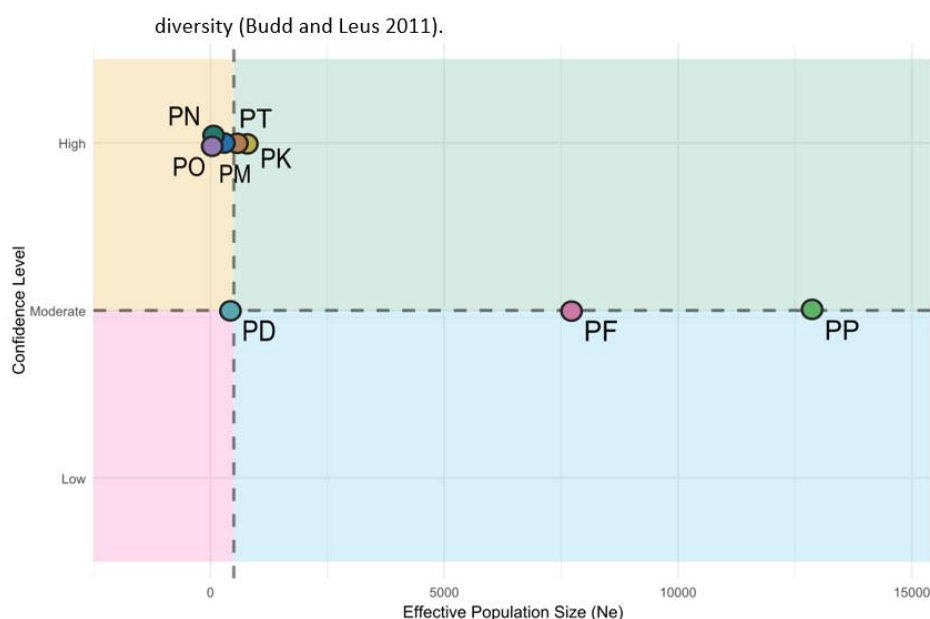


Figure 2. Effective population size compared to confidence in the value. Colour of points and labelling corresponds to the colour for the ESU in Table 1. Dashed lines divide the x axis into above and below N_e500 , and the y axis into low and high confidence. ESUs in the low confidence quadrant should be further surveyed to increase confidence in the evaluation. Those with high confidence below N_e500 should have increased genetic management.

1Proportion of populations within species with an effective population size (N_e) greater than 500

(<https://www.gbif-indicators.org/metadata/headline/A-4>)

2Proportion of populations maintained within species

(https://ccgenetics.github.io/guidelines-genetic-diversity-indicators/docs/2_Theoretical_background/PM-indicator.html)

Genetic 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.

IUCN Status:

- Global: Least concern (indicated below)
- South Africa: Vulnerable



- **Limitations and 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.
- 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..

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Consultation

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

Acknowledgements

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Queries

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

Management Level

Subspecies

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

- ***Tragelaphus oryx oryx*** (Cape eland, Pallas 1766): South Africa, Namibia, southern Botswana, south-western Zimbabwe)
- ***Tragelaphus oryx livingstonii*** (Livingstone's eland P.L. Sclater, 1864): Angola, northern Namibia, northern Botswana, Zimbabwe, Mozambique, Zambia, southern DRC, Malawi.)
- ***Tragelaphus oryx pattersonianus*** (Patterson's or East African eland, Lydekker 1906): Tanzania, Rwanda, Burundi, Uganda, Kenya, southern South Sudan, southern Ethiopia.)

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.

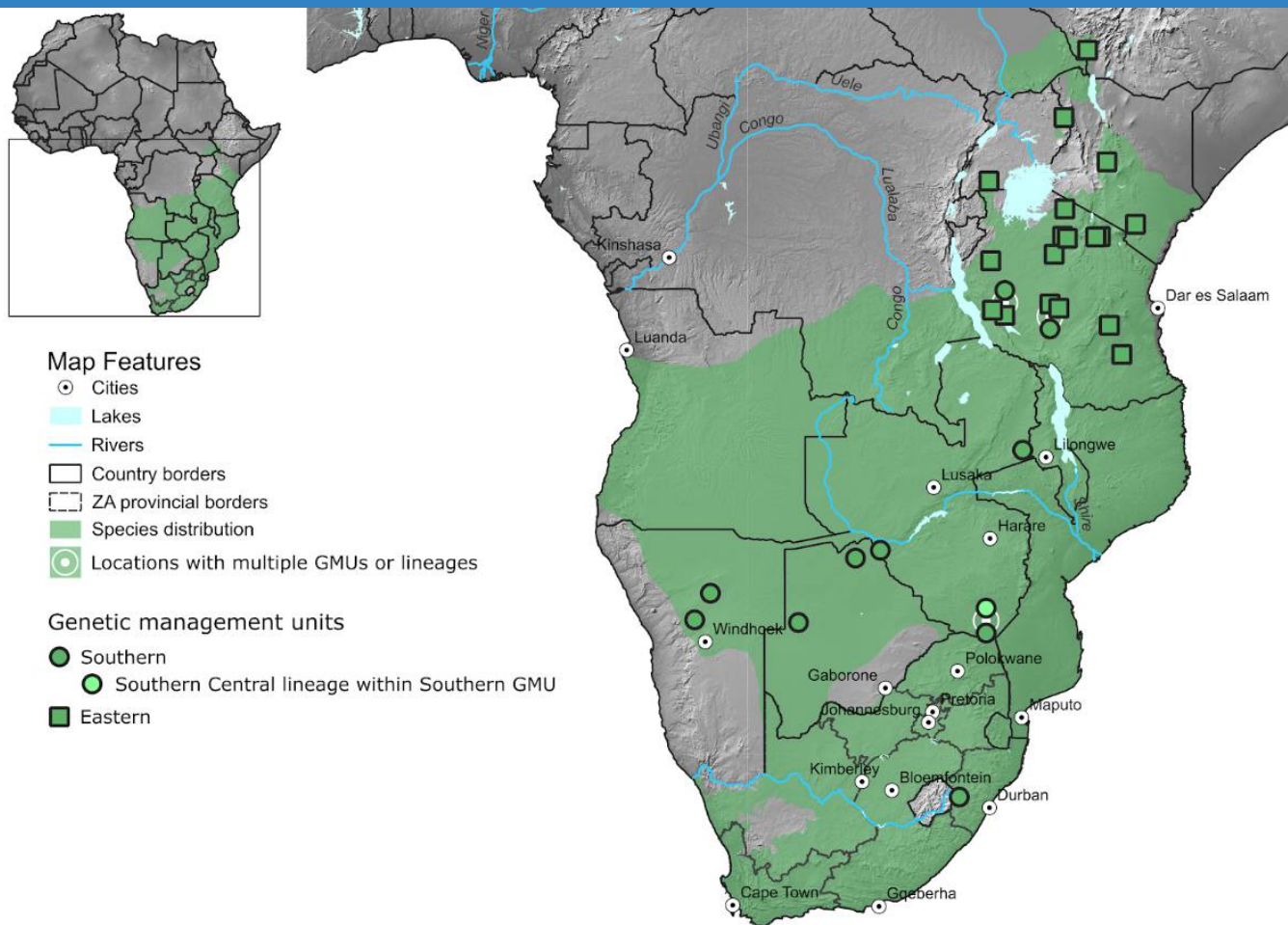


Figure 1: Natural distribution of common eland (*Tragelaphus oryx*) in green shading. Genetic Management Units (GMUs) are indicated by different symbols. Each point represents a locality which has been sampled for genetic data and thus the GMU (symbol) designation of each locality is based on genetic 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 - Continued

Evolutionarily Significant Units (ESUs)

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

Genetic Management Units (GMUs)

- **Eastern (EE)**
- **Southern (SO)**
- **Central (CE); tentative, referred to as "intermediate" by Lorenzen et al. (2010)**

Management Boundaries

See **Figure 1** for visual representation. Text descriptions follow.

- **Genetic Management Units (GMUs, based on genetic data from Lorenzen et al. (2010))**
 - Eastern (EE): South Sudan, Ethiopia, Uganda, Rwanda, Burundi, Kenya, Tanzania.
 - Southern (SO): Zambia, Zimbabwe, Botswana, Namibia, Angola, South Africa, Mozambique.
 - Central (CE): Southern Zimbabwe

Genetic Risk

There are three subspecies currently recognised for this species, but their validity remains disputed. For this evaluation, genetic management units were used.

- Global population Nc: 90,000-110,000 (IUCN 2016).
- South African population Nc: 34,925-45,648 (Venter and da Silva 2025).
- Genetic indicators are calculated at GMU level. This is based on a best case scenario where gene flow is maintained within GMUs.
- If values are reported as a range, the average is used for subsequent calculations.

Table 1. Effective population size, Ne500 indicator, and confidence in the values calculated per ESU for common eland. Colour of the ESU label is linked to the colour used in Figure 1. Colour of Ne500 and confidence text corresponds to positive (**green**) or negative interpretation (**orange/red**). Overall Ne500 indicates the proportion of the total ESUs that have an Ne over 500.

GMU	Nc	Ne	Ne500 indicator ¹	Confidence
Eastern (EE)	28,154	2,815-9,446	> 500	Moderate
Southern (SO)	84,183	8,416-25,249	> 500	Moderate
Central (CE)	Unknown	Unknown	Unknown	N/A
Overall	90,000-110,000	N/A	2/3 GMUs have an Ne > 500 = 1	Moderate

- **Genetic indicators**

- **Ne500 indicator¹:**

- **Eastern (EE)** individuals: > 40,220 (East 1999). With assumed maturity percentage of 70 % (Buijs et al. 2016), Nc: 28,154. Using an Nc:Ne ratio of 0.1-0.3, Ne = 2,815-9,446.
- **Southern (SO)** Nc: 84,163 (East 1999; Venter and da Silva 2025). Using an Nc:Ne ratio of 0.1-0.3, Ne = 8,416-25,249.
- **Central (CE)** Nc: Unknown.
Eastern and southern management units have an Ne above 500 which indicates each GMU will maintain genetic diversity, assuming gene flow is maintained within GMUs, thus indicating lower genetic risk. The central GMU lacks sufficient data to evaluate.

- **Proportion of populations maintained (PM2)**

- The global populations of the common eland comprise three GMUs, therefore the proportion of populations maintained globally: $3/3 = 1$.

- **Diversity loss**

- **Functional variation**

- There is risk of functional variation loss due to increasingly fragmented, intensively managed populations that are often admixed or bred in small founder groups. Due to this, there has likely been a loss of traits that were adapted to specific habitats.

- **Divergent lineages**
 - There is little risk of losing current divergent lineages due to high effective population numbers for EE and SO GMUs. The CE GMU is the most at risk as is a much smaller group.
- **Hybridisation/introgression**
 - There is little risk of hybridisation for common eland with other closely related species. There have been cases of eland hybridisation with greater kudu, however this was only in captivity with rare circumstances and the offspring was sterile (Jorge et al. 1976). No introgression has been seen in genetic studies of eland (Kubatova et al. 2020).
 - Crosses between GMUs within common eland are a more pressing risk as once individuals of another GMU are 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).
- Lower turnover/constraints on adaptive opportunities
 - Founder effects in subpopulations within managed areas and translocation without consideration for unique genetic groups pose risk to adaptive potential.
- **In situ genetic threat level**
 - *In situ Risk* (**Low**)
Common eland exist in small, fragmented populations, however eastern and southern genetic management units have an N_e well above 500 and are relatively stable, therefore with facilitation of gene flow between populations within GMUs, risk is low (IUCN 2016; Buijs et al. 2016). More data is needed on the central GMU to comment. For more threats, see the IUCN Red List and South African Red List.
 - **Confidence in in situ threat level**
 - Confidence score (**Moderate**)
 - Confidence is moderate as the assessment is based on IUCN or regional assessment data from within the last decade (IUCN 2016; Buijs et al. 2016; Venter and da Silva 2025). However, population numbers per GMU to calculate N_{e500} were assumed from data provided in East (1999) as well as the South African red list assessment (Buijs et al. 2016; Venter and da Silva 2025) and the population is assumed to have remained stable (IUCN 2016). The in situ risk score is based on several assumptions and could potentially misrepresent current population census sizes and change interpretations.
- **Ex situ representation**
 - Common eland exists in captive populations within southern Africa, particularly South Africa. Many of these are game ranches outside of their natural range (IUCN 2016).
 - Globally, they are found in 148 institutions across 46 countries (within North Central, and South America, Europe, Asia, and Africa).
 - Hybridisation between the GMUs in captive populations may be widespread.

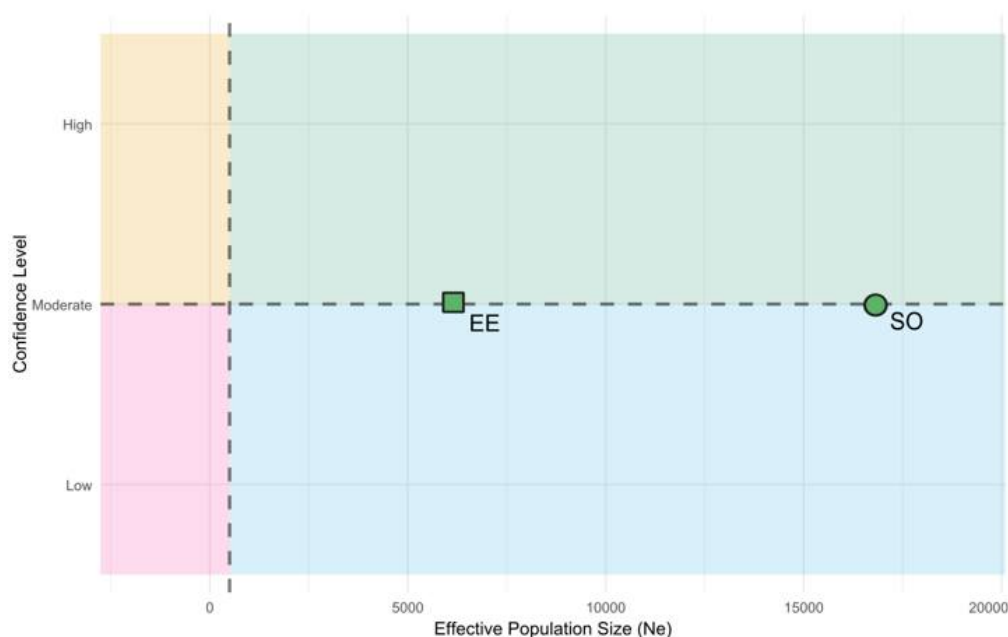


Figure 2. Effective population size compared to confidence in the value. Colour and shape of points and labelling corresponds to the GMU in Figure 1 and Table 1. Dashed lines divide the x axis into above and below Ne500, and the y axis into low and high confidence. GMUs in the low confidence quadrant should be further surveyed to increase confidence in the evaluation. Those with high confidence below Ne500 should have increased genetic management. Note that the CE GMU is not shown due to data deficiency.

¹**Proportion of populations within species with an effective population size (Ne) greater than 500**

(<https://www.gbf-indicators.org/metadata/headline/A-4>)

²**Proportion of populations maintained within species**

(https://ccgenetics.github.io/guidelines-genetic-diversity-indicators/docs/2_Theoretical_background/PM-indicator.html)

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 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.
- Both GMUs have $N_e > 500$ under the assumption of gene flow within GMUs. Therefore, management must strive to facilitate natural migration and gene flow between isolated populations within each GMU, while taking cognisance of the other guidelines above.

IUCN Status:

- Global: Least concern (indicated below)
- South Africa: Vulnerable



• Limitations and 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.
 - “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 CE lineage (equivalent to the “intermediate” lineage from Lorenzen et al. 2010) 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.
- Additional range-wide surveys to accurately report census sizes to enable more confident calculations of effective population sizes.
- 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.

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Consultation

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

Acknowledgements

We are grateful to Prof Eline Loenzen 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).

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.

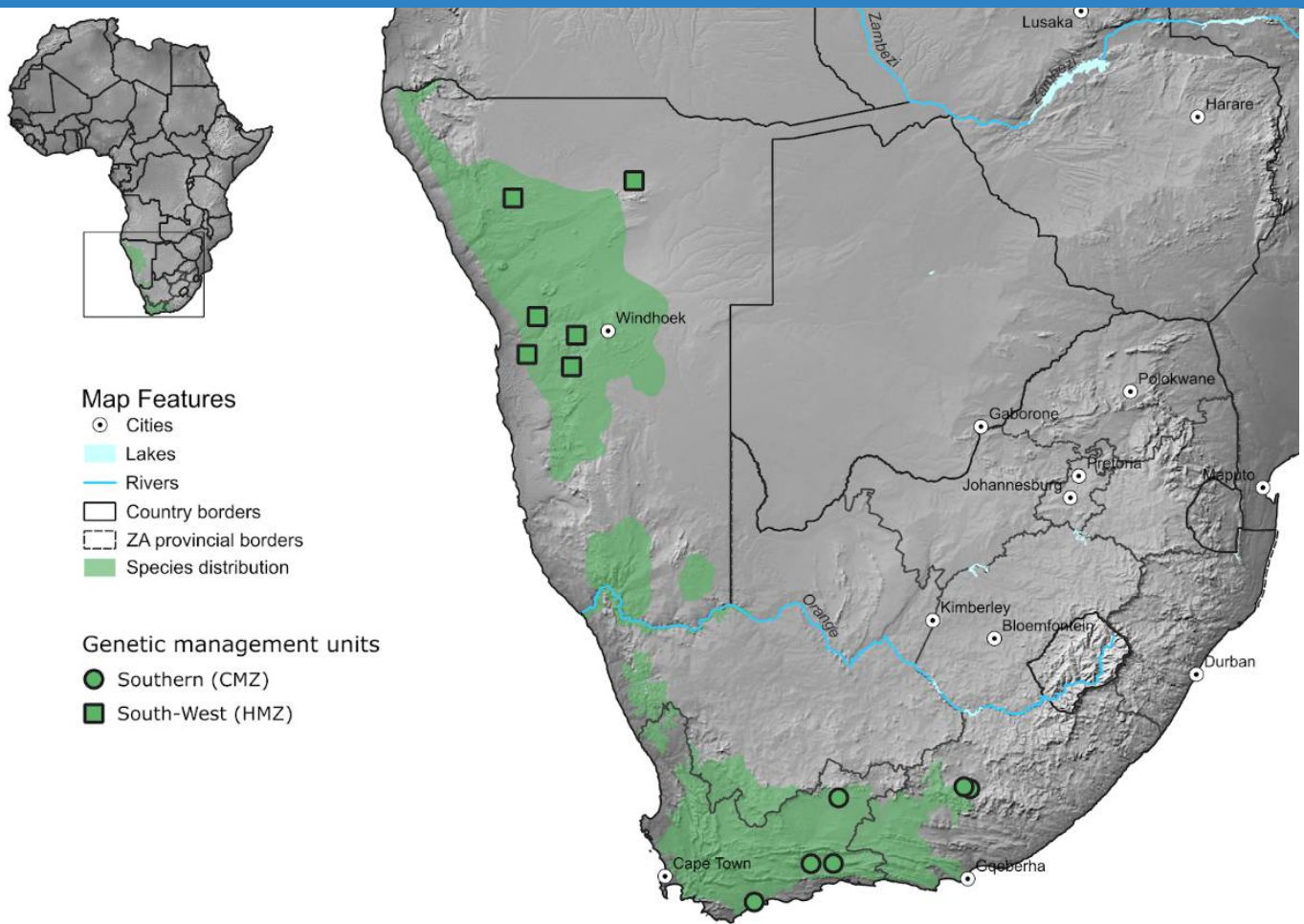


Figure 1: Natural distribution of mountain zebra (*Equus zebra*) in green shading. Genetic Management Units (GMUs) are indicated by different symbols. Each point represents a locality which has been sampled for genetic data and thus the GMU (symbol) designation of each locality is based on genetic data. 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*.

Management Level - Continued

Evolutionarily Significant Units (ESUs)

No ESUs are recognised at present.

Genetic Management Units (GMUs)

There are two GMUs within the species corresponding to the two subspecies.

- **South-West (SW):** (HMZ, *E. z. hartmannae*)
- **Southern (SO):** (CMZ, *E. z. zebra*)

Management Boundaries

See **Figure 1** for visual representation. Text descriptions follow.

- 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

Genetic Risk

- Global Nc:** 37,017 (de Villiers et al. 2025; Patel et al. 2025)
- South African Nc:** 2,852-3,889 (de Villiers et al. 2025)
- Genetic indicators are calculated at **GMU level**. This is based on a best case scenario where gene flow is maintained.
- If values are reported as a range, the average is used for subsequent calculations.

Table 1. Effective population size, Ne500 indicator, and confidence in the values calculated per ESU for mountain zebra. The colour of the GMU label is linked to the colour used in Figure 1. Colour of Ne500 and confidence text corresponds to positive (green) or negative interpretation (orange/red). Overall Ne500 indicates the proportion of the total GMUs that have an Ne over 500.

Genetic group:	Nc	Ne	Ne500 indicator ¹	Confidence
South-West (SW)	33,646	3,365-10,094	>500	High
Southern (SO)	2,852-3,889	337-1,011	>500	High
Overall	37,017	N/A	2/2 GMUs have an Ne>500 = 1	High

- Population genetic indicators**
 - Ne500 indicator¹:
 - South-West (SW) Nc: 33,646. Using an Nc:Ne ratio of 0.1-0.3, Ne = 3,365-10,094 (Patel et al. 2025).
 - Southern (SO) Nc: 2,852-3,889. Using an Nc:Ne ratio of 0.1-0.3, Ne = 337-1,011 (de Villiers et al. 2025).
 Both management units have an Ne above 500 which indicates each GMU will maintain genetic diversity, assuming gene flow is maintained within GMUs, thus indicating lower genetic risk.
 - Proportion of populations maintained (PM2):**
 - Global populations of mountain zebra comprise 2 GMUs (de Villiers et al. 2025; Patel et al. 2025), therefore the proportion of populations maintained globally: $2/2 = 1$.
- Diversity loss**
 - Functional variation:** There is risk of functional variation loss, particularly in E. z. zebra, due to massive reduction in historical range causing fragmented/isolated populations with little potential for natural gene flow. This leaves CMZ at risk of genetic drift and inbreeding. Due to this, there has likely been a loss of traits that were adapted to habitats the species formerly occupied.
 - Divergent lineages:** There is risk of losing divergent lineages due to small remaining population sizes in several areas of its range. Genetic divergence among the relic subpopulations of E. z. zebra is 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 2007).
- Hybridisation/introgression**
 - Cape mountain zebra and Hartmann's mountain zebra are known to hybridise, with 28% of the CMZ population currently thought to be at risk (Hrabar et al. 2015).

- There is some evidence of hybridisation between Cape mountain zebra (*E. z. zebra*) and plains zebra (*Equus quagga burchelli*). No introgression has been seen as it is likely offspring between the two species are infertile (Dalton et al. 2017).
- **Lower turnover/constraints on adaptive opportunities**
 - Historical bottlenecks have led to a narrow gene pool for mountain zebra, constraining their adaptive potential. This is furthered by founder effects in subpopulations derived from these original bottlenecked populations. Studies have documented low heterozygosity within the species in comparison to other zebra and equine species (Kotze et al. 2019).
- **In situ genetic threat level**
 - In situ risk (High)
Mountain zebras are at risk of continued diversity loss through fragmented habitats and isolated populations. Low heterozygosity within remaining populations may pose future risk. The Cape mountain zebra exists in smaller numbers than Hartmann's mountain zebra and are potentially at an increased risk. There is also significant risk of hybridisation, which could further affect diversity loss in the form of divergent lineage and functional variation loss. For other threats, see the IUCN Red List, South African Red List (CMZ), and South African Red List (HMZ) .
- **Confidence in in situ threat level**
 - Confidence score (High)
Confidence levels are supported by data on heterozygosity from recent genomic studies using microsatellite markers (Kotze et al. 2019) and IUCN or regional assessment data from within the last decade (de Villiers et al. 2025; Gosling et al. 2019; Hrabar et al. 2015; Patel et al. 2025).
- **Ex situ representation**
 - Hartmann's mountain zebra exists in captive populations globally, with 226 individuals within 59 institutions, in 15 countries and five continents (Europe, Asia, Central America, North America, and Africa) (Langenhorst 2025).
 - Cape mountain zebra exists within six captive populations in South Africa, totalling 143 individuals (Hrabar et al. 2015).
 - Captive populations may contain both GMUs and other zebra species, potentially complicating the genetic integrity of some ex situ stocks.

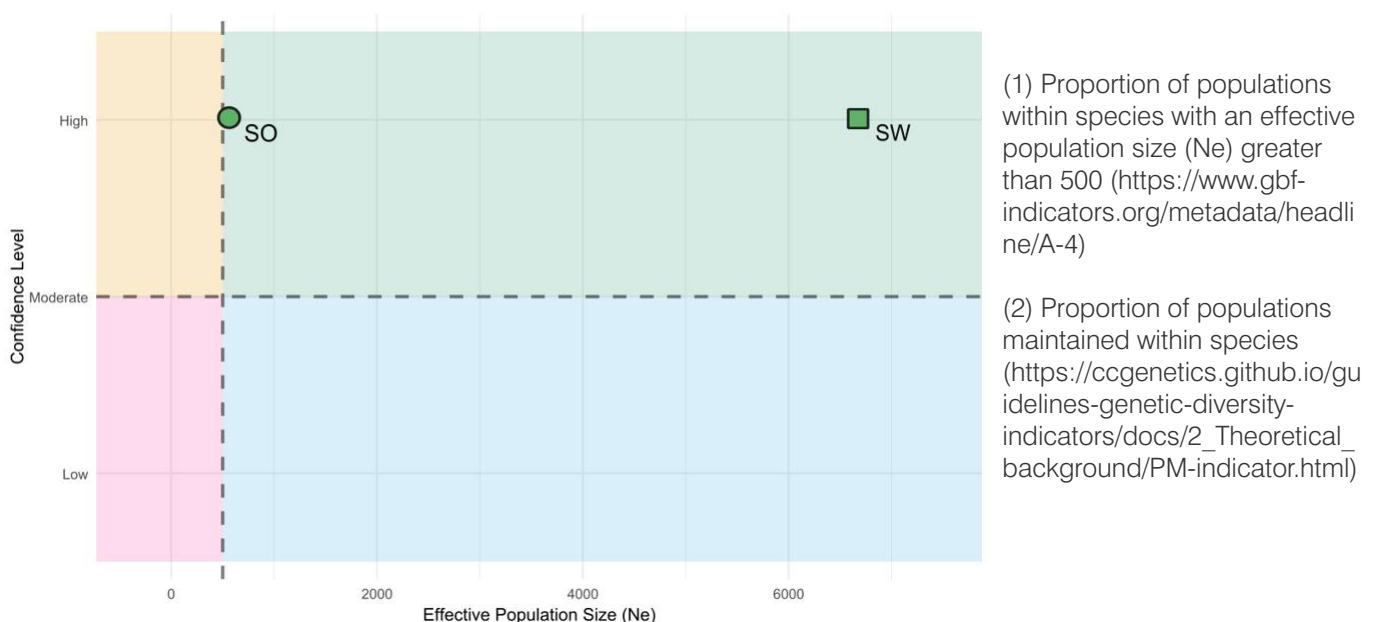


Figure 2. Effective population size compared to confidence in the value. Colour and shape of points and labelling corresponds to the GMUs in Figure 1 and Table 1. Dashed lines divide the x axis into above and below N_e500 , and the y axis into low and high confidence. GMUs in the low confidence quadrant should be further surveyed to increase confidence in the evaluation. Those with high confidence below N_e500 should have increased genetic management.

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).

IUCN Status:

- Global: Least concern (indicated below)
- South Africa: Vulnerable



Limitations and assumptions:

- Some level of hybridisation between *E. z. zebra* and *E. burchelli* have 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.

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Consultation

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

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Queries

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



African Buffalo

(*Syncerus caffer*)

Within *S. caffer*, four subspecies have generally been accepted based on morphological characteristics, namely *S. c. caffer* (Cape or Savannah buffalo – large, blackish, large horns), *S. c. nanus* (forest or dwarf buffalo – small, reddish/brown, small horns), *S. c. brachyceros* (Sudan buffalo – intermediate size and colour compared to Cape and forest buffalo), and *S. c. aequinoctialis* (Nile buffalo – intermediate size and colour compared to Cape and forest buffalo) (see Smits et al. 2013 for a summary of morphological differences). However, **genetic studies show support for only two lineages: a West-Central lineage** consisting of forest, Sudan, and Nile buffalo (*S. c. nanus*, *S. c. brachyceros*, and *S. c. aequinoctialis*) and **South-East lineage** consisting of Cape buffalo (*S. c. caffer*) (van Hooft et al. 2002, Smits et al. 2013, Talenti et al. 2024). While there is some shared genetic variation between these two lineages, this current assessment has defined them as two distinct Evolutionarily Significant Units (ESUs) – the West-Central (WC) ESU and South-East (SE) ESU. This is based on the combined

evidence of: (i) high genetic differentiation between the two lineages/ESUs (FCT mitochondrial DNA = 0.42 – 0.48 (van Hooft et al. 2002, Smits et al. 2013), mean F_{ST} genome-wide data = 0.13 (Talenti et al. 2024)), (ii) distinct number of chromosomes ($2n = 52$ for Cape buffalo and $2n = 54$ for forest buffalo (Wurster & Benirschke, 1968)), (iii) substantial morphological differences, and (iv) different preferred habitats of the WC ESU and SE ESU buffalo.

The main evolutionary driving force of genetic differentiation in Cape buffalo (SE ESU, *S. c. caffer*) is isolation-by-distance (Simonsen et al. 1998, van Hooft et al. 2000, van Hooft et al. 2002, Talenti et al. 2024), with some exceptions (see Appendix). Within the SE ESU, there are several populations currently known to be threatened by inbreeding due to past bottlenecks and subsequent isolation: **Addo Elephant National Park (NP)** and **Hluhluwe-iMfolozi Park** in South Africa (O’Ryan et al. 1998, Smits et al. 2014, de Jager et al. 2020, de Jager et al. 2021, Quinn et al. 2023, Talenti et al. 2024), and **Catuane, Namaacha, Marromeu National Reserve**, and **Gorongosa NP** in Mozambique (Colangelo et al. 2024). These populations require urgent genetic supplementation and highlight the vulnerability of Cape buffalo populations to genetic threats as a result of isolation from other populations. The WC ESU requires more in-depth genetic studies.

Management Level

Four subspecies of African buffalo are described based on morphological characteristics.

Syncerus caffer caffer (Cape buffalo)

Syncerus caffer nanus (Forest buffalo)

Syncerus caffer brachyceros (Sudan buffalo)

Syncerus caffer aequinoctialis (Nile buffalo)

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.

Management Level - Continued

Evolutionarily Significant Units (ESUs)

- West-Central (WC) (*S. c. nanus*, *S. c. brachyceros* and *S. c. aequinoctialis*)
- South-East (SE) (*S. c. caffer*)

Genetic Management Units (GMUs)

- West-Central (WC)
 - No GMUs are recognised at present due to lack of appropriate data.
- South-East (SE)
 - Functionally, East African and southern African populations should be considered as different GMUs due to the vast distances between them. But given the gradual increase in differentiation with distance (i.e. the isolation-by-distance pattern of genetic variation), it is difficult to define distinct GMU boundaries and thus we do not do so here. See the management guidelines for more details.

Additionally, some individual populations require special attention in terms of genetic management, due to being threatened by inbreeding, or because they already contain a non-ideal mixture of buffalo from different sources. See the management guidelines for more details.

Management Boundaries

Evolutionarily Significant Units (ESUs)

- West-Central (WC) (*S. c. nanus*, *S. c. brachyceros* and *S. c. aequinoctialis*): Central to West Africa, potentially including south-western Africa.
- South-East (SE) (*S. c. caffer*): East Africa to southern Africa.

Genetic Management Units (GMUs)

- West-Central ESU: None defined at present.
- South-East ESU: None defined at present, though some populations require specific considerations (see management guidelines).

Genetic Risk

- **Global population Nc:** 398,000-401,000 (IUCN 2019).
- **South African population Nc:** 48,917 (Venter et al. 2025).
- Genetic indicators are calculated at **ESU level**. This is based on a best case scenario where gene flow is maintained within ESUs. However, the SE ESU does show potential isolation-by-distance, and therefore GMUs may be present that have yet to be defined (Talent et al. 2024).
- If values are reported as a range, the average is used for subsequent calculations.

Table 1. Effective population size, Ne500 indicator, and confidence in the values calculated per ESU for African Buffalo. Colour of the ESU label is linked to the colour used in Figure 1. Colour of Ne500 and confidence text corresponds to positive (**green**) or negative interpretation (**orange/red**). Overall Ne500 indicates the proportion of the total ESUs that have an Ne over 500.

ESU	Nc	Ne	Ne500 indicator ¹	Confidence
West-central (WC)	67,200	6,720-20,160	> 500	Moderate
South-east (SE)	331,100	33,110-99,330	> 500	High
Overall	399,500	N/A	2/2 ESUs have an Ne > 500 = 1	High

Genetic Indicators

• Ne500 indicator¹

- **Western Central (WC)** individuals: 96,000 (Cornelis et al. 2014). With assumed maturity percentage of 70 % (Venter et al. 2025; IUCN 2019), Nc: 67,200. Using an Nc:Ne ratio of 0.1-0.3, Ne = 6,720-20,160.
- **South-east (SE)** individuals: 473,000 (Cornelis et al. 2014). With assumed maturity percentage of 70 % (Venter et al. 2025; IUCN 2019), Nc: 331,100. Using an Nc:Ne ratio of 0.1-0.3, Ne = 33,110-99,330.
- Both ESUs have an Ne above 500 which indicates each will maintain genetic diversity, assuming gene flow is maintained, thus indicating lower genetic risk.

• Proportion of populations maintained (PM2):

- The global populations of African buffalo comprise 2 ESUs, therefore the proportion of populations maintained globally: $2/2 = 1$.

Diversity Loss

- **Functional variation:** There is some risk of functional variation loss in *S. caffer* due to having areas of fragmented or isolated population due to human agriculture and disease control (Venter et al. 2025). Trophy hunting in natural populations that target breeding males may lead to unintentional changes in gene frequencies in the population (genetic drift). Only males older than 10 years (thus, past their breeding prime) should be targeted for trophy hunting. Addo Elephant NP, Mokala NP, Waterberg Plateau NP, and private ranches are generally free from major bovid diseases (bovine tuberculosis, foot-and-mouth disease and theileriosis). These disease-free populations of Cape buffalo (*S. c. caffer*) represent an “insurance policy” for the South-East ESU, in the event that a disease outbreak causes major population declines in southern Africa.
- **Divergent lineages:** There is moderate risk of losing divergent lineages as both ESUs have seen population decline in mature individuals in recent decades with an overall loss of 18% between 1999 and 2014 (East 1999; Cornelis et al. 2014). The subspecies *S. c. aequinoctialis* has seen the most decline, with a drop of 61% documented in the same time period (East 1999; Cornelis et al. 2014). Addo Elephant NP harbours an unique, highly divergent mitochondrial lineage (de Jager et al. 2025), which is threatened by the high inbreeding levels in this population.

Hybridisation/introgression

- There is no major risk to genetic structure through hybridisation between ESUs as rates are low and within restricted geography; detected instances appear to be natural or historic.
- Natural contact zones within the range between ESUs may be facilitating hybridisation, especially for localities in Uganda (See figure 1). Intermediate individuals that may be hybrids between *S. c. nanus* and *S. c. aequinoctialis* (Talent et al. (2024).

Lower turnover/constraints on adaptive opportunities

- There is a high risk of constraints on adaptive potential, especially in isolated populations, as effective population sizes have substantially declined across much of the buffalo’s range (Talent et al. 2024). Human mediated translocation and selective breeding may have a negative impact on African buffalo populations’ ability to adapt via narrowing of the gene pool and creating fragmented populations (de Jager et al. 2020). Additionally, disease resilience may also be limited locally through populations facing natural selection from bovine tuberculosis and

foot-and-mouth disease (Lane-deGraff et al. 2016). In Mozambique and other regions such as parts of South Africa, high levels of genome-wide homozygosity and reduced genetic variation have been documented (Colangelo et al. 2024; Talenti et al. 2024; Quinn et al. 2023; de Jager et al. 2021). African buffalo populations seem to be particularly prone to strong genetic drift when isolated from other populations, leading to a loss of genetic variation and eventually inbreeding and inbreeding depression. This is illustrated by an increasing number of studies and populations (see Population-specific guidelines above).

In situ genetic threat level

- ***In situ risk (High)***

- African buffalo exist in fragmented populations, and have evidence of inbreeding and low heterozygosity within populations. Despite both ESUs having an N_e well above 500, there is decline seen in numbers of mature individuals and several threats to genomic diversity, including selective breeding, disease, and trophy hunting, put the species at risk. For more threats, see the IUCN Red List and South African Red List.

- ***Confidence in *in situ* threat level***

- Confidence score (**High**)

Confidence is high as the assessment is based on regional assessment data published within the last year (Venter et al. 2025) and overall species range assessment from the last decade (IUCN 2019). Genetic risk evaluation has been based on numerous studies from within the last six years across the species range (Colangelo et al. 2024; de Jager et al. 2020; Talenti et al. 2024; Quinn et al. 2023). Population numbers may not be entirely accurate due to the nature of surveying migratory species, however confidence can be had in the ESUs N_e 500 indicator results.

Ex situ representation

- The African buffalo is found in 59 institutions across 24 countries, with a total of 463 individuals in captivity, the majority being within Europe (IUCN 2019).
- Knowledge of genetics in ex situ populations outside of Africa is limited.



¹Proportion of populations within species with an effective population size (N_e) greater than 500 (<https://www.gbf-indicators.org/metadata/headline/A-4>)

²Proportion of populations maintained within species (https://ccgenetics.github.io/guidelines-genetic-diversity-indicators/docs/2_Theoretical_background/PM-indicator.html)

Figure 2. Effective population size compared to confidence in the value. Colour of points and labelling corresponds to the ESU in Figure 1 and Table 1. Dashed lines divide the x axis into above and below Ne500, and the y axis into low and high confidence. ESUs in the low confidence quadrant should be further surveyed to increase confidence in the evaluation. Those with high confidence below Ne500 should have increased genetic management.

Management Guidelines

- No introductions of West-Central ESU into the range of the South-East ESU, and vice versa.
- **South-East (SE)**
 - No translocations directly from East Africa to southern Africa, and vice versa.
 - Translocations should instead follow a step-wise pattern between neighbouring or nearby populations to mimic the natural isolation-by-distance pattern of genetic differentiation.
 - Promote natural migration/gene flow between populations where possible.
- **Population-specific guidelines**
 - South Africa:**
 - **Addo Elephant NP:** Genetic supplementation is required due to high levels of inbreeding (O’Ryan et al., 1998, de Jager et al., 2020, 2021, Quinn et al., 2023) and thus to prevent inbreeding depression. Due to strict disease control regulations and with Addo Elephant NP being a disease-free population, the most appropriate source population is Mokala NP, which harbours disease-free Kruger NP buffalo. One buffalo bull should be translocated per buffalo generation (every approximately 7.5 years) (O’Ryan et al., 1998). Note that Addo Elephant NP contains unique mitochondrial DNA diversity (de Jager et al. 2025) and thus only bulls (males) should be introduced, as they do not pass on mitochondrial DNA and thus the unique mitochondrial diversity of Addo will be retained.
 - **Hluhluwe-iMfolozi Park:** Similar to Addo Elephant NP, although inbreeding is less severe in this population (de Jager et al., 2021, Quinn et al., 2023). Thus, introducing one buffalo bull every 1-2 buffalo generations (7.5-15 years) might be sufficient to prevent inbreeding depression. The most appropriate genetic source would be buffalo of Kruger NP origin due to their geographic proximity and high genetic diversity. Southern Mozambique (for example Namaacha or Catuane) is another potential source, though populations studied in this region also have low genetic diversity and high inbreeding levels, which risks introducing novel deleterious alleles into the population (Colangelo et al., 2024). See Priority research for more on this.
 - **Private ranches:** No translocation of buffalo from private ranches to national parks or natural populations of buffalo in southern Africa should occur, unless no other appropriate source population is available, as per the guidelines under South-East ESU above. While many populations or herds were established with disease-free Addo Elephant NP buffalo, and later Kruger NP-origin buffalo from Mokala NP were also introduced (de Jager et al., 2020), it is well known that buffalo of East African origin have also been introduced into the South African private ranch system. This breaks down the evolutionarily established pattern of isolation-by-distance and is in opposition to the first guideline under South-East ESU above. Consequently, the private ranch buffalo population network should be considered as a separate system and a last resort for conservation translocations, reintroductions, or introductions.
 - Mozambique:**
 - **Catuane, Namaacha, Marromeu National Reserve, and Gorongosa NP:** While Smits et al. (2014) did not observe particularly low genetic diversity in Mozambique populations using microsatellites (including Marromeu and Gorongosa), Colangelo et al. (2024) observe alarmingly low levels of diversity and high levels of inbreeding in the above mentioned populations using more powerful markers (genomic SNPs). Thus, these populations require urgent genetic supplementation to prevent inbreeding depression. The most appropriate source population depends on the geographic location of the receiving population, with buffalo of Kruger NP origin likely an appropriate source for the southern and central Mozambique populations due to their high diversity and geographic proximity. However, caution must be taken not to genetically swamp these native Mozambican populations with Kruger buffalo. Thus, introducing 1-2 Kruger NP bulls per generation (approximately 7.5 years) should be sufficient. Hluhluwe-iMfolozi Park might be another appropriate source for

the southern populations, but as with the converse scenario, Colangelo et al. (2024) caution that careful genomic studies are required prior to translocation between two populations with low diversity to prevent the introduction of additional deleterious genetic variants. See Priority research for more on this.

- **Namibia:**

- **Waterberg Plateau NP:** This is an introduced population north of Windhoek (green dot on the map in Figure 1), with source buffalo from Addo Elephant NP and potentially East Africa via a Namibian game dealer (de Jager et al., 2020). While predominantly showing a genetic signature of Addo Elephant NP, another genetic cluster is present, as with private ranches in South Africa (de Jager et al., 2020). Thus, this population should be considered as part of the private ranch network and the same guidelines apply.
- Additionally, Namibia may also naturally harbour the WC ESU, as indicated by the purple dot at Okahandja, near Windhoek. The sample linked to this location, with a WC ESU mitochondrial control region haplotype, was sourced from the Antwerpen Zoo (Belgium), but its mother was from Okahandja and father from Windhoek. Given that mitochondrial DNA is passed only from mother to offspring, it suggests that the WC ESU may have occurred naturally in Namibia, assuming that its mother naturally occurred around Okahandja and was not introduced there.
- Zambezi Region (previously Caprivi Strip): These populations have only been studied with nuclear data in a local context (Epps et al., 2013), but they may represent a historical contact zone between the SE and WC ESUs. Thus, they are here designated as having an uncertain ESU affiliation until further studies are conducted (for example mitochondrial DNA studies, or nuclear DNA studies with other SE or WC ESU populations included).

- **Zambia:**

- **Simalaha Conservancy (near Mwandi):** Buffalo were introduced from Waterberg Plateau NP (Namibia) (*Pers. Comm. R. D. Taylor 2021*). Thus, it should be treated as part of the private ranch system. Ideally, this population should have been established with buffalo from the nearby Chobe NP (Botswana), or from the Zambezi Region (previously Caprivi Strip) (Namibia). Thus, the same guidelines as for Waterberg Plateau NP and private ranches in South Africa apply to this population. The location with uncertain ESU affiliation in south-west Zambia is due to a lack of mitochondrial data in Smits et al. (2014) where this sample was only studied in a local context with microsatellite data. However, this region might represent a contact zone between the WC and SE ESUs. The GPS location of this sample is unknown and was approximated from the map in Smits et al. (2014).

- **Angola:**

- Very little data are available from Angola, with potentially only one sample analyzed, as it is unclear whether Smits et al. (2014) genotyped the same sample with microsatellites as van Hooft et al. (2002) sequenced at the mitochondrial control region. The latter showed that the sample harboured a WC ESU mitochondrial haplotype (van Hooft et al., 2002, de Jager et al., 2025), while the microsatellite data was not analyzed in a broad enough context to make an ESU designation, hence the uncertain ESU designation as well. Note that the location of the Angolan samples are unknown, and thus the centroid of the country was used. The sample from van Hooft et al. (2002) was from the Dresden Zoo (Germany), but its great-grandmother was from Angola and with mitochondrial DNA being passed down to offspring only along the maternal line, this suggests that the WC ESU was or is present in Angola. This is also supported by the reporting of a "dwarf-buffalo-like" population in Angola based on morphology (Smits et al., 2013 cite Prins 1996), suggesting that south-western Africa, potentially including Namibia and Zambia (or parts thereof), represented a link between the WC and SE ESUs.
- Both ESUs within the species have an N_e greater than 500 under the assumption of gene flow. Therefore, management must strive to facilitate natural migration and gene flow between isolated populations, while taking cognisance of the other guidelines above.

IUCN Status:

- Global: Least threatened (indicated below)
- South Africa: Least concern



Limitations and assumptions:

- Translocations of buffalo from East to southern African private ranches, and from private ranches to other National Parks and Reserves have already complicated interpretation of natural genetic patterns.

Priority Research

- Sample natural populations in Angola, Namibia, and Zambia (or museum specimens representing these populations). Both mitochondrial and nuclear data should be generated and analyzed in a broad context (i.e. with both SE and WC ESU reference samples) to determine their ESU affiliation. This region may represent an historical contact zone between the WC and SE ESUs.
- A comprehensive study of African buffalo across the continent is required, combining both nuclear and mitochondrial data, to facilitate direct comparisons of genetic diversity and structure. While many genetic studies have been conducted on African buffalo, they have used different combinations of data and populations, each with their own limitations. For example, the study by Talenti et al. (2024) was the most comprehensive to date (195 whole genome sequences from all four subspecies, representing both ESUs), but lacked mitochondrial data, which can provide valuable insights into phylogeography. By combining the genomic data from de Jager et al. (2021), Quinn et al. (2023), Colangelo et al. (2024), and Talenti et al. (2024), such a comprehensive study should be possible and will be highly informative for these guidelines and other management initiatives.
- With reference to Hluhluwe-iMfolozi Park (South Africa) and the southern Mozambique populations from Colangelo et al. (2024) (e.g. Namaacha and Catuane), a genomic study comparing runs-of-homozygosity (ROHs) between these populations could be informative regarding whether it is appropriate to exchange individuals between them. If there is a large overlap in the location of ROHs within the genomes of individuals from these populations and the genetic variants within ROHs between populations are the same, then genetic exchange would do little to boost the genetic diversity of either population. However, if the location of ROHs in the genome are, to a large extent, complementary and/or the genetic variants within ROHs are different between the populations, then genetic exchange should be beneficial to both populations, as new genetic variation is then introduced.

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Species name for permits in southern Africa:

- Namibia: *Syncerus caffer caffer*
- South Africa: *Syncerus caffer caffer*

Consultation

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

Acknowledgements

We are grateful to Drs Nathalie Smitz and Russell Taylor 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.



Nile Crocodile

(*Crocodylus niloticus*)

Within Africa, the Nile crocodile *Crocodylus niloticus* (Laurenti 1768), is one of five currently recognised crocodilian species. The species is found in 26 countries, from Egypt down to South Africa (Iseburg et al. 2019). The Nile crocodile was previously considered a single species but recent studies have clarified there are 2 distinct lineages: the Nile crocodile (*C. niloticus*) and the African crocodile (*C. suchus*), found in West and Central Africa. This distinction was made through phylogenetic analysis of mitochondrial and nuclear markers (Cunningham et al. 2016; Hekkala et al. 2011). For permitting purposes, *Crocodylus niloticus* is used across the entirety of its range. There are no currently recognised subspecies since *C. suchus* has been elevated to species level. There is evidence of biogeographical structuring based on mitochondrial DNA and microsatellite data within *C. niloticus* following the major river basins across

northern, eastern, and southern Africa (van Asch et al. 2019; Versfeld 2016). This assessment used genetic evidence as the basis for naming two Evolutionarily Significant Units (ESUs) within Africa, and assigning eight Genetic Management Units (GMUs) within those. Figure 1 visualises these ESUs and GMUs across Africa.

Management Level

• Subspecies

- There are no current subspecies identified currently for Nile crocodiles. 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)

- North-eastern (NE)
- Southern (SO)

• Genetic Management Unit (GMUs)

- **North-eastern (NE)**
 - Central-eastern (CEA) (Tana river system)
 - Central (CE) (Semliki, Victoria Nile, and Albert Nile river systems)
 - North-Nile (NN) (Lake Nasser and lower Nile river system)
- **Southern (SO)**

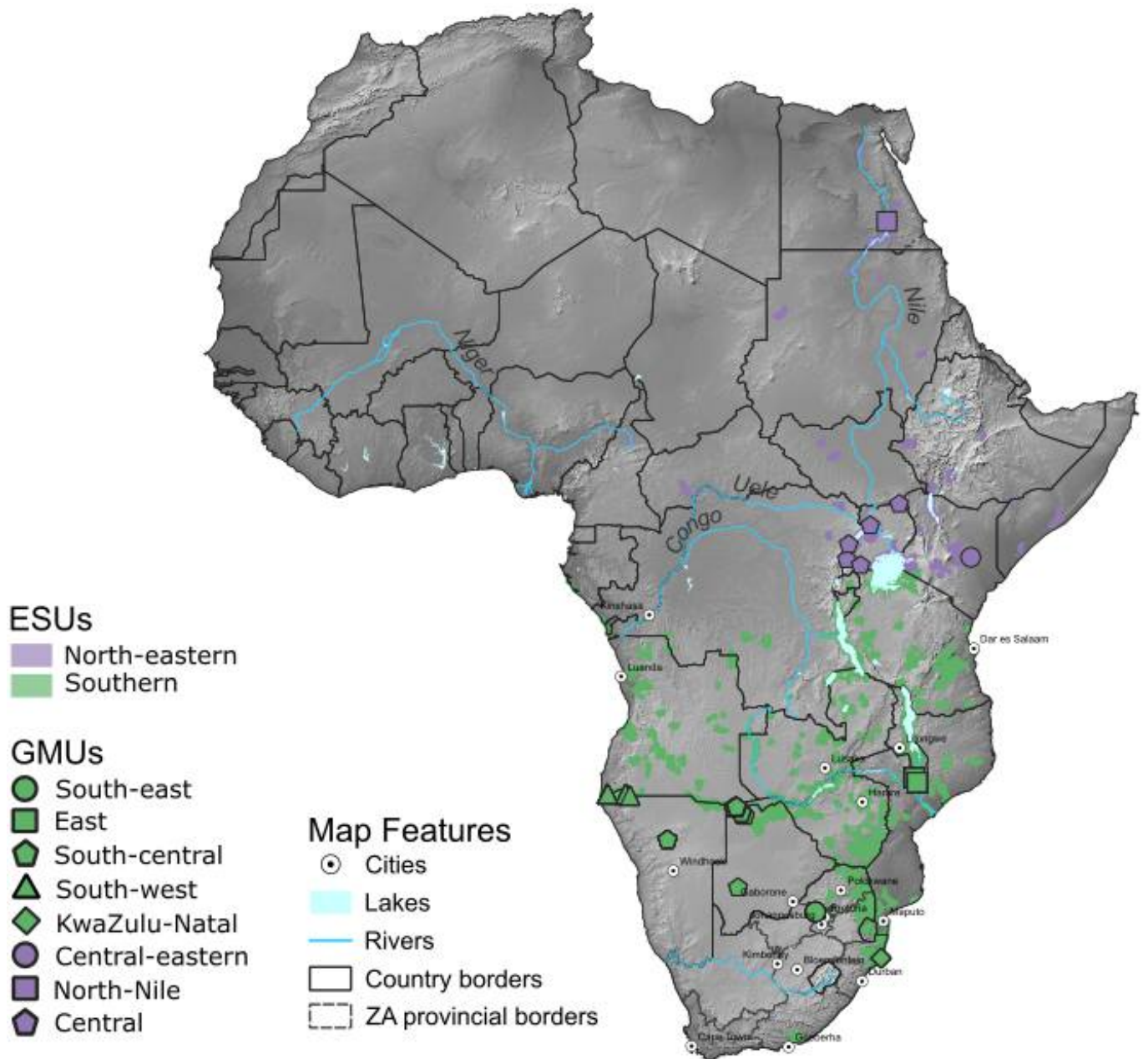


Figure 1: Natural distributions of Nile crocodiles in Africa. Current distribution and its management units are indicated by coloured regions. Points represent a locality which has been sampled for genetic data and correspond through colour to the ESU they are within. The shape of these points indicates different management units within an ESU and are based on genetic data. ESU ranges are based on genetic data of populations. Distribution data source: Isberg, S., Combrink, X., Lippai, C. and Balaguera-Reina, S.A. 2019. *Crocodylus niloticus*. *The IUCN Red List of Threatened Species* 2019:e.T45433088A3010181. <https://dx.doi.org/10.2305/IUCN.UK.2019-1.RLTS.T45433088A3010181.en> [Accessed 14th November 2025]. Point data source: van Asch, B. et al. 2019. Phylogeography, genetic diversity, and population structure of Nile crocodile populations at the fringes of the southern African distribution. *PLoS ONE*, 14. <https://doi.org/10.1371/journal.pone.0226505>.

Management Level - Continued

- South-western (SW) (Kunene river system)
- South-central (CS) (Okovango river and lower Zambezi river systems)
- Eastern (EE) (Lake Nyassa and upper Zambezi river system)
- South-eastern (SE) (Limpopo river system)
- KwaZulu-Natal (KZN) (Coastal wetlands and estuaries)

Management Boundaries

See **Figure 1** for visual representation. Text descriptions follow.

- **Genetic Management Units (GMUs, Based on genetic data from van Asch et al. (2019), Versfeld (2016))**
 - **Southern (SO):**
 - **South-west (SW):** Namibia and Angola (Also potentially Gabon, Cameroon, and Equatorial Guinea).
 - **South-central (SC):** Okavango Delta, Botswana, upstream or adjacent populations in central Zimbabwe.
 - **South-east (SE):** Limpopo river system including adjacent populations in South Africa, central Mozambique, southern Zimbabwe.
 - **Eastern (EE):** Lower shire in Southern Malawi (Lake Nyasa), southern Mozambique, Tanzania, southern Zambia, northern Zimbabwe, Rwanda, Madagascar.
 - **KwaZulu-Natal (KZN):** KwaZulu-Natal coastal wetlands and estuaries, South Africa.
 - **North-eastern (NE):**
 - **Central-eastern (CEA):** Kenya
 - **Central (CE):** Uganda
 - **North-Nile (NN):** Egypt
 - Unknown: Sudan, South Sudan, Somalia.

Genetic Risk

- **Global Nc:** 50,000-60,000 (Isburg et al. 2019)
- **South African Nc:** 4,000 (Isberg et al. 2019)
- Genetic indicators are calculated at **GMU level**. This is based on a best case scenario where gene flow is maintained.
- If values are reported as a range, the median is used for subsequent calculations.

