

# Genetic guidelines for the translocations of lions

## Executive summary

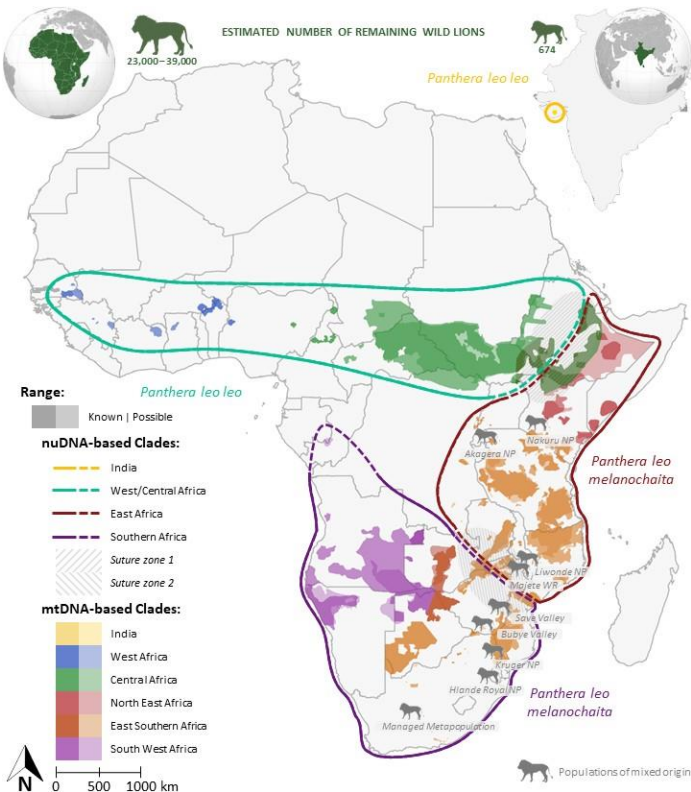
In order to effectively conserve biodiversity, genetic diversity within species must be taken into account. Management interventions, such as translocations, should incorporate genetics by building on the vast data available in the literature. Here, we summarize all available information on lion genetics, infer genetic assignments of populations for which data are currently lacking, and translate this into recommendations for translocations.



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## Background

Data from the CITES Trade Database illustrate that in the past 40 years more than 1000 lions have been translocated into lion range states. Although there has been a variety of sources and purposes for these translocations, we estimate that there often is a risk of unintentionally affecting local lion genetics. Hereby, the natural distribution of genetic diversity in the lion can be negatively affected. **We therefore urge managers to take genetics into account when selecting source/target populations for management interventions.**



## Genetic markers

Genetic assignments to a particular clade (=group) are studied through different genetic markers, each representing a different part of the genome. By combining the information from these different genetic markers, we can obtain a more complete picture of the diversity within species:

- Mitochondrial DNA (mtDNA): widely used, represents maternal lineage, tends to overestimate structure
- Nuclear DNA (nuDNA): less widely used, provides a more complete image of the evolutionary history

## Proposed suitability score

We assess all 132 lion populations/Lion Conservation Units for available genetic data, and assign them to specific genetic clades. For populations without data available, we infer their genetic assignment, based on knowledge from neighbouring populations.

Based on data from mtDNA and nuDNA genetic markers, we propose the following suitability for source/target combinations for translocations:

