

LION GENETICS & TRANSLOCATION

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THE CABELA FAMILY FOUNDATION

RE: LION SOURCE-POPULATION GENETICS FOR TRANSLOCATION

AN INTRODUCTION TO REINTRODUCTIONS

The CABELA FAMILY FOUNDATION, in cooperation with the IVAN CARTER WILDLIFE CONSERVATION ALLIANCE and ZAMBEZE DELTA SAFARIS, are undertaking an ecological restoration initiative, amongst other projects, that will re-establish a viable wild lion *Panthera leo* population in an area of over 9 000 km² of their historic domain. With the current conservation status of the species as either ‘*Threatened*’ or ‘*Endangered*’ throughout its extant range, such initiatives are crucial to ensuring the future survival of lions in the wild. As both Keystone and Umbrella species, and the apex predator wherever they occur, lions are of critical importance to the functional ecosystem.

Cynically, conservation is a history of compounded anthropogenic errors; where solving one problem often creates more, philosophically referred to as so-called ‘unintended consequences’. It is therefore an incumbent responsibility on conservationists that any initiative involving intervention is properly understood from the outset. With regard to the spatial translocation of an organism for ecological restoration, there are several key factors that must be comprehensively studied before any move is made (*and for the purposes of this document, here we refer to conservation in the traditional sense; involving the maintenance of wild animals in their natural environment where they historically occurred*).



With regard to a general assessment of the probable viability of a species reintroduction, we need to first evaluate the ecological situation (*past, present, & future*):

1. *Why did the species locally disappear?*
2. *Why did the species not recover?*
3. *Have the factors that led to the decline been identified and dealt with?*
4. *Is the current environment suitable for a viable population of the species?*

When these general points have been sufficiently researched, and the results show that a successful reintroduction is both possible and beneficial to the conservation status of the species, as well as the ecological and anthropogenic environment, then several more specific topics need to be addressed regarding the actual future seed population:

5. *survival ability*
6. *infectious disease transmission risk*
7. *genetic suitability*

Points **1 – 4** have already been carefully investigated, as far as practical given the retrospective nature of certain aspects, with regard to the reintroduction of lion to the Zambeze Delta; and indicate that all the environmental conditions exist to ensure success in re-establishing a viable and healthy free-ranging wild lion population (*available in a previous document*).

Point **5** is fairly straightforward with regard to the survival ability of the seed population – **only free-ranging wild lions will be selected for the translocation**. These individuals were not bred or born in captivity and have never been caged; these animals already naturally fend for themselves in the wild without any human intervention.

Point **6** is an important consideration in a translocation exercise, as introducing diseases to an area puts other wildlife at risk, and could negate any potential for a positive contribution to conservation. However, the topic of disease is easily dealt with at the source during the first phase of the seed population selection: a wildlife veterinarian is leading the capture and quarantine phases of the translocation, and all relevant disease screening and inoculation against disease is done in situ at source before the lions are moved. Only lions that



produce negative results for all infectious diseases tested for will be considered for translocation.

This document will thus focus on the final point, **7**, with regard to the genetic composition of the seed population. Taking genetics into account when planning a translocation is critical, as introducing the wrong types to an area effectively creates aliens, which in the case of different species could result in either hybridisation with or out-competition of the indigenous population, or in the case of the same species could dilute certain historical traits of a particular area or population. With regard to lions and our reintroduction project, there is little worry about in terms of either issue – lions are not alien to the release site in the Zambeze Delta where they historically occurred, and there is no extant indigenous population to dilute.

However, it is still critical to meticulously investigate all facets of such an enormous undertaking, if only to rule-out the chance of making errors; and so here we discuss the topic of lion genetics throughout their range in Africa, and how this pertains to a spatial translocation.

THE EXTANT GENETICS OF VARIOUS LEVELS OF LION POPULATION

With regard to the translocation and reintroduction of lion between spatially distinct sites (*in this case from South Africa to neighbouring Mozambique*), the genetic implications may be considered at two levels: *i. species & subspecies*, and *ii. population & subpopulation*:

- i. At the species level, lions were historically abundant and widespread throughout Africa and parts of Asia – and being a large and wide-ranging apex carnivore there was no isolation between populations (until relatively recently with the expansion of human civilisation) and thus there originally existed little impediment to gene flow (see Figure 1). As such, throughout the extent of their range, there are currently only two formally recognised extant subspecies of modern lion (based on mtDNA):
 - *P. l. leo* (Endangered), which is represented by the Asiatic and west and north African populations;
 - *P. l. melanochaita* (Threatened), which is represented by all of the southern and eastern African lions.



- ii. At the population and subpopulation level, within a subspecies, the topic of lion genetics is more complicated: in the current conservation era, many restored populations now available as sources were themselves founded with individuals of mixed historical lineages from a range of localities (which even though were once contiguous, many are now genetically isolated due to expansive human activity). Many minor genetic differences between isolated populations within the subspecific range result from reduced diversity, which in turn result from reduced connectivity between populations, rather than because of any real historical natural selection and adaptation towards distinct traits.

Many physical characteristics of wild lions, for example manes, are phenotypically (environmentally) influenced: individuals at higher altitudes and in sparser and colder environments have larger manes than those in lower and more humid and denser habitats; mane size is also affected by age and physical condition of the animals, and varies throughout their lives. Morphology alone was originally used to classify subspecies such as the famous Barbary and Cape lions, which had the largest and most distinctive manes (Asiatic lions usually have sparser manes than the average African lion), as taxonomists previously believed that distinct subspecies could be defined by external physical characteristics, such as mane size, shape and colour (see Appendices I & II). However, lions in captivity tend to have much larger manes, free from the survival stresses facing wild lions, as well as dense vegetation that snags the hair. For example, the cooler ambient temperatures in European and North American zoos has been linked to their lions developing heavier and darker manes. Physical attributes alone are therefore not reliable markers for classifying subspecies, and this has been resolved in the modern era through the development and use of more definitive genetic testing.

ECOLOGICAL JUSTIFICATION FOR LARGE CARNIVORE RESTORATIONS

Regardless of relatively minor genetic differences between populations, all lions fill the same biological niche, being the apex predator wherever they occur, exerting top-down control on the ecosystem: preying on the sick and the weak and the over abundant, thus maintaining healthy prey populations and preventing mass die-off in poor seasons; reducing competition and exclusion between herbivores; facilitating other large carnivores whilst stemming meso-



predator release; and increasing the overall biodiversity and general health and stability of the environment.

Obviously, in the perfect world, there would be no need for reintroductions; and if there were, then individuals would be sourced from the same genetic lineage that historically occurred at that particular site. In reality, however, we no longer have the luxury of choice, and the genetic constitution of the source population is moot – if there are no individuals locally available with the historic genetic composition of that particular area, then animals from further afield must be considered; the alternative being that no reintroduction occurs, and an ecosystem that historically included lions as the apex predator remains devoid of them. This is difficult to argue as the preferable course of action, especially given the current conservation status of the overall species. Restoration of the intact ecosystem should remain the priority.

THE DESTINATION

The Zambeze Delta in Mozambique is an area of over 9 000 km² of pristine habitat and former lion range. This is an example of an area for which there are no locally available source populations from which to restore the species to the area; necessity dictates looking further afield.

Written records (both historic and relatively recent) indicate that lions were once abundant and occurred at high densities in Mozambique, but were reduced to unviable levels during the country's brutal and protracted civil war. There is evidence that both the direct persecution and the depletion of their prey base resulted in the local declines and eventual extirpations of the lion; reducing connectivity and subsequently the ability of populations to naturally recover.

THE SOURCES

Because the remnant lion populations in Mozambique are few, small, and relatively unknown in terms of robust scientific data, we therefore plan to source 25 lions for the reintroduction program from large, healthy, and well-managed free-ranging wild lion populations in South Africa, and for which exists data on population trends, demographics, genetics, and behaviour (Figure 1).

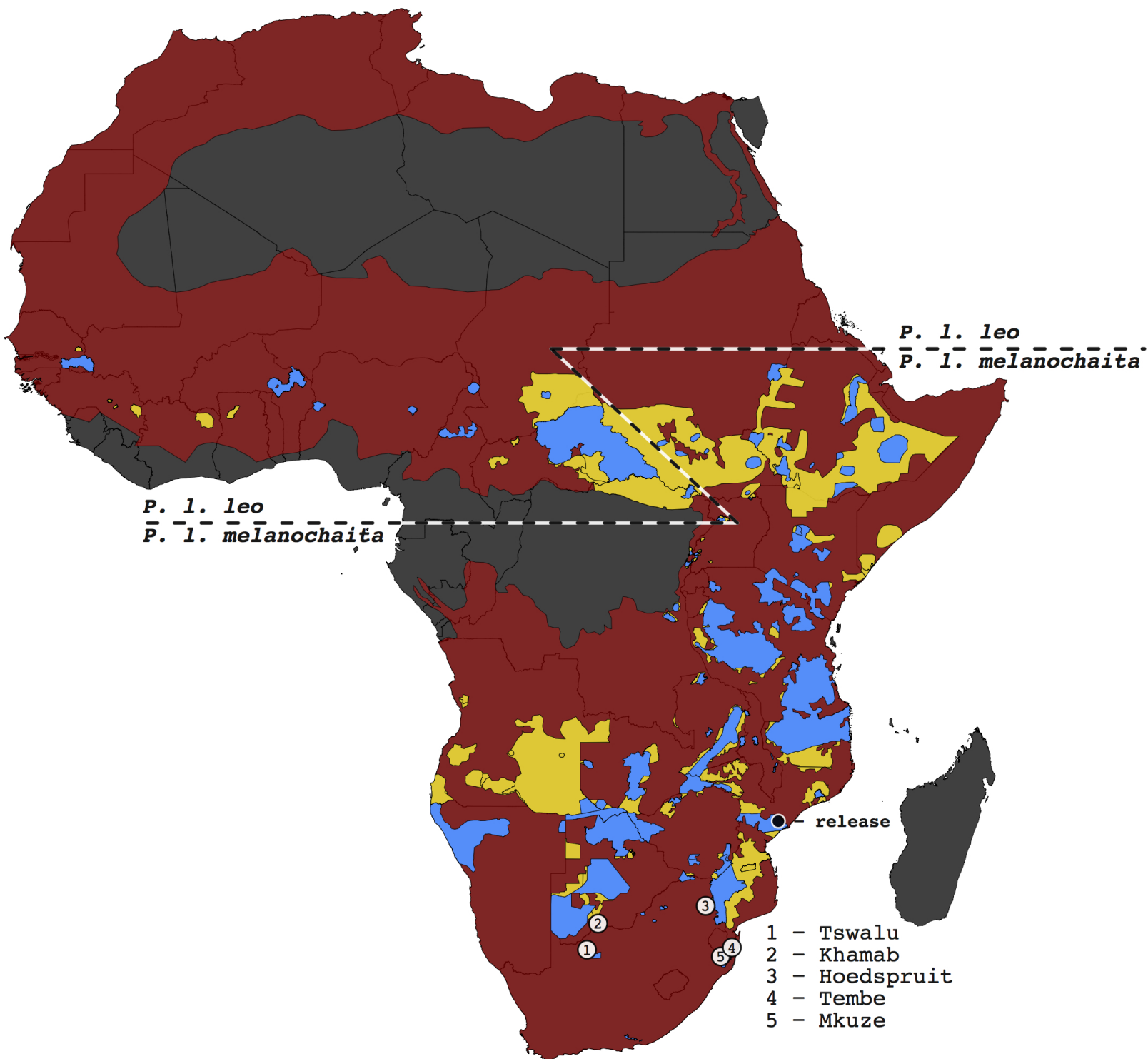


FIGURE 1: Map of the lion's *Panthera leo* range in Africa

RED – the extensive historical range of lion in Africa; only major deserts and rainforests

YELLOW – it is suspected that lion have gone extinct from these areas in recent years

BLUE – the current known range of Africa's extant lion

It is quite apparent that the lion once enjoyed unrestricted movement throughout the African continent, unimpeded by the general obstacles to population connectivity, such as rivers and mountain ranges, that may affect smaller and less mobile species – and it is mainly for this reason that there exist only two extant subspecies.

The approximate boundary between the subspecies *P. l. leo* (north) and *P. l. melanochaita* (south) is indicated by the dashed line – however, there is obviously some overlap in range, and some genetic intermingling where this occurs.

The release site in Mozambique is indicated on the map with a black point, and the source sites are numbered in white points (note that some sources are closer to the destination than to each other).



The specific lion source populations selected for the translocation (Figure 1) are:

1. **Twsalu** (*includes Kalahari genetics*)
2. **Khamab** (*include Kalahari and Kruger genetics*)
3. **Hoedspruit** (*Kruger genetics, from the Mozambican border*)
4. **Tembe** (*from Pilansberg, originally from Khamab, include Kruger genetics*)
5. **Mkuze** (*from Phinda, which came from Pilansberg, originally from Khamab*)

For obvious reasons, only private reserves are available as source populations, and National Parks are off-limits. This is not a disadvantage. Even large National Parks suffer the same modern isolation as smaller reserves, which often have an advantage in genetic diversity, originally sourced from a range of areas. These populations also have the luxury of more intensive management strategies and private veterinarian care. Tuberculosis, a contagious and fatal disease in lion, is not present in the source populations on the private reserves, but is highly prevalent in the Kruger National Park lion population and therefore completely precludes this population from being a source for any future translocations.

PRECEDENCE

In terms of rewilding private areas, a good reason for introducing individuals from different areas was indeed to increase genetic diversity in the necessarily small seed populations, and prevent the negative effects of genetic bottlenecks and inbreeding. With regard to subsequent translocations out of these subpopulations, and despite excellent previous work in genetic testing, it is largely impossible to trace any descendent of the original individuals back to a specific locale, but this is actually unimportant insofar as the lions all represent the same local subspecies.

The original source population that we intended to use for the translocation to the Zambeze Delta (prior to encountering political blockages actually unrelated to our project) was that of the Buby Valley Conservancy in Zimbabwe – this population itself deriving from 13 lions imported from throughout South Africa and the region in 1999. Genetic testing has subsequently shown that the current population of approximately 500 individuals is genetically diverse and healthy (*no doubt aided in part by the odd break-in of vagrant individuals over the years*).

Recently, in a well publicised and highly praised move, African Parks successfully reintroduced lions into Rwanda's Akagera National Park; restoring an important ecosystem and national pride, in what has been lauded as a huge win for conservation – despite the fact that these lions were sourced from private



game reserves in South Africa, at the furthest extent of the lion range and extant genetics in Africa, as there were none available closer to the destination. Conversely, Mozambique shares a common border with neighbouring South Africa, and before modern agriculture and development destroyed much of their habitat, the lion populations within these two countries were connected and contiguous – and genetically, the remnant populations of Mozambican lions are very closely related to those in South Africa, and all classified as *P. l. melanochaita*. (*Note that several of the source populations are closer to the release site in Mozambique than they are to the other source sites in South Africa*).

GENETICS THAT WE HAVE AVOIDED

South Africa unfortunately has the infamous reputation for captive lion breeding programs that supply the canned hunting industry. Official figures vary, but it is estimated that there are more lions in captivity in South Africa than there are in the wild. These lions, apart from the fact that they are reportedly often inbred, are behaviourally, and possibly psychologically, not suitable for reintroduction to the wild, especially where they may come into contact with people.

To be clear; the lions that we have selected for reintroduction all historically originated from wild populations within the region, and are currently living as free-ranging animals; none of these individuals were captive bred, nor have they ever been caged. There has also obviously not been any artificial selection for physical attributes, such as mane or body size, and the only possible anthropogenic selection criterion (if we can even call it that) imposed is that every individual for translocation is disease free and fending for itself on properly and responsibly managed areas (*intact social groups are captured together where possible*).