Figure 1: Table 1. Effective population size, Ne500 indicator, and confidence in the values calculated per ESU for Nile crocodiles. The colour of the GMU label is linked to the colour used in Figure 1. Colour of Ne500 and confidence text corresponds to positive (**green**) or negative interpretation (**orange/red**). Overall Ne500 indicates the proportion of the total GMUs that have an Ne over 500.

GMU	Nc	Ne	Ne500 indicator ¹	Confidence
South-west (SW)	567	57-170	< 500	Low
South-central (SC)	582-698	64-192	< 500	Low
South-east (SE)	3,904	390-1,171	> 500	Low
Eastern (EE)	10,270-17,614	1,394-4,183	> 500	Moderate
KwaZulu-Natal (KZN)	620	62-186	<500	Moderate
Central-eastern (CEA)	Unknown	Unknown	Unknown (Likely > 500)	N/A
Central (CE)	Unknown	Unknown	Unknown	N/A
North-Nile (NN)	3,000-4,000	350-1,050	> 500	Moderate
Overall	50,000-60,000	N/A	Likely 4/8 GMUs have an Ne > 500 = 0.5	Moderate

• Population genetic indicators

- Ne500 indicator (1):
 - South-west (SW) Nc: 567. Using an Nc:Ne ratio of 0.1-0.3, Ne = 57-170 (Lyet et al. 2016)
 - South-central (SC) Nc: 582-698. Using an Nc:Ne ratio of 0.1-0.3, Ne = 64-192 (Combrink et al. 2019)
 - South-east (SE) Nc: 3,904. Using an Nc:Ne ratio of 0.1-0.3, Ne = 390-1,171 (Combrink et al. 2019)
 - Eastern (EE) Nc: 10,270-17,614. Using an Nc:Ne ratio of 0.1-0.3, Ne = 1,394-4,183 (Combrink et al. 2019)
 - KwaZulu-Natal (KZN) individuals: 1,512. With assumed maturity percentage of 41 % specifically in this GMU (Combrink et al. 2019), Nc: 620. Using an Nc:Ne ratio of 0.1-0.3, Ne = 62-186.
 - Central-eastern (CEA): Information is only available Kenya and other localities within the north-eastern ESU where this GMU may be present are unknown. From Kenya alone, Nc: > 4,000 (Combrink et al. 2019). Using an Nc:Ne ratio of 0.1-0.3, Ne = 400-1,200. Based on this, it can be assumed the Ne for the whole GMU is above 500.
 - Central (CE): There is limited information on the number of Nile crocodiles in Uganda where this GMU is identified. Other localities within the north-eastern ESU where this GMU may be present are unknown and therefore Ne500 cannot be calculated.
 - North-Nile (NN) Nc: 3,000-4,000 (Combrink et al. 2019). Using an Nc:Ne ratio of 0.1-0.3, Ne = 350-1,050. Based on Ne500, the south-west, south-central, and KZN GMUs are most at genetic risk. GMUs with Ne < 500 are highly susceptible to rapid loss of genetic diversity and are at high risk of extinction due to genetic threats. The north-eastern GMUs are understudied and more information is needed both on their genetics and numbers to be able to confidently calculate Ne500. Figure 2 summarises findings.
- **PM indicator (2):**
 - Global populations of Nile crocodile comprise 8 GMUs across 2 ESUs (van Asch et al. 2019), therefore the proportion of populations maintained globally: $8/8 = 1$

• Diversity loss

- Functional variation: There is risk of functional variation loss due to human interference in river systems causing fragmented/isolated populations, as well as overall small sub-population numbers in areas of its range. Other anthropogenic activity such as overexploitation through hunting for skin and human-crocodile conflict poses a threat to population numbers (Combrink et al. 2019). Due to this, there has likely been a loss of traits that were adapted to habitats the species formerly occupied.
- Divergent lineages: There is risk of losing divergent lineages due to small remaining population sizes in several areas of its range.

- **Hybridisation/introgression**

- There is substantial risk of introgression and hybridisation between the African crocodile (*C. suchus*) and the Nile crocodile (*C. niloticus*) due to them being considered the same species, with *C. suchus* as a subspecies of *C. niloticus* until 2011 (Hekkala et al. 2011). They had been managed as a singular species until that point. Presence of *C. suchus* individuals in the same gene pools as *C. niloticus* has been identified within the central (CE) GMU (van Asch et al. 2019).
- Breeding between ESUs is likely to occur at contact zones such as lake victoria. There is evidence of some breeding and introgression between GMUs within the southern ESU (van Asch et al. 2019).

- **Lower turnover/constraints on adaptive opportunities**

- Within Nile crocodiles, there has been a noted decline in effective population size, leading to reduced genetic diversity, inbreeding depression, and decreased ability to adapt to environmental change (Bishop et al. 2009).

- **In situ genetic threat level**

- In situ risk (Moderate)
- Nile crocodiles are at risk of diversity loss through fractured habitats and isolated populations. Decline in effective population sizes within remaining populations may pose future risk. Several areas of the distribution are understudied and may be at risk. There is also significant risk to these subspecies of hybridisation with the African crocodile, which could further affect diversity loss in the form of divergent lineage and functional variation loss. The overall assessment of the species indicates that populations are stable (Iseburg et al. 2016). For more threats, see the IUCN Red List and South African Red List.

- **Confidence in in situ threat level**

- Confidence score (Low)

Confidence levels are supported by data from recent genomic studies (van Asch et al. 2019; Versfeld 2016), IUCN data on populations from within the last decade (Iseburg et al. 2019), and conservation surveys (Combrink et al. 2019). Large portions of the range are still lacking data on population numbers of Nile crocodile (such as Sudan, South Sudan, and other areas of the northern distribution) and available information does not provide a full picture of their numbers for many areas due to the study and survey limitations (SW, SE, and SC GMUs).

- **Ex situ representation**

- Nile crocodiles exist in captive populations globally, with 4600 individuals held within 91 institutions across 35 countries (The majority within Europe, North America, and South Africa) (Iseburg et al. 2016)
- Captive populations may contain multiple GMUs or ESUs with no distinction as well as other crocodile species, potentially complicating the genetics of some ex situ stocks.

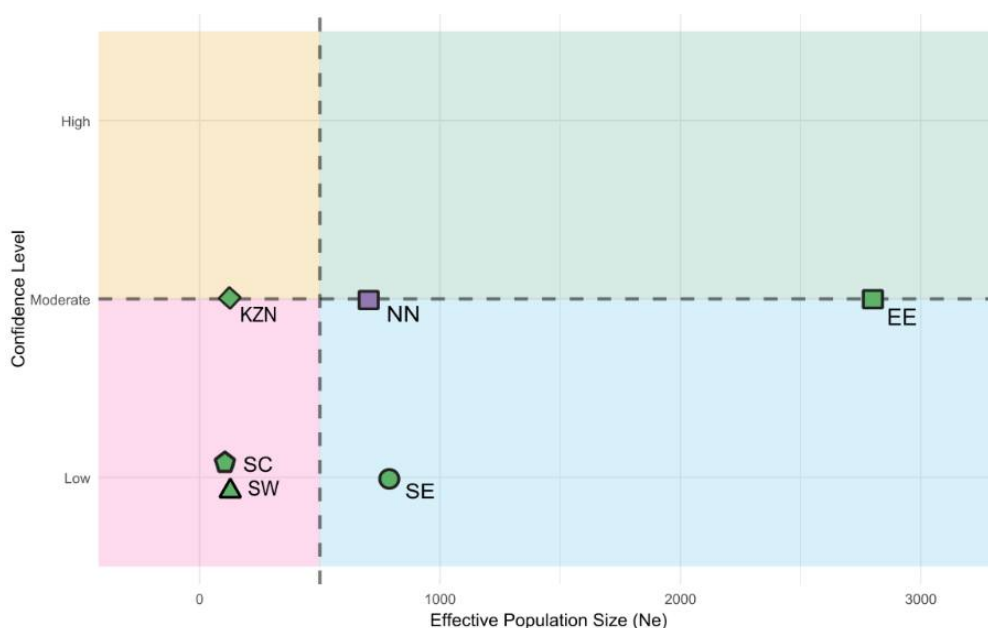


Figure 2. Effective population size compared to confidence in the value. Colour and shape of points and labelling corresponds to the GMU in Figure 1 and Table 1. Dashed lines divide the x axis into above and below Ne500, and the y axis into low and high confidence. ESUs in the low confidence quadrant should be further surveyed to increase confidence in the evaluation. Those with high confidence below Ne500 should have increased genetic management. Note that the CEA and CE GMUs are not shown due to data deficiency.

¹Proportion of populations within species with an effective population size (Ne) greater than 500
(<https://www.gbf-indicators.org/metadata/headline/A-4>)

²Proportion of populations maintained within species
(https://ccgenetics.github.io/guidelines-genetic-diversity-indicators/docs/2_Theoretical_background/PM-indicator.html)

Management Guidelines

- No translocation between GMUs (defined by microsatellites) until further genetic information is provided, however natural migration and gene flow should not be hindered.
- Captive bred individuals and those on private ranches must be genetically tested before translocation to ensure no admixture between GMUs, ESUs, or hybrid individuals.
- If populations are at imminent risk of extinction, due to reduced effective population size or inbreeding, Translocation should be permitted between GMUs.

IUCN Status:

- Global: Least threatened (indicated below)
- South Africa: Vulnerable



Limitations and assumptions:

- River basins in central and northern Africa remain under-sampled or simply not sampled at all and data from these areas may change ESUs or GMUs currently proposed.
- Genetic data that is available is based on small sample sizes.
- Private ranches in South Africa may have some individuals from other GMUs found in more northern populations such as those in the Zambezi or Okavango rivers.
- Translocation of individuals from different GMUs and from the once considered subspecies, *C. suchus*, has already occurred.

Priority Research

- Additional samples from both ESUs should be assessed to help clarify if the suggested GMUs and ESUs should be considered distinct. Current proposed separation is precautionary until further testing can be done.
- Surveys in areas currently lacking census data (primarily central and east Africa), as well as more comprehensive surveys across the species' distribution.
- 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.

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- Versfeld, W. F. 2016. Nile crocodile (*Crocodylus niloticus*) genetic diversity and population structure, within the lower Kunene and Okavango Rivers of northern Namibia. Msc Thesis. Stellenbosch University.

Additional references:

- Turner, A. and Marais, J. 2017. *Crocodylus niloticus*. Red List of South African Species. South African Biodiversity Institute. [Accessed 14th November 2025]

Queries

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



Black Rhinoceros

(*Diceros Bicornis*)

The black rhinoceros *Diceros bicornis* (Linnaeus 1758), belonging to the family Rhinocerotidae, is one of two extant species of African rhinoceros. It is a large herbivorous mammal endemic to Sub-Saharan Africa, with a broad historical range now significantly reduced. It is found along the east of Africa, from South-Sudan to the tip of South Africa, and west into Angola and Namibia. For permitting purposes in southern Africa, *D. b. bicornis* (the south-western black rhino) is recognised in Namibia and Angola, and *D. b. minor* (the south-central black rhino) is recognised in South Africa, Zimbabwe, Eswatini, and Mozambique, with South Africa additionally using *D. b. Bicornis* and *D. b. michaeli*. There are 9 presumed subspecies of black rhino, with 7 currently considered extant (Moodley and Robovsky 2025). This assessment adopted morphological and genetic evidence of nine subspecies, providing basis to recognise seven

Evolutionarily Significant Units (ESUs) across the continent, having several contact zones, and no Genetic Management Units (GMUs) seen within them. Figure 1 visualises estimated ESUs and the presumed natural contact zones between them, as well as point data where samples were collected.

Management Level

• Subspecies

- There are currently nine proposed black rhino subspecies, two of which are considered extinct.
 - *D. b. longipes* (North-west Africa)
 - *D. b. brucii* (North-east Africa)
- There are seven extant subspecies among contemporary populations (Moodley and Robovsky 2025).
 - *D. b. occidentalis* (south-west Africa)
 - *D. b. bicornis* (south-east/north Africa)
 - *D. b. holmwoodi* (eastern Africa - Maasai region)
 - *D. b. ladoensis* (eastern Africa)
 - *D. b. michaeli* (central Africa)
 - *D. b. rosvoldi* (south-eastern Tanzania, likely extinct)
 - *D. b. rendilis* (Northern Rift, status unknown)
- 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:

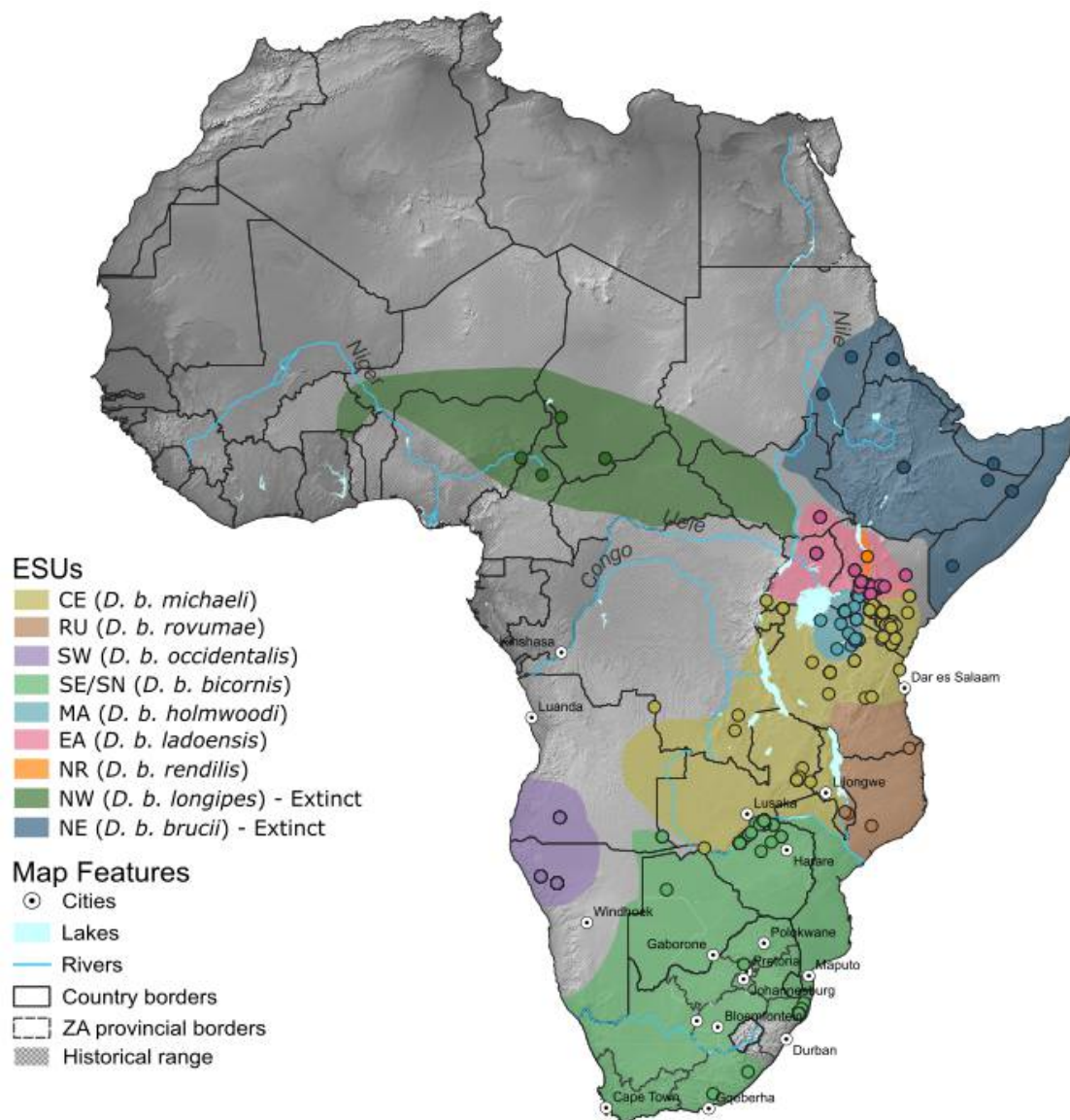


Figure 1: Natural distribution of black rhinoceros in Africa. Base colours show the current and historical distribution of the species across Africa. Historical range based on the IUCN distribution for the species is shown as hashed white regions. Current distribution and its management units are indicated by coloured regions. NW (North-West) and NE (North-East) ESUs are extinct. Points represent a locality which has been sampled for genetic data and correspond through colour to the ESU they are within. ESU ranges are based on genetic data of populations. Distribution data sources: ESU ranges estimated from sampling locations of Sánchez-Barreiro et al. (2023) and Moodley and Robovský (2025). Historical range - Emslie, R. 2020. *Diceros bicornis*. The IUCN Red List of Threatened Species 2020, e.T6557A152728945. <https://dx.doi.org/10.2305/IUCN.UK.2020-1.RLTS.T6557A152728945.en>. (Accessed 10th November 2025)

Management Level - Continued

- **Evolutionarily Significant Units (ESUs)**

- **South-West (SW)** (*D. b. occidentalis*)
- **South-East/ South-North (SE/SN)** (*D. b. bicornis*)
- **Maasai Mara (MA)** (*D. b. holmwoodi*)
- Eastern Africa (EA) (*D. b. ladoensis*)
- **Central Africa (CE)** (*D. b. michaeli*)
- **Ruvuma (RU)** (*D. b. rovumae*)
- **Northern Ridge (NR)** (*D. b. rendilis*)

- **Genetic Management Unit (GMUs)**

- No GMUs are recognised at present.

Management Boundaries

See **Figure 1** for visual representation. Text descriptions follow.

- **Evolutionarily Significant Units (ESUs, based on proposed subspecies from Moodley and Robovsky 2025)**

- **South-west (SW):** Northern Namibia, South-western Angola.
- **South-east/south-north (SE/SN):** South of Zambezi River, South Africa, Zimbabwe, Botswana*, Eswatini*, southern Mozambique*, eastern Angola, Tanzania.
- **Central (CE):** Central Africa north of Zambezi River, Malawi*, Zambia*, Democratic Republic of Congo*, Tanzania, Kenya, Uganda*, Angola*.
- **Ruvuma (RU):** East of Lake Malawi, Shire-Zambezi and Kilombero rivers in east-central Africa (possibly extinct).
- **East (EA):** East Africa north of Zambezi River, Mozambique*, Zambia*, Democratic Republic of Congo*, Tanzania, Kenya, southern Somalia*, Uganda*, South Sudan*.
- **Northern ridge (NR):** Northern Kenya (possibly extinct).
- **Maasai Mara (MA):** South-western Kenya, Northern Tanzania.
- **North-West (NW):** West of the Shari-Logone rivers*, Cameroon* and Nigeria* (extinct).
- **North-East (NE):** Ethiopia*, Eritrea*, Northern Sudan*, Northern Somalia* (extinct).

* Extinct in these countries.

Genetic Risk

- **Global Nc:** 3,598 (Emslie 2020; Ferreira et al. 2024b).
- South African Nc: 818 (Ferreira et al. 2025).
- Genetic indicators are calculated at **ESU level**. These calculations are based on a best case scenario where gene flow is maintained.
- If values are reported as a range, the average is used for subsequent calculations.

Table 1. Effective population size, Ne500 indicator, and confidence in the values calculated per ESU for black rhinoceros. Colour of the ESU label is linked to the colour used in Figure 1. Colour of Ne500 and confidence text corresponds to positive (**green**) or negative interpretation (**orange/red**). Overall Ne500 indicates the proportion of the total ESUs that have an Ne over 500.

ESU	Nc	Ne	Ne500 indicator ¹	Confidence
South-West (SW) (<i>D. b. occidentalis</i>)	1,221	122-366	< 500	Moderate
South-east / South-north (SE/SN) (<i>D. b. bicornis</i>)	1,244	124-373	< 500	Moderate
Maasai Mara (MA) (<i>D. b. holmwoodi</i>)	28	3-8	< 500	Moderate
Eastern Africa (EA) (<i>D. b. ladoensis</i>)	479	50-144	< 500	Moderate
Central Africa (CE) (<i>D. b. michaeli</i>)	236	24-71	< 500	Moderate
Ruvuma (RU) (<i>D. b. rovumae</i>)	Unknown	Unknown	Unknown (Likely < 500)	N/A
Northern Ridge (NR) (<i>D. b. rendilis</i>)	Unknown	Unknown	Unknown (Likely < 500)	N/A
Overall:	3,598	N/A	Likely 0/7 ESUs have an Ne > 500 =0	Moderate

Genetic indicators

• Ne500 indicator¹:

- **South-west (SW)** individuals: 2,188 (Emslie 2020). With assumed maturity percentage of 55.8 % (Emslie 2020), Nc: 1,221. Using an Nc:Ne ratio of 0.1-0.3, Ne = 122-366.
- **South-east/South-north (SE/SN)** Individuals: 2,229 (Emslie 2020). With assumed maturity percentage of 55.8 % (Emslie 2020), Nc: 1,244. Using an Nc:Ne ratio of 0.1-0.3, Ne = 124-374
- **Maasai Mara (MA)** Individuals: Approximately 50 (Narok County Government 2023). With assumed maturity percentage of 55.8 % (Emslie 2020), Nc: 28. Using an Nc:Ne ratio of 0.1-0.3, Ne = 3-8.
- **Central (CE)** individuals: 422 (Emslie 2020; Kenya Wildlife Services 2025). With assumed maturity percentage of 55.8 % (Emslie 2020), Nc: 236. Using an Nc:Ne ratio of 0.1-0.3, Ne = 24-71.
- **Eastern (EA)** individuals: 859 (International Rhino Foundation 2025). With assumed maturity percentage of 55.8 % (Emslie 2020), Nc: 479. Using an Nc:Ne ratio of 0.1-0.3, Ne = 50-144.
- **Ruvuma (RU)**: Unknown
- **Northern Ridge (NR)**: Unknown

Of the seven genetic management units, five have an Ne below 500 based on population data, and two are assumed to have an Ne below 500 based on comments on abundance within their ranges and population data for the country in which they occur. ESUs with Ne < 500 are highly susceptible to rapid loss of genetic diversity and are at high risk of extinction due to genetic threats.

• Proportion of populations maintained (PM2):

- The global populations of black rhinoceros comprise 9 ESUs relating to 9 proposed subspecies, with 7 of those being extant. Therefore the proportion of populations maintained globally: $7/9 = 0.78$

• Diversity loss

- **Functional variation:** There is risk of functional variation loss due to massive reduction in historical range causing fragmented/isolated populations. Due to this, there has likely been a loss of traits that were adapted to habitats the species formerly occupied. Ongoing poaching of the black rhinoceros especially in South Africa may further exacerbate this. Range expansion that is inconsistent with population and management boundaries (e.g. SE in Malawi and Zambia, and SW in northern and -western South Africa) may lead to the genetic erosion of locally evolved variation.

- **Divergent lineages:** There is risk of losing divergent lineages due to small remaining population sizes in several areas of its range. The North-west and North-east ESUs are already extinct and there is suggestion that the RU and NR ESUs may also be extinct as there has been little information on the presence of individuals in the regions in which they occur (Moodley and Robovsky 2025).
- **Hybridisation/introgression**
 - There is strong risk of hybridisation and introgression between black rhino subspecies due to past translocation (Moodley et al. 2017; Sánchez-Barreiro et al. 2023).
 - There is no risk of hybridisation with white rhinos as no inter-species crosses have been recorded in the wild or in captivity.
- Lower turnover/constraints on adaptive opportunities
 - There has been a significant decrease in black rhino population densities since the 1970s (Mellya et al. 2025). Early colonisation and more recent land-use changes within the SE/SN ESU has resulted in low levels of genetic diversity, and long term geographic isolation and possible ecological specialisation in an arid environment within the SW ESU may have resulted in a low effective population size and genetic diversity. These will have an impact on population turnover for the species, constraining adaptive opportunities.
- **In situ genetic threat level**
 - *In situ risk* (**High**)
Black rhinos exist in small, fragmented populations and are targets of poaching. Hybridisation between ESUs presents genetic risks in reduction of functional variation. Early colonisation and more recent land-use changes have resulted in low levels of genetic diversity for the SE/SN ESU. Genetic diversity is low across the species and their ability to adapt quickly to environmental or population level changes is low. For more threats, see the IUCN Red List and South African Red List.
- **Confidence in in situ threat level**
 - Confidence score (**Moderate**)
Confidence is moderate as the evaluation is based on scientific papers (Mellya et al. 2025; Moodley et al. 2017; Moodley and Robovsky 2025; Sánchez-Barreiro et al. 2023) and IUCN or regional assessment data from within the last decade (Emslie 2020; Ferreira et al. 2025). However, population numbers per ESU to calculate N_{e500} were inconsistent and may not have captured the true presence of this species across the continent.
- **Ex situ representation**
 - Black rhinos exist in captive populations within South Africa, North America, Europe, and Asia with 168 individuals across 63 institutions in 16 countries. The highest quantity is in North America with 56 individuals (Emslie et al. 2020).
 - Captive individuals in Europe predominantly from the CE ESU (Elsner-Gearing 2023).
 - South African captive CE ESU individuals show admixture with at least one southern (SE/SN) black rhino male and this admixture is extensive within the population (Elsner-Gearing 2023).



Figure 2. Effective population size compared to confidence in the value. Colour of points and labelling corresponds to the ESU in Figure 1 and Table 1. Dashed lines divide the x axis into above and below Ne500, and the y axis into low and high confidence. ESUs in the low confidence quadrant should be further surveyed to increase confidence in the evaluation. Those with high confidence below Ne500 should have increased genetic management. Note that the RU and NR ESUs are not shown due to data deficiency.

¹ Proportion of populations within species with an effective population size (Ne) greater than 500 (<https://www.gbf-indicators.org/metadata/headline/A-4>)

² Proportion of populations maintained within species (https://ccgenetics.github.io/guidelines-genetic-diversity-indicators/docs/2_Theoretical_background/PM-indicator.html)

Management Guidelines

- No translocation between ESUs across Africa, however, natural migration should not be hindered.
- Southern ESUs (SW, SE/SN) should be managed separately. The SW MU inhabits a water scarce region and it is still unknown whether this population contains local environmental adaptations. This is another reason to manage SW separately for now, despite its historical connection with the SE/SN MU, to the east.
- If populations are at imminent risk of extinction, due to reduced effective population size or inbreeding, Translocation should be permitted.
- To make up a viable founding group 16 to 20 individuals should be used.
- Efforts must be made to increase the effective population size of all ESUs to over 50 in for short term survival, and over 500 for long term genetic diversity.
- To maintain within population heterozygosity, one breeding male should be introduced every seven years (Pers. comm. P. Goodman, 2021) or one male and one female should be introduced every 14 years.

IUCN Status:

- Global: Least threatened (indicated below)
- South Africa: Vulnerable



Limitations and assumptions:

- RU and NR ESUs were assumed to be extant although previous data suggests they are at significant risk of extinction, so this may not still be the case.
- South-north and South-east populations are considered a singular ESU based on Moodley and Robovský (2025).
- Studies used to determine distribution also included historical (museum samples) to investigate historical vs modern genetic diversity within black rhinoceros.

Priority Research

- Investigation into the continuation of smaller or assumed likely extinct populations/ESU such as the NR or RU ESUs, enabling a better picture of their distribution.
- Genetic sampling from smaller populations to properly assess current risk of inbreeding and rate of loss of genetic diversity.
- The SW MU contains two monophyletic lineages which could possibly be classified as two separate MUs. Samples have been stored at the University of Pretoria (Onderstepoort) to conduct this work.
- Samples from southern Namibia are still required to determine the natural southern limit of the SW population in that country. The Cape of Good Hope was naturally populated by SE.
- Future whole genome data are required for further genetic resolution and to determine the adaptive value of population genetic variation.

- 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.

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Consultation

- Global: Least threatened (indicated below)
- South Africa: Vulnerable

Acknowledgements

- We are grateful to Drs Peter Goodman, Richard Emslie and Prof Oliver Ryder 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.co.za



Black Wildebeest

(*Connochaetes gnou*)

The black wildebeest *Connochaetes gnou* (Zimmermann, 1780) is endemic to South Africa and was driven to near extinction in the early 1900's due to over-exploitation, disease outbreaks and habitat destruction (Von Richter, 1974). A severe drought in 1933 caused the population to go through a second bottleneck and by 1938 there were only an estimated 300 animals remaining (Kirkman, 1938). Numbers have subsequently recovered and according to the IUCN, the population is currently listed as least concern and total population size is estimated at 11,158 animals (IUCN, 2017). They have been widely reintroduced on nature reserves and private farms throughout their natural distribution range (including Eswatini and Lesotho). Black wildebeest have also been introduced outside their natural distribution range, with animals currently present on privately owned farms in Namibia and Botswana

(Grobler et al., 2018; Liu et al., 2024). For permitting purposes in southern Africa, Namibia and South Africa currently utilise *Connochaetes gnou*. There is only one recognised species with no ESUs or GMUs. Figure 1 illustrates the geographic distribution of the species.

Management Level

- **Subspecies**
 - No subspecies are recognised at present.
- **Evolutionarily Significant Units (ESUs)**
 - No ESUs are recognised at present.
- **Genetic Management Units (GMUs)**
 - No GMUs are recognised at present.

Management Boundaries

• *Connochaetes gnou*: Endemic to South Africa, eSwatini and Lesotho. Introduced into Namibia. The species formerly occurred in Lesotho, eSwatini and South Africa (the Northern Cape, Western Cape, Eastern Cape, throughout the Free State, northward into the North West province, Gauteng and Mpumalanga, extending into western KwaZulu-Natal).

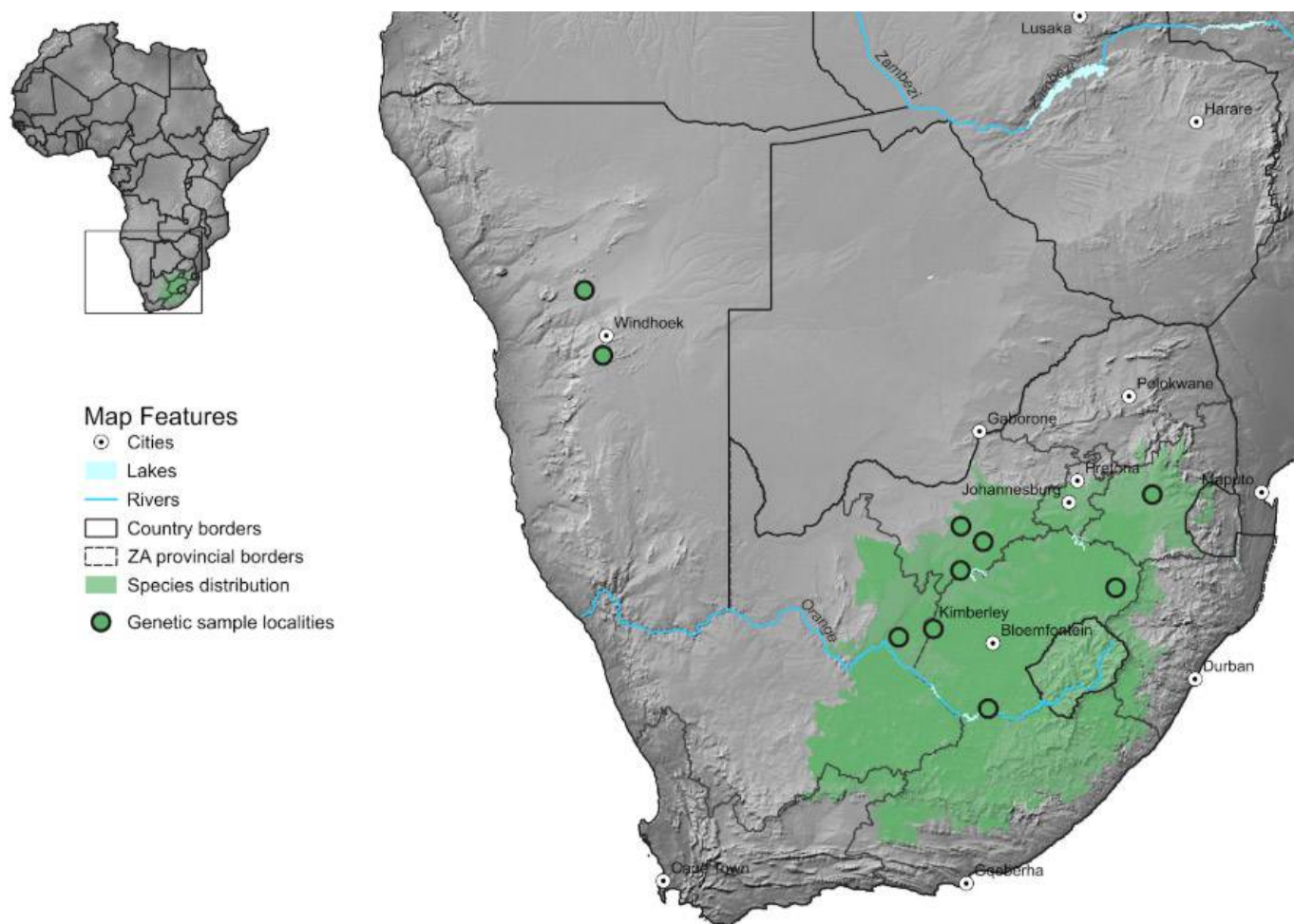


Figure 1: Natural distribution of black wildebeest (*Connochaetes gnou*) in green shading. Points represent a locality which has been sampled for genetic data. The inset indicates the part of Africa shown in the main map. Distribution data source: Birss, C., Rushworth, I., Collins, N. B., Peinke, D. & Buijs, D. 2017. *Inferred natural distribution ranges of certain large mammals in South Africa*. Unpublished GIS coverage.

Genetic Risk

- **Global population Nc:** 13,593-15,859 (Shrader and da Silva 2025; Vrahimis et al. 2017).
- **South African population Nc:** 9,393-10,959 (Shrader and da Silva 2025)
- Genetic indicators are calculated at **species level** as there are no GMUs or ESUs within the species.
- If values are reported as a range, the average is used for subsequent calculations.

Figure 1: Effective population size, Ne500 indicator, and confidence in the values calculated per ESU for black wildebeest. Colour of the ESU label is linked to the colour used in Figure 1. Colour of Ne500 and confidence text corresponds to positive (green) or negative interpretation (orange/red). Overall Ne500 indicates the proportion of the total ESUs that have an Ne over 500.

ESU	Nc	Ne	Ne500 indicator ¹	Confidence
<i>C. gnou</i>	13,593-15,859	1,473-4,418	> 500	High
Overall	13,593-15,859	N/A	The species has an Ne > 500 = 1	High

Genetic Indicators

• Ne500 indicator¹

- *C. gnou* individuals: 22,655, comprising 15,655 in South Africa (Shrader and da Silva 2025) and >7,000 in Namibia (Vrahimis et al. 2017). With assumed maturity percentage of 60-70 % (Shrader and da Silva 2025; Vrahimis et al. 2017), Nc: 13,593-15,859. Using an Nc:Ne ratio of 0.1-0.3, Ne = 1,473-4,418.

gnou has an Ne above 500 which indicates the species will maintain genetic diversity, assuming gene flow is maintained between populations, thus indicating lower genetic risk.

• Proportion of populations maintained (PM2):

- The global populations of the black wildebeest do not have any GMUs or ESUs and are endemic to South Africa, therefore the proportion of populations maintained globally: $1/1 = 1$.

Diversity Loss

- **Functional variation:** There is risk of functional variation loss due to intensive management of the species that are often bred in small founder groups. Hunting and diseases also pose risk to potentially functionally adapted populations (Grobler et al. 2018). Due to this, there has likely been a loss of traits that were adapted to specific habitats.
- **Divergent lineages:** There is little risk of losing current divergent lineages due to high effective population numbers and the current lack of any clear genetic structuring within the species.

Hybridisation/introgression

- There is risk of hybridisation for black wildebeest with the closely related species, blue wildebeest (Power 2014). Some game ranches still stock the two species together and introgression is seen within the blue wildebeest genome (Grobler et al. 2018). There are at least 1,347 individuals that are purely black wildebeest within South Africa (Shrader and da Silva 2025). There are signals of historic hybridisation as well as current extant hybrids (Grobler et al. 2018).

Lower turnover/constraints on adaptive opportunities

- Black wildebeest faced near extinction in the early 20th century, but have since recovered. Signals of this historical bottleneck can still be seen in their genetics, with the species having a lower genetic diversity than blue wildebeest (Grobler et al. 2018). Fragmented populations due to game ranching exist across their range which could have constraints on gene flow and therefore adaptive opportunities.
- In situ genetic threat level

- **In situ Risk (Moderate)**

Black wildebeest are seen to be increasing in population number across their distribution and have an effective population size above 500 (Vrahimis et al. 2017). Hybridisation with blue wildebeest is the most significant threat to their genetic diversity. With facilitation of gene flow between populations and caution towards mixing any potential hybrids, risk is moderate. For more threats, see the IUCN Red List and South African Red List.