WRAPPING UP

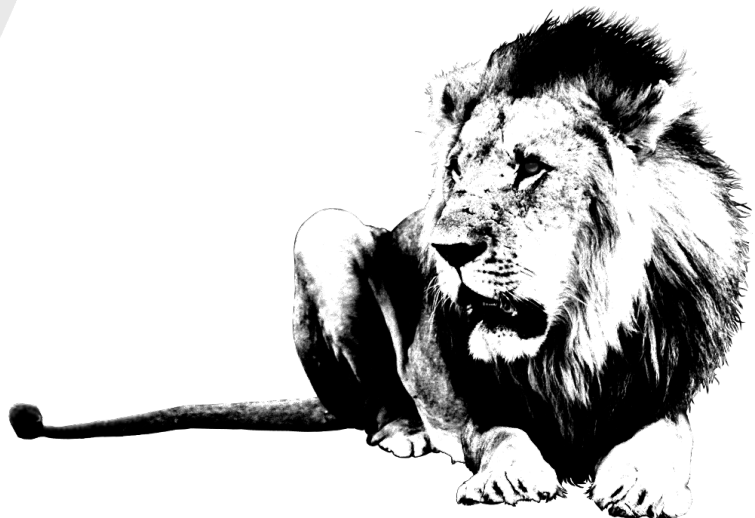
It is absolutely ethically imperative that responsible conservationists consider the genetic implications of translocation, however we also need to consider the implications of not translocating individuals for the future survival of their species: given that the subspecies historically occurred in an area, if one were to let minor genetic variations between areas – which naturally occur within populations of all species – affect the decision whether or not to reintroduce a species, then conservation suffers as a result of misplaced intentions and false concern. Take, for example, the critically endangered black rhino *Diceros bicornis* – it is imperative that remaining individuals be removed from danger zones and relocated to areas where they may be better protected – the alternative is that they die in situ in their natural environments, which does not appear to be a better solution for their conservation.



From a geographical proximity perspective, the Kruger lion population would superficially appear to be an ideal source, however the fact that it is a National Park and contains diseased lions absolutely disqualifies this population for translocation. As the area and project management and ecologists, we are more than confident that the lions we have selected for translocation to Mozambique from several source populations in South Africa represent the most ideal available genetic constitution, and best possible opportunity, for the successful restoration of this apex predator to a significant portion of its former range – to further enhance both the species' conservation status and the protection of the area for its unique biodiversity.

For further information, please do not hesitate to contact us.

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APPENDIX I: FORMER CLASSIFICATIONS OF EXTANT SUBSPECIES

Prior to modern genetic testing, the previous lion subspecies classifications included:

	(CURRENTLY)	(FORMERLY)
ASIATIC LION	<i>P. l. leo</i>	<i>P. l. persica</i>
NORTH AFRICAN LION	<i>P. l. leo</i>	<i>P. l. nubica</i> <i>P. l. somaliensis</i>
BARBARY LION	<i>P. l. leo</i>	<i>P. l. nubica</i> <i>P. l. somaliensis</i>
MASAI LION	<i>P. l. leo</i>	<i>P. l. nubica</i>
WEST AFRICAN LION	<i>P. l. leo</i>	<i>P. l. senegalensis</i> <i>P. l. kamptzi</i>
CENTRAL AFRICAN LION	<i>P. l. leo</i>	<i>P. l. azandica</i>
CONGO LION	<i>P. l. leo</i>	<i>P. l. azandica</i>
EAST AFRICAN LION	<i>P. l. melanochaita</i>	<i>P. l. leo</i> <i>P. l. massaica</i> <i>P. l. sabakiensis</i> <i>P. l. roosevelti</i> <i>P. l. nyanzae</i> <i>P. l. hollisteri</i> <i>P. l. webbiensis</i>
ETHIOPIAN LION	<i>P. l. melanochaita</i>	<i>P. l. roosevelti</i>
SOUTHWEST LION	<i>P. l. melanochaita</i>	<i>P. l. bleyenberghi</i>
SOUTHERN AFRICAN LION	<i>P. l. melanochaita</i>	<i>P. l. leo</i> <i>P. l. bleyenberghi</i> <i>P. l. krugeri</i> <i>P. l. vernayi</i>
TRANSVAAL LION	<i>P. l. melanochaita</i>	<i>P. l. krugeri</i>

(Hybridisation between *P. l. leo* and *P. l. melanochaita* occurs at the intersection of their range)

APPENDIX II: THE 'BARBARY' LION (*Panthera leo leo*)



[SULTAN THE LION]