- **Confidence in in situ threat level**

- Confidence score (**High**)

Confidence is high as the assessment is based on IUCN and regional assessment data from within the last decade (Vrahimis et al. 2018; Shrader and da Silva 2025) as well as scientific papers on the species genetics using microsatellites (Grobler et al. 2018).

Ex situ representation

- Black wildebeest are held in 22 institutions, across 14 countries (North, South, and Central America, Europe, and Asia) with the majority in Europe. The total number of individuals is 114 (Vrahimis et al. 2017).
- Populations within European zoos may represent genetics of the species before large-scale translocation occurred within South Africa as were founded in the 1950s and 60s, therefore not containing hybrid individuals (Shrader and da Silva 2025).

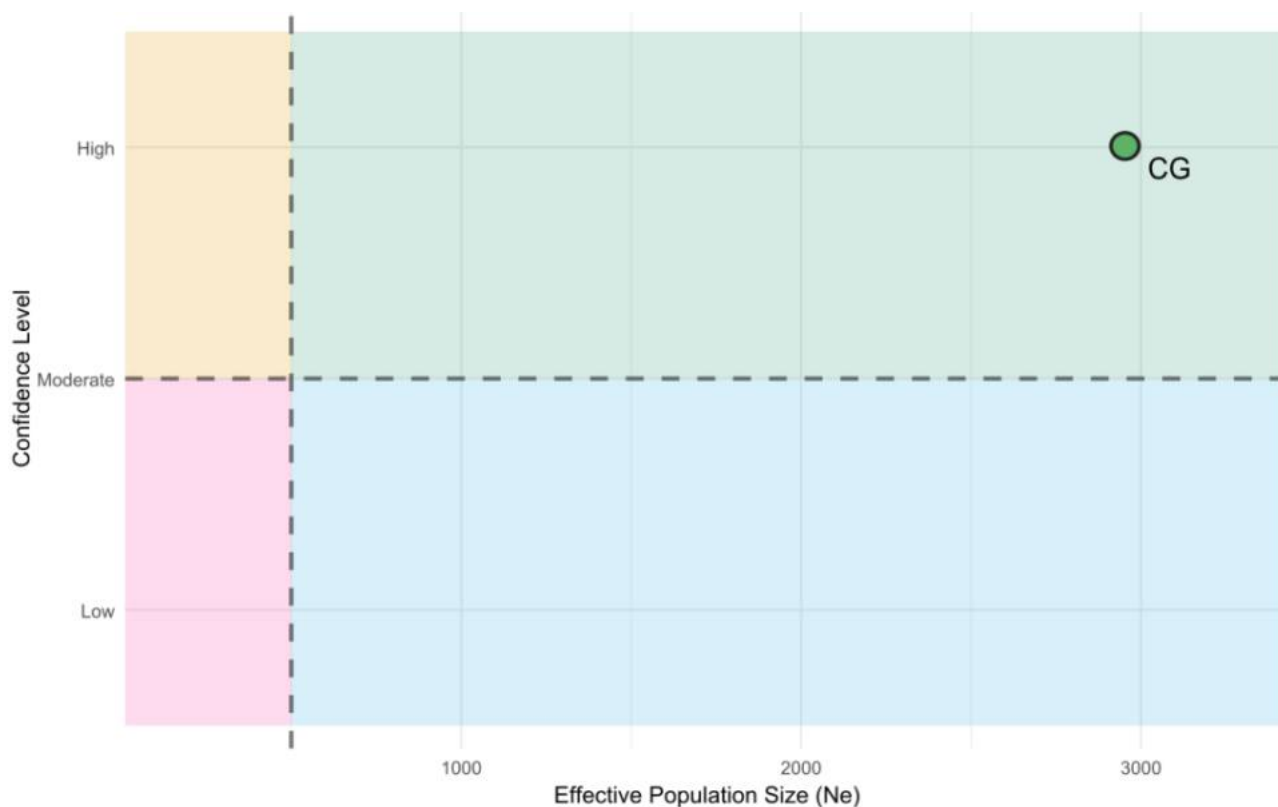


Figure 2. Effective population size compared to confidence in the value. Colour of points and labelling corresponds to Figure 1 and Table 1. Dashed lines divide the x axis into above and below Ne500, and the y axis into low and high confidence. ESUs in the low confidence quadrant should be further surveyed to increase confidence in the evaluation. Those with high confidence below Ne500 should have increased genetic management.

¹ Proportion of populations within species with an effective population size (Ne) greater than 500 (<https://www.gbf-indicators.org/metadata/headline/A-4>)

² Proportion of populations maintained within species (https://ccgenetics.github.io/guidelines-genetic-diversity-indicators/docs/2_Theoretical_background/PM-indicator.html)

Management Guidelines

- Black wildebeest should be managed as a metapopulation.
- If both blue- and black wildebeest are (or were) kept on the same property, all animals should be genetically tested before translocation to ensure no hybrid individuals are moved.
- No imports/exports from/to Namibia.
- The species is indicated to have an $N_e > 500$ under the assumption of gene flow. Therefore, management must strive to facilitate natural migration and gene flow between isolated populations, while taking cognisance of the other guidelines above.

IUCN Status:

- Global: Least threatened (indicated below)
- South Africa: Vulnerable



- Black wildebeest has been widely translocated within and outside of its natural distribution range without taking hybridisation with blue wildebeest into account. Therefore, admixed individuals may have been used as founders of new black wildebeest populations as well as mixed with pure black wildebeest individuals.

Priority Research

- A more powerful panel of molecular markers is required to increase the confidence with which hybrids (especially 2nd or 3rd generation backcrosses) can be detected and to preserve the genetic integrity of the species.
- Wider sampling from localities holding the species.

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Consultation

- Global: Least threatened (indicated below)
- South Africa: Vulnerable

Acknowledgements

- We are grateful to Profs Paul Grobler and Rouvay Roodt-Wilding and Dr David Mallon 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.co.za



Blue Wildebeest

(*Connochaetes gnou*)

Ansell (1972) listed the following five subspecies of blue wildebeest: brindled wildebeest (*C. t. taurinus* Burchell, 1823), Cookson's wildebeest (*C. t. cooksoni* Blaine, 1914); Nyassa wildebeest (*C. t. johnstoni* Sclater, 1896); eastern white-bearded wildebeest (*C. t. albojubatus* Thomas, 1892); and western white-bearded wildebeest (*C. t. mearnsi* Heller, 1913). The brindled wildebeest is widely distributed in southern Africa (Angola, Zambia, Namibia, Mozambique and South Africa), whereas the Cookson's wildebeest has a restricted distribution in Zambia in the Luangwa Game Reserve. The Nyassa wildebeest went extinct from Nyasaland by the end of the 19th century, however, this subspecies still occurs north of the Zambezi River in Mozambique and into east-central Tanzania.

The Gregory Rift Valley in Kenya and Tanzania divides the eastern-and-western white-bearded wildebeest distribution areas. These subspecies are used for permitting purposes in southern Africa. Genetics research (Arctander et al. 1999), including recent genome-level analyses (Liu et al. 2024), supports the five subspecies that are herein treated as Evolutionarily Significant Units (ESUs, Figure 1). There are at least two Genetic Management Units (GMUs, Figure 1), within the brindled ESU that is separated by the Zambezi river.

Management Level

Subspecies

Five subspecies of blue wildebeest are recognised, based on genetic and morphological data.

- *Connochaetes taurinus mearnsi* (western white-bearded wildebeest)
- *Connochaetes taurinus albojubatus* (eastern white-bearded wildebeest)
- *Connochaetes taurinus cooksoni* (Cookson's wildebeest)
- *Connochaetes taurinus johnstoni* (Nyassa or Johnston's wildebeest)
- *Connochaetes taurinus taurinus* (brindled gnu/wildebeest)
- 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.

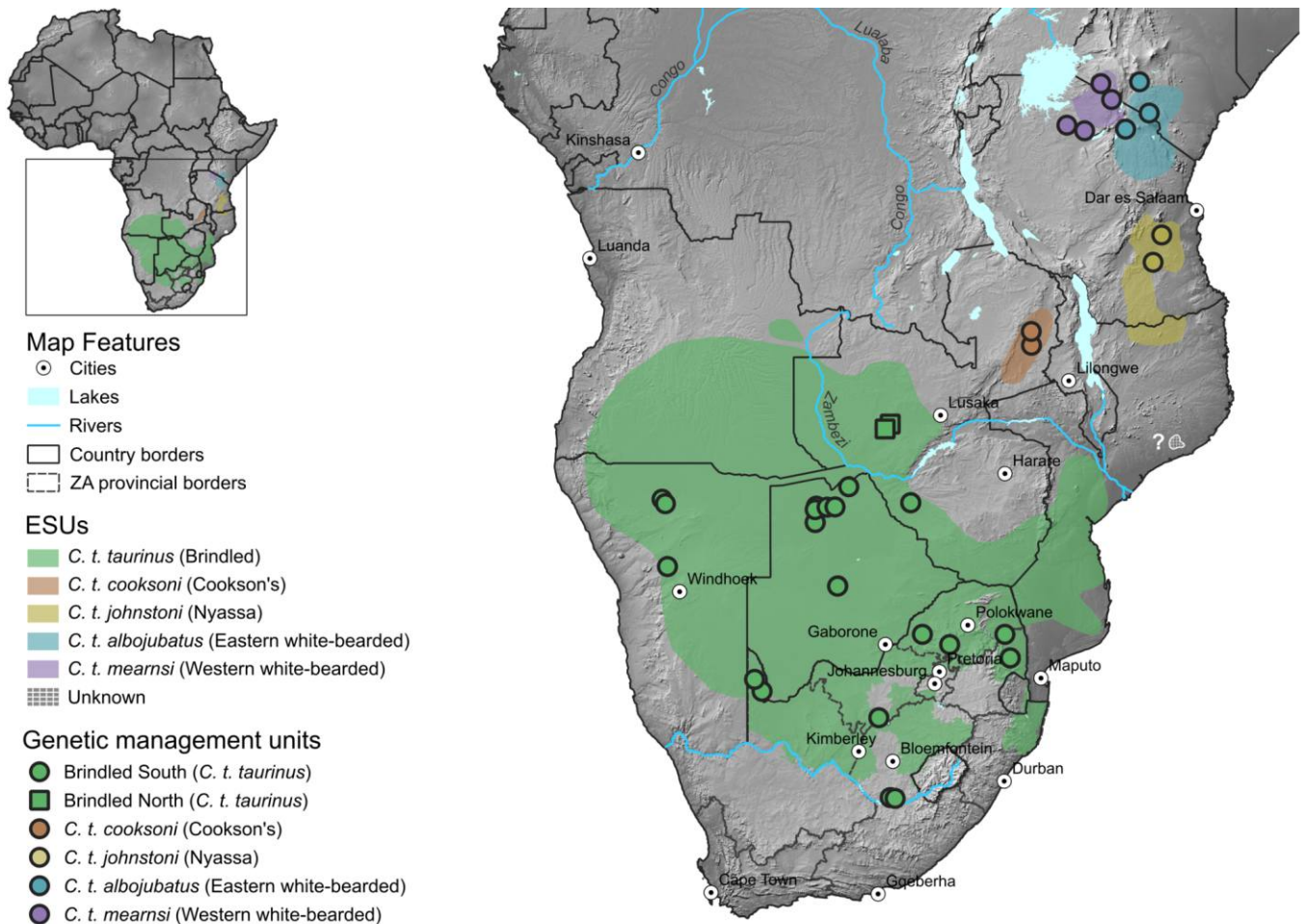


Figure 1: Natural distribution of blue wildebeest (*Connochaetes taurinus*) subspecies shown in different colours. Points represent a locality which has been sampled for genetic data. The inset indicates the part of Africa shown in the main map. Distribution data sources: South Africa, Lesotho and eSwatini – 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) 2016. *Connochaetes taurinus*. The IUCN Red List of Threatened Species. Version 2021-1. <https://www.iucnredlist.org>

Management Level - Continued

Genetic Management Units (GMUs)

- *Connochaetes taurinus mearnsi*
 - No GMUs
- *Connochaetes taurinus albojubatus*
 - No GMUs
- *Connochaetes taurinus cooksoni*
 - No GMUs
- *Connochaetes taurinus johnstoni*
 - No GMUs
- *Connochaetes taurinus taurinus*
 - Brindled North: Brindled population in Kafue and potentially other populations north of the Zambezi river.
 - Brindled South: Brindled populations south of the Zambezi river. However, additional sampling may reveal further genetic structure within this GMU. See priority research.

Management Boundaries

Subspecies

- ***Connochaetes taurinus mearnsi***: Serengeti-Mara ecosystem of northern Tanzania and southern Kenya west of the Gregory Rift Valley.
- ***Connochaetes taurinus albojubatus***: northern Tanzania to central Kenya south of the Equator and west to the Gregory Rift Valley.
- ***Connochaetes taurinus cooksoni***: restricted distribution in Zambia in the Luangwa Game Reserve.
- ***Connochaetes taurinus johnstoni***: north of the Zambezi River in Mozambique and into east-central Tanzania.
- ***Connochaetes taurinus taurinus***: Angola, Zambia, Namibia, Mozambique and South Africa.

Management Level

- *Connochaetes taurinus taurinus*
 - Brindled North: Brindled population in Kafue and potentially other populations north of the Zambezi river.
 - Brindled South: Brindled populations south of the Zambezi river. However, additional sampling may reveal further genetic structure within this GMU. See priority research.

Genetic Risk

- **Global Nc**: 1,085,000 (IUCN 2016; Patel and da Silva 2025).
- **South African Nc**: 13,000 (Patel and da Silva 2025).
- Genetic indicators are calculated at **ESU level**. These calculations are based on a best case scenario where gene flow is maintained.
- Risk levels for GMUs can be assumed based on the Ne500 at ESU level.
- If values are reported as a range, the average is used for subsequent calculations.

Table 1. Effective population size, Ne500 indicator, and confidence in the values calculated per ESU for blue wildebeest. Colour of the ESU label is linked to the colour used in Figure 1. Colour of Ne500 and confidence text corresponds to positive (green) or negative interpretation (orange/red). Overall Ne500 indicates the proportion of the total ESUs that have an Ne over 500.

ESU	Nc	Ne	Ne500 indicator ¹	Confidence
Cookson's (CS) <i>C. t. cooksoni</i>	5,250	525-1,575	> 500	High
Eastern white-bearded (EWB) <i>C. t. albojubatus</i>	4,900	490-1,470	> 500	Moderate
Nyassa (NS) <i>C. t. johnstoni</i>	43,750	4,375-13,125	> 500	High
Western white-bearded (WWB) <i>C. t. mearnsi</i>	910,000	91,00-273,000	> 500	High
Brindled (BR) <i>C. t. taurinus</i>	91,000	91,000-27,300	> 500	High
Overall:	1,085,000	N/A	5/5 ESUs have an Ne > 500 = 1	High

Genetic Indicators

• Ne500 indicator¹

- **Cookson's (CS)** individuals: 5,000-10,000 (Estes and East 2009). With assumed maturity percentage of 70 % (Patel and da Silva 2025), Nc: 5,250. Using an Nc:Ne ratio of 0.1-0.3, Ne = 525-1,575.
 - **Eastern white-bearded (EWB)** individuals: 6,000-8,000 (Estes and East 2009). With assumed maturity percentage of 70 % (Patel and da Silva 2025), Nc: 4,900. Using an Nc:Ne ratio of 0.1-0.3, Ne = 490-1,470.
 - **Nyassa (NS)** individuals: 50,000-75,000 (Estes and East 2009). With assumed maturity percentage of 70 % (Patel and da Silva 2025), Nc: 43,750. Using an Nc:Ne ratio of 0.1-0.3, Ne = 4,373-13,125.
 - **Western white-bearded (WWB)** individuals: 1,300,000 (Estes and East 2009). With assumed maturity percentage of 70 % (Patel and da Silva 2025), Nc: 910,000. Using an Nc:Ne ratio of 0.1-0.3, Ne = 91,000-273,000.
 - **Brindled (BR)** individuals: 130,000 (Estes and East 2009). With assumed maturity percentage of 70 % (Patel and da Silva 2025), Nc: 91,000. Using an Nc:Ne ratio of 0.1-0.3, Ne = 9,100-27,300.
- All ESUs have an Ne above 500 which indicates each will maintain genetic diversity, assuming gene flow is maintained, thus indicating lower genetic risk.

• Proportion of populations maintained (PM2):

- The global populations of blue wildebeest make up five subspecies relating to the five ESUs. Therefore the proportion of populations maintained globally: $5/5 = 1$.

Diversity Loss

- **Functional variation:** There is risk of functional variation loss due to massive reduction in historical range. Due to this, there has likely been a loss of traits that were adapted to habitats the species formerly occupied. Several colour variants of blue wildebeest (e.g. golden and king) are routinely bred on private wildlife ranches in the region. Escapees from such ranches threaten the genetic integrity of natural populations.
- **Divergent lineages:** There is risk of losing divergent lineages if the EWB ESU continues to see decline at the same rate as has been occurring since the 90s.

Hybridisation/introgression

- There is risk of hybridisation for blue wildebeest with the closely related species, black wildebeest (Power 2014). Some game ranches still stock the two species together and introgression is seen within the blue wildebeest genome (Grobler et al. 2018). There are signals of historic hybridisation as well as current extant hybrids (Grobler et al. 2005; 2018).
- Admixture between ESUs within the species has not been detected (Liu et al. 2024).

Lower turnover/constraints on adaptive opportunities

- The population numbers of blue wildebeest have remained relatively stable since the 1990s, with only the EWB showing decline. Increased human disruption within migration routes have shown to decrease the population of blue wildebeest within those areas. This has particularly affected the EWB ESU which has seen significant decline since the 90s and shows signs of low genetic diversity (Caspers et al. 2020; East 1999; Liu et al. 2024).

In situ genetic threat level

• In situ risk (Low)

Blue wildebeest exist in relatively large populations, with the Serengeti having upwards of a million individuals. The species faces issues due to hybridisation with black wildebeest (*Connochaetes gnou*). Hybridisation presents genetic risks in reduction of functional variation. All ESUs have an N_e above 500, with EWB being the ESU most at risk due to past declines. For more threats, see the IUCN Red List and South African Red List.

• Confidence in in situ threat level

◦ Confidence score (High)

Confidence is high as the evaluation is based on scientific papers (Grobler et al. 2018; Liu et al. 2024) and IUCN or regional assessment data from within the last decade (IUCN 2016; Patel and da Silva 2025). Population numbers per ESU to calculate N_e500 were assumed from data provided in Estes and East (2009) and the population is assumed to have remained stable (IUCN 2016).

Ex situ representation

- Blue wildebeest exist in captive populations within South Africa, Egypt, Asia, Europe, and North America, with a total of 935 individuals across 113 in 31 countries. North America has the largest ex situ stock, with 264 individuals.
- North American captive individuals are predominantly from the EWB ESU; despite instances of introduction of other ESUs, there does not seem to be any introgression (Caspers et al. 2020).

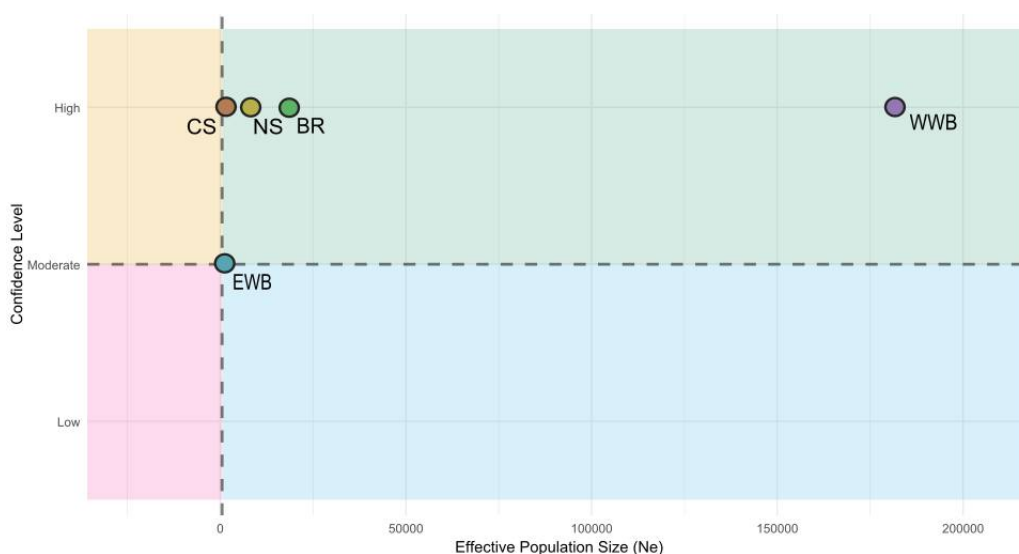


Figure 2: Effective population size compared to confidence in the value. Colour of points and labelling corresponds to the ESU in Figure 1 and Table 1. Dashed lines divide the x axis into above and below Ne500, and the y axis into low and high confidence. ESUs in the low confidence quadrant should be further surveyed to increase confidence in the evaluation. Those with high confidence below Ne500 should have increased genetic management.

¹ Proportion of populations within species with an effective population size (Ne) greater than 500
<https://www.gbf-indicators.org/metadata/headline/A-4>

² Proportion of populations maintained within species
https://ccgenetics.github.io/guidelines-genetic-diversity-indicators/docs/2_Theoretical_background/PM-indicator.html

Management Guidelines

- Manage blue wildebeest as five separate subspecies with no imports of the other four subspecies into southern Africa.
- Translocations must mimic a stepwise pattern between geographically close natural populations.
- If both blue- and black wildebeest are (or were) kept on the same property, all animals should be genetically tested before translocation to ensure no hybrid individuals are moved.
- All ESUs within the species have an Ne > 500 under the assumption of gene flow. Therefore, management must strive to facilitate natural migration and gene flow between isolated populations, while taking cognisance of the other guidelines above.

IUCN Status:

- Global: Least threatened (indicated below)
- South Africa: Vulnerable



Limitations & Assumptions

- Blue wildebeest (specifically the brindled wildebeest subspecies, *C. t. taurinus*) has been widely translocated within and outside of its natural distribution ranges in South Africa, without taking hybridisation with black wildebeest into account. Therefore, admixed/hybrid individuals may have been used as founders of new blue wildebeest populations and/or mixed with pure blue wildebeest populations.

Priority Research

- A comprehensive study on *C. t. taurinus*, including all areas in the natural distribution should be conducted to get a better picture of genetic differentiation and potential cryptic diversity (Grobler & Van der Bank, 1993; Liu et al. 2024).
- A more powerful panel of molecular markers is required to increase the confidence with which hybrids (especially 2nd or 3rd generation backcrosses) can be detected and to preserve the genetic integrity of the species (Grobler et al. 2018).

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Consultation

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

Acknowledgements

- We are grateful to Profs Paul Grobler and Rouvay Roodt-Wilding and Dr David Mallon for their valuable comments and for taking the necessary time and effort to critically review the initial guidelines.

Queries

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Southern Giraffe

(*Giraffa giraffa*)

Recent genetic studies (Bertola et al. 2024; Coimbra et al. 2021; Fennessy et al. 2016; Winter et al. 2018) showed that there are four separate giraffe lineages with different demographic histories. These lineages correspond to four recognised species of giraffe (see Appendix, Figure A1 for their distribution): *Giraffa camelopardalis* (northern), *Giraffa reticulata* (reticulated), *Giraffa tippelskirchi* (Masai), *Giraffa giraffa* (southern). For permitting purposes, South Africa recognise *Giraffa camelopardalis giraffa* (updated taxonomy *Giraffa giraffa giraffa*; Coimbra et al. 2021), and within Namibia, both *Giraffa camelopardalis angolensis* (updated taxonomy *Giraffa giraffa angolensis*; Coimbra et al. 2021) and *Giraffa camelopardalis giraffa* (updated taxonomy *Giraffa giraffa giraffa*; Coimbra et al. 2021) are used. Currently the International Union for Conservation of Nature (IUCN) only

recognises a single species with nine subspecies. **Here we treat southern giraffe (*G. giraffa*) as a single species based on the genetic evidence provided.**

Management Level

• Subspecies

Two subspecies of southern giraffe are recognised based on genetic data (Coimbra et al. 2021, Bertola et al. 2024).

- ***Giraffa giraffa angolensis*** (Angolan)
- ***Giraffa giraffa giraffa*** (South African)

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.

• Genetic Management Units (GMUs)

- Angolan (AO)
- Southern African (SA)
- Southern Central (SC)

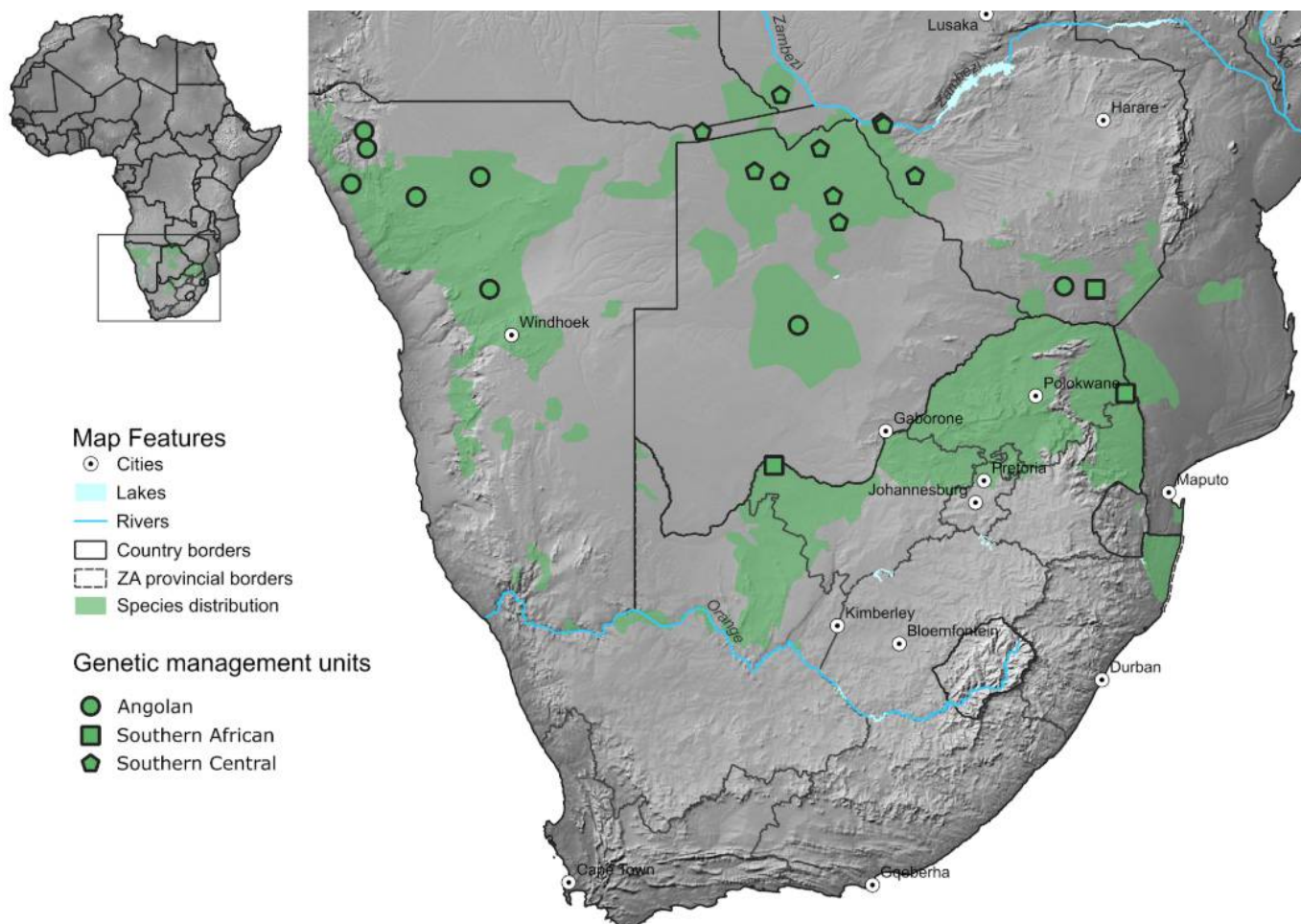


Figure 1: Natural distribution of southern giraffe (*Giraffa giraffa*) in green shading. Genetic Management Units (GMUs) are indicated by different symbols. Each point represents a locality which has been sampled for genetic data and thus the GMU (symbol) designation of each locality is based on genetic data. The inset indicates the part of Africa shown in the main map. Distribution data sources: South Africa and eSwatini - 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) 2018. *Giraffa camelopardalis*. *The IUCN Red List of Threatened Species*. Version 2021-1. <https://www.iucnredlist.org>. Downloaded on 23/04/2021.

Management Boundaries

See **Figure 1** for visual representation. Text descriptions follow.

- **Genetic Management Units (GMUs)**

- Angolan (AO): central Botswana, Namibia.
- Southern African (SA): South Africa, southern Botswana, western Mozambique, southern Zimbabwe, eSwatini.
- Southern Central (SC): southern Zambia, northern Botswana, northern Zimbabwe

Management Boundaries

- **Global population Nc:** 48,186 (Marneweck et al. 2025).
- **South African population Nc:** 20,821 (Marneweck et al. 2025; Hoffman et al. 2025).
- Genetic indicators are calculated at **GMU level**. This is based on a best case scenario where gene flow is maintained within GMUs.
- If values are reported as a range, the average is used for subsequent calculations.

Table 1. Effective population size, Ne500 indicator, and confidence in the values calculated per ESU for blue wildebeest. Colour of the ESU label is linked to the colour used in Figure 1. Colour of Ne500 and confidence text corresponds to positive (green) or negative interpretation (orange/red). Overall Ne500 indicates the proportion of the total ESUs that have an Ne over 500.

GMU	Nc	Ne	Ne500 indicator ¹	Confidence
Angolan (AO)	10,964	1,096-3,289	> 500	High
Southern African (SA)	25,109-28,330	2,672-8,016	> 500	Moderate
Southern central (SC)	11,819-15,040	1,343-4,029	> 500	Moderate
Overall	48,186	N/A	3/3 GMUs have an Ne > 500 = 1	Moderate

- **Genetic indicators**

- **Ne500 indicator¹:**

- **Angolan (AO)** individuals: 15,663 (Marneweck et al. 2025). With assumed maturity percentage of 70 % (Muller et al. 2018), Nc: 10,964. Using an Nc:Ne ratio of 0.1-0.3, Ne = 1,096-3,289.
- **Southern Africa (SA)** individuals: 35,870-40,471 (Marneweck et al. 2025; Hoffman et al. 2025). With assumed maturity percentage of 70 % (Muller et al. 2018), Nc: 25,109-28,330. Using an Nc:Ne ratio of 0.1-0.3, Ne = 2,672-8,016.
- **Southern central (SC)** individuals: 16,884-21,486 (Marneweck et al. 2025). With assumed maturity percentage of 70 % (Muller et al. 2018), Nc: 11,819-15,040. Using an Nc:Ne ratio of 0.1-0.3, Ne = 1,343-4,029.

- All three genetic management units have an Ne above 500 which indicates each GMU will maintain genetic diversity, assuming gene flow is maintained within GMUs, thus indicating lower genetic risk.

- **Proportion of populations maintained (PM2)**

- The global populations of southern giraffes comprise three GMUs, therefore the proportion of populations maintained globally: $3/3 = 1$.

- **Diversity loss**

- Functional variation

There is risk of functional variation loss in *G. g. angolensis* due to having smaller, historically bottlenecked populations (e.g., desert-dwelling Angolan giraffe in northwest Namibia) which are particularly susceptible to loss of adaptive genetic variants (Prochotta et al. 2024).

- **Divergent lineages**
There is low risk of losing divergent lineages as both of the subspecies, covering all three GMUs, have shown population increase in recent decades.
- **Hybridisation/introgression**
 - There is evidence of introgression between Angolan and South African giraffes at certain contact zones, with admixture analyses showing intermediate ancestry in populations such as those in the Central Kalahari Game Reserve (CKGR). This hybridisation is not widespread across all populations (Prochotta et al. 2024).
- **Lower turnover/constraints on adaptive opportunities**
 - There has been reduction of genetic diversity genome wide and runs of heterozygosity in *G. g. angolensis*, especially within smaller, isolated groups, indicating inbreeding (Prochotta et al. 2024). These low levels of heterozygosity and high levels of inbreeding are seen across southern giraffes, likely due to a historical bottleneck, and may still constrain adaptive opportunities despite population growth, especially alongside pressures such as changing climate.
- **In situ genetic threat level**
 - In situ Risk (**Moderate**)
Southern giraffes exist in fragmented populations, and have evidence of inbreeding and low heterozygosity within populations. However genetic management units have an Ne well above 500 and are relatively stable so with facilitation of gene flow between populations, risk is moderate (Hoffman et al. 2025; Marneweck et al. 2025). For more threats, see the IUCN Red List and South African Red List.
 - **Confidence in in situ threat level**
 - Confidence score (**Moderate**)
Confidence is moderate as the assessment is based on regional assessment data published within the last year (Marneweck et al. 2025; Hoffman et al. 2025). However, population numbers per GMU to calculate Ne500 were assumed from population data per country or subspecies provided in Marneweck et al. (2025) as well as the South African red list assessment (Hoffman et al. 2025). These assumptions of individuals per GMU may potentially misrepresent the exact current population census sizes.
- **Ex situ representation**
 - The southern giraffe is more uncommon in traditional zoos than other giraffe species, with only 20 Angolan and 45 from the southern GMUs in zoos worldwide (Tuttings et al. 2013).
 - High levels of inbreeding were detected in the genetic analysis of captive southern giraffes, with low levels of heterozygosity and known cases of mating with relatives (Frasier et al. 2026).



Figure 2: Effective population size compared to confidence in the value. Colour and shape of points and labelling corresponds to the colour and title of the GMU in Figure 1 and Table 1. Dashed lines divide the x axis into above and below Ne500, and the y axis into low and high confidence. GMUs in the low confidence quadrant should be further surveyed to increase confidence in the evaluation. Those with high confidence below Ne500 should have increased genetic management.

¹ Proportion of populations within species with an effective population size (Ne) greater than 500
(<https://www.gbf-indicators.org/metadata/headline/A-4>)

² Proportion of populations maintained within species
(https://ccgenetics.github.io/guidelines-genetic-diversity-indicators/docs/2_Theoretical_background/PM-indicator.html)

Management Guidelines

- Other species of giraffe should not be imported from the rest of Africa to southern Africa.
- Manage the Southern African, Southern Central and Angolan GMUs as separate units to maintain genetic separation between the two subspecies.
- In 1991 (Kruger 1994), animals from Namibia (*Giraffa giraffa angolensis*) were translocated to the Kgalagadi National Park in South Africa. Animals for this park must be genetically tested before translocation to avoid any further admixture between GMUs.
- Animals on private ranches should be tested genetically before translocations to prevent mixing of different GMUs.
- All GMUs have $N_e > 500$ under the assumption of gene flow within GMUs. Therefore, management must strive to facilitate natural migration and gene flow between isolated populations within each GMU, while taking cognisance of the other guidelines above.

IUCN Status:

- Global: Least threatened (indicated below)
- South Africa: Vulnerable



- Other species of giraffe should not be imported from the rest of Africa to southern Africa.
- Manage the Southern African, Southern Central and Angolan GMUs as separate units to maintain genetic separation between the two subspecies.
- In 1991 (Kruger 1994), animals from Namibia (*Giraffa giraffa angolensis*) were translocated to the Kgalagadi National Park in South Africa. Animals for this park must be genetically tested before translocation to avoid any further admixture between GMUs.
- Animals on private ranches should be tested genetically before translocations to prevent mixing of different GMUs.
- All GMUs have $N_e > 500$ under the assumption of gene flow within GMUs. Therefore, management must strive to facilitate natural migration and gene flow between isolated populations within each GMU, while taking cognisance of the other guidelines above.

Limitations & Assumptions

- Previous translocations have occurred, without taking genetic structure between the species (ESUs) or within the southern giraffe (GMUs) into account.
- Private ranches are likely to have individuals from other ESUs or these ranches have descendants from ESUs outside of southern Africa.

Priority Research

- Generate genetic data from undersampled southern African populations of both *G. g. giraffa* and *G. g. angolensis*.
- Identify important corridors or natural dispersal routes for populations at local and regional levels.
- Undertake genetic analysis to determine the level of hybridisation within translocated populations/newly established populations.

Limitations & Assumptions

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Consultation

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

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Queries

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Impala

(*Giraffa giraffa*)

A single species of impala *Aepyceros melampus* (Lichtenstein, 1812), the sole extant member of the Aepycerotini, is currently recognised across the broad geographic distribution in southern and East Africa. In the past up to six subspecies were proposed (Ansell 1972), yet at present conservation authorities only accept two subspecies, the common impala *A. m. melampus* (Lichtenstein, 1812) in southern and East Africa, and the vulnerable black-faced impala *A. m. petersi* (Bocage, 1879) restricted to north-western Namibia and south-western Angola. These subspecies are used for permitting purposes in southern Africa. Genetics research, including recent genome-level analyses, support at least three subspecies that are herein treated as Evolutionarily Significant Units (ESUs, Figure 1). There are at least five Genetic Management Units (GMUs, Figure 1), although additional priority research should refine the status and guidelines for these units.

Management Level

Subspecies

Three subspecies of impala are recognised across Africa based on genetic and morphological data (Frost 2014, Garcia-Erill et al. 2024), although some sources only recognise the black-faced and common impala (Selier et al. 2016).

- *Aepyceros melampus petersi* (black-faced impala)
- *Aepyceros melampus melampus* (common or southern impala)
- *Aepyceros melampus rendilis* (East African impala)
- 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.

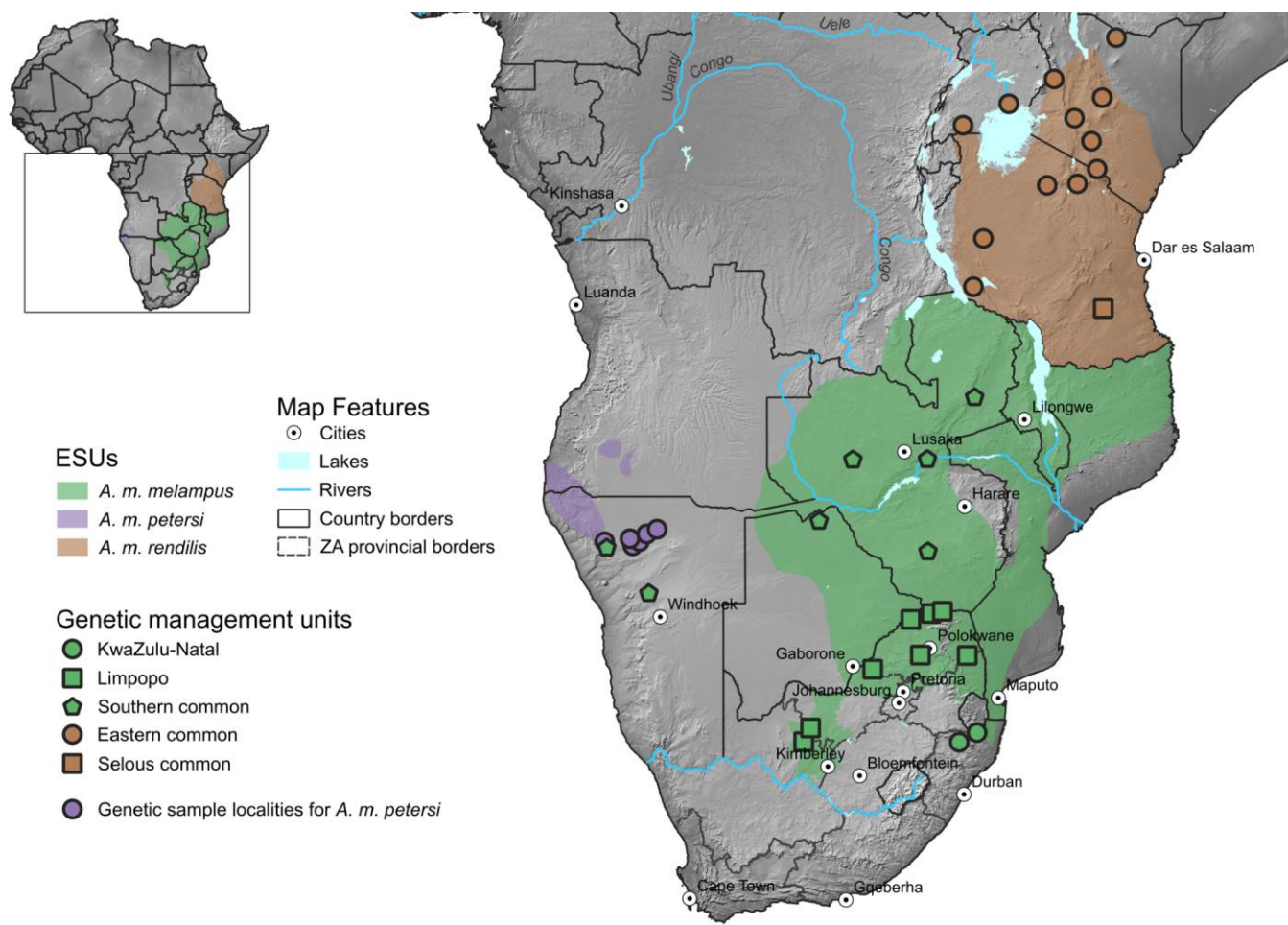


Figure 1: Natural distribution of impala (*Aepyceros melampus*) subspecies indicated by different colours. Genetic Management Units (GMUs) are indicated by different symbols, with the colour corresponding to the ESU to which it belongs. Each point represents a locality which has been sampled for genetic data and thus the GMU (symbol) and ESU (colour) designation of each locality is based on genetic data. Note that the points in and near Etosha National Park have been slightly adjusted so that all points are visible. 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) 2016. *Aepyceros melampus*. *The IUCN Red List of Threatened Species*. Version 2021-1. <https://www.iucnredlist.org>.

Management Level

Genetic Management Units (GMUs)

- **Black-faced impala**
 - No GMUs recognised at present but see Priority research
- **Common or southern impala**
 - KwaZulu-Natal (KZN)
 - Limpopo (LP)
 - Southern common (SO)
- **East African impala**
 - Selous common (SE)
 - Eastern common (EA)

Management Boundaries

Subspecies

- *Aepyceros melampus petersi*: North-western Namibia and south-western Angola.
- *Aepyceros melampus melampus*: South Africa, eSwatini, north-eastern Namibia (Zambezi Region – previously Caprivi Strip), south-eastern Angola, Botswana, Zimbabwe, Mozambique, Zambia, southern Democratic Republic of the Congo, Malawi.
- *Aepyceros melampus rendilis*: Tanzania, Kenya, Uganda, Rwanda, Burundi (possibly extinct).

Genetic Management Units (GMUs)

- **Common or southern impala**
 - KwaZulu-Natal (KZN): northern KwaZulu-Natal Province of South Africa.
 - Limpopo (LP): Limpopo Province of South Africa.
 - Southern common (SO): north-eastern Namibia, Botswana, Zimbabwe, Zambia.
- **East African impala**
 - Eastern common (EA): Western Tanzania, Kenya and Uganda.
 - Selous common (SE): Selous Nature Reserve (now Nyerere National Park), Tanzania.

Genetic Risk

- **Global population Nc**: 2,000,000 (IUCN 2016; East 1999).
- **South African population Nc**: 540,936-631,092 (East 1999).
- Genetic indicators are calculated at **GMU level**. This is based on a best case scenario where gene flow is maintained within GMUs.
- If values are reported as a range, the average is used for subsequent calculations.

Table 1. Effective population size, Ne500 indicator, and confidence in the values calculated per GMU for impala. Colour of the GMU label is linked to the colour used in Figure 1. Colour of Ne500 and confidence text corresponds to positive (green) or negative interpretation (orange/red). Overall Ne500 indicates the proportion of the total GMUs that have an Ne over 500.

GMU	Nc	Ne	Ne500 indicator ¹	Confidence
<i>A. m. petersi</i> (AMP)	3,000-4,000	350-1,050	> 500	Moderate
KwaZulu-Natal (KZN)	Unknown	Unknown	Unknown (Likely > 500)	N/A
Limpopo (LP)	Unknown	Unknown	Unknown (Likely > 500)	N/A
Southern common (SO)	269,850-314,825	29,234-87,701	> 500	Moderate
Eastern common (EA)	122,280-142,600	13,247-39,741	> 500	Moderate
Selous common (SE)	17,713-20,665	1,919-5,757	> 500	Moderate
Overall	~2,000,000	N/A	Likely 6/6 GMUs have an Ne > 500 = 1	Moderate

Genetic Indicators

• Ne500 indicator¹

- *A. m. petersi* (AMP) Nc: 3,000-4,000 (IUCN 2017). Using an Nc:Ne ratio of 0.1-0.3, Ne = 350-1,050.
- **South Africa:**
- **KwaZulu-Natal (KZN)** and **Limpopo (LP)** individuals: 901,560 (East 1999). Both GMUs are reported to have sufficient population sizes to meet the Ne > 500 threshold (Shrader and da Silva 2025).
- **Southern common (SO)** individuals: 449,750 (East 1999). With assumed maturity percentage of 60-70 % (Shrader and da Silva 2025), Nc: 269850-314,825. Using an Nc:Ne ratio of 0.1-0.3, Ne = 29,234-87,701.
- **Eastern common (EA)** individuals: 203,800 (East 1999). With assumed maturity percentage of 60-70 % (Shrader and da Silva 2025), Nc: 122,280-142,660. Using an Nc:Ne ratio of 0.1-0.3, Ne = 13,247-39,741.
- **Selous common (SE)** individuals: 29,500 (UNESCO 2011). With assumed maturity percentage of 60-70 % (Shrader and da Silva 2025), Nc: 17,713-20,665. Using an Nc:Ne ratio of 0.1-0.3, Ne = 1,919-5,757.
- Of the six genetic management units, four have an Ne above 500 based on population data, and two are assumed to have an Ne above 500 based on comments on abundance within their ranges and population data for the country in which they occur. Ne > 500 indicates each GMU will maintain genetic diversity, assuming gene flow is maintained within GMUs, thus indicating lower genetic risk.

• Proportion of populations maintained (PM²):

- The global populations of impala comprise six GMUs, therefore the proportion of populations maintained globally: 6/6 = 1.

Diversity Loss

- **Functional variation:** There is moderate risk of functional variation loss in impala due to their large population size and wide distribution, yet isolated populations exist in fenced areas therefore localised loss is a potential concern. Levels of genetic diversity are low in isolated groups and groups subjected to intensive and selective breeding (Grobler & Van der Bank 1994, Lorenzen et al. 2006, Garcia-Erill et al. 2024).
- **Divergent lineages:** There is a moderate risk of losing divergent lineages as the subspecies *A. m. petersi* occurs at lower densities and is more geographically restricted than *A. m. melampus* or *A. m. rendilis* (Lorenzen et al 2006; Grobler et al. 2011).

Hybridisation/introgression

- There is evidence of hybridisation and introgression between impala subspecies, with *A. m. melampus* being moved into areas historically occupied by *A. m. petersi* in southern Africa by human-mediated translocation for game ranching and hunting (Nersting and Arctander 2001; Lorenzen and Siegismund 2004; Lorenzen et al. 2006; Miller et al. 2020). This hybridisation is a particular threat to *A. m. petersi* as it is less widespread (Grobler et al. 2011).

Lower turnover/constraints on adaptive opportunities

- Lower levels of genetic diversity have been detected in the black-faced impala and East African impala compared with the common or southern impala (Nersting and Arctander 2001; Lorenzen and Siegismund 2004; Lorenzen et al. 2006; Miller et al. 2020; Garcia-Erill et al. 2024). Adaptive opportunities may be constrained locally in fenced or intensively managed populations, especially alongside pressures such as changing climate.

In situ genetic threat level

• In situ risk (Moderate)

Impala remain abundant and genetically diverse across the majority of their range. However, when assessed at the subspecies level, risks increase due to lineage mixing, habitat fragmentation, and uneven management practices, especially affecting *A. m. petersi*. Continued unregulated translocations may elevate long-term genetic risk despite stable census numbers. For more threats, see the IUCN Red List assessments for impala as a species, common impala and black-faced impala and the South African Red List for common impala.

• Confidence in in situ threat level

◦ Confidence score (Moderate)

Confidence is moderate as the assessment is based on IUCN or regional assessment data from within the last decade (IUCN 2016; IUCN 2017; Shrader and da Silva 2025). However, population numbers for some GMUs to calculate N_{e500} were assumed from data provided in East (1999) as well as the South African red list assessment (Shrader and da Silva 2025), IUCN assessments (IUCN 2017), and UNESCO data sheets (UNESCO 2011). The in situ risk score is based on several assumptions and could potentially misrepresent current population census sizes. Confidence is supported by mitochondrial and nuclear genetic studies demonstrating high diversity but clear subspecies structure (Lorenzen et al. 2006; Grobler et al. 2011).

Ex situ representation

- Impala are present in private game reserves, wildlife ranches, and managed conservation areas rather than traditional zoo breeding programs.
- Several colour variants of common impala (e.g. black and saddle-back) are routinely bred on private wildlife ranches in the region. Escapees from such ranches threaten the genetic integrity of natural populations.

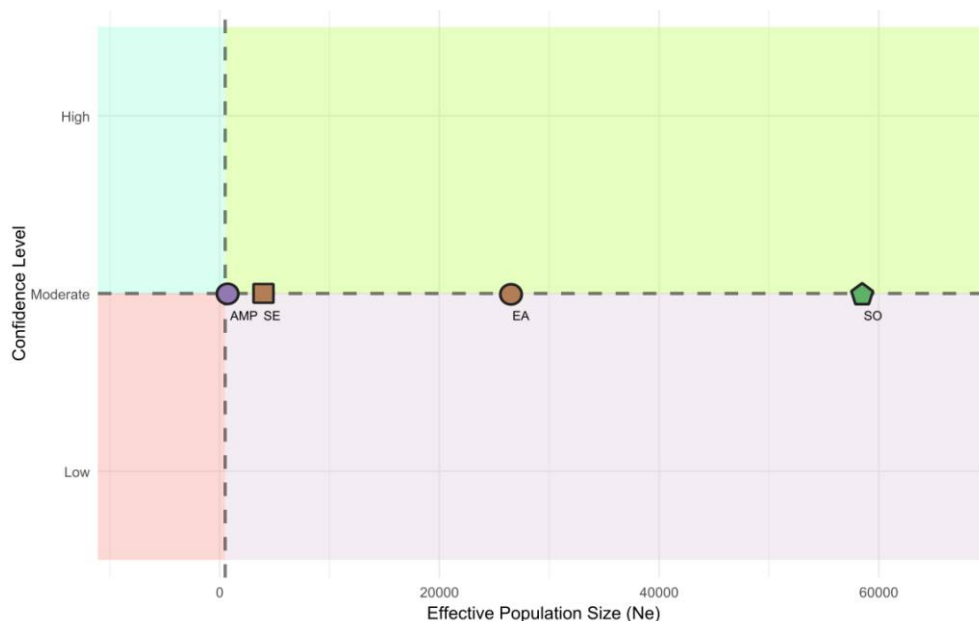


Figure 2: Effective population size compared to confidence in the value. Colour and shape of points and labelling corresponds to the GMU in Figure 1 and Table 1. Dashed lines divide the x axis into above and below Ne500, and the y axis into low and high confidence. GMUs in the low confidence quadrant should be further surveyed to increase confidence in the evaluation. Those with high confidence below Ne500 should have increased genetic management. Note that the KZN and LP GMUs are not shown due data deficiency.

¹ Proportion of populations within species with an effective population size (Ne) greater than 500 (<https://www.gbf-indicators.org/metadata/headline/A-4>)

² Proportion of populations maintained within species (https://ccgenetics.github.io/guidelines-genetic-diversity-indicators/docs/2_Theoretical_background/PM-indicator.html)

Management Guidelines

- No mixing of the three subspecies on the same property.
- No new introductions of one subspecies into the range of the other subspecies.
- **Black-faced impala**
 - Genetic testing is required to ensure that only pure black-faced impala is present in a population. The buffer zone in Namibia is crucial for the genetic integrity of the vulnerable subspecies (Matson 2006, Miller et al. 2020).
- **Common or southern impala**
 - No translocations between GMUs but allow natural migration.
- **East African impala**
 - No translocations between GMUs but allow natural migration.
- All GMUs are indicated to have an Ne > 500 under the assumption of gene flow within GMUs. Therefore, management must strive to facilitate natural migration and gene flow between isolated populations within each GMU, while taking cognisance of the other guidelines above.

IUCN Status:

- Global: Least threatened (indicated below)
- South Africa: Vulnerable



Limitations & Assumptions

- Genetic evaluation for any South African impala populations outside of KZN and Limpopo has not been carried out (Schwab et al. 2012). The latter study did an analysis including mitochondrial DNA sequences from previous studies (Nersting & Arctander 2001, Lorenzen et al. 2006) but re-analysis and interpretation is required (See Priority research).
- Previous studies did not include samples from South Africa (Nersting & Arctander 2001, Lorenzen et al. 2006, Garcia-Erill et al. 2024), thus the relationships of the Limpopo GMU and KwaZulu-Natal GMU (Schwab et al. 2012) within the broader Southern common (SO) group need further investigation.
- Several studies reported isolated populations and lower levels of adaptability in East Africa (Nersting & Arctander 2001, Lorenzen et al. 2006, Garcia-Erill et al. 2024). The assessment of GMU status based on wider sampling is required.
- Parts of the species distributional range are data deficient and therefore difficult to assign ESU/GMU status. The status of eSwatini, southern Angola, Mozambique, Malawi, Rwanda and Burundi populations with respect to ESUs and GMUs should be determined. There are suggestions that the species is extinct in Burundi.

Priority Research

- More populations of black-faced impala must be sampled across Namibia and Angola (currently no data) to investigate the levels of genetic diversity, inbreeding in the subspecies, and genetic substructure across its distribution, to determine if GMUs are present. Lorenzen et al. (2006) suggested some differentiation among sites in Etosha National Park.
- The consequences of subspecies hybridisation should be investigated.
- More extensive sampling of impala in natural populations in South Africa and Mozambique outside of Limpopo Province and KZN, in order to conduct a finer scale phylogeographic study of this region.
- More extensive sampling of impala in Central and East Africa given the sampling gaps and findings of previous studies (Nersting & Arctander 2001, Lorenzen et al. 2006, Garcia-Erill et al. 2024) and to refine the distribution of the East African subspecies/ESU *A. m. rendilis*.

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Consultation

- IUCN SSC Conservation Genetics Specialist Group
- IUCN SSC Antelope Specialist Group
- Namibia Ministry of Environment, Forestry and Tourism (black-faced impala)

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Queries

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



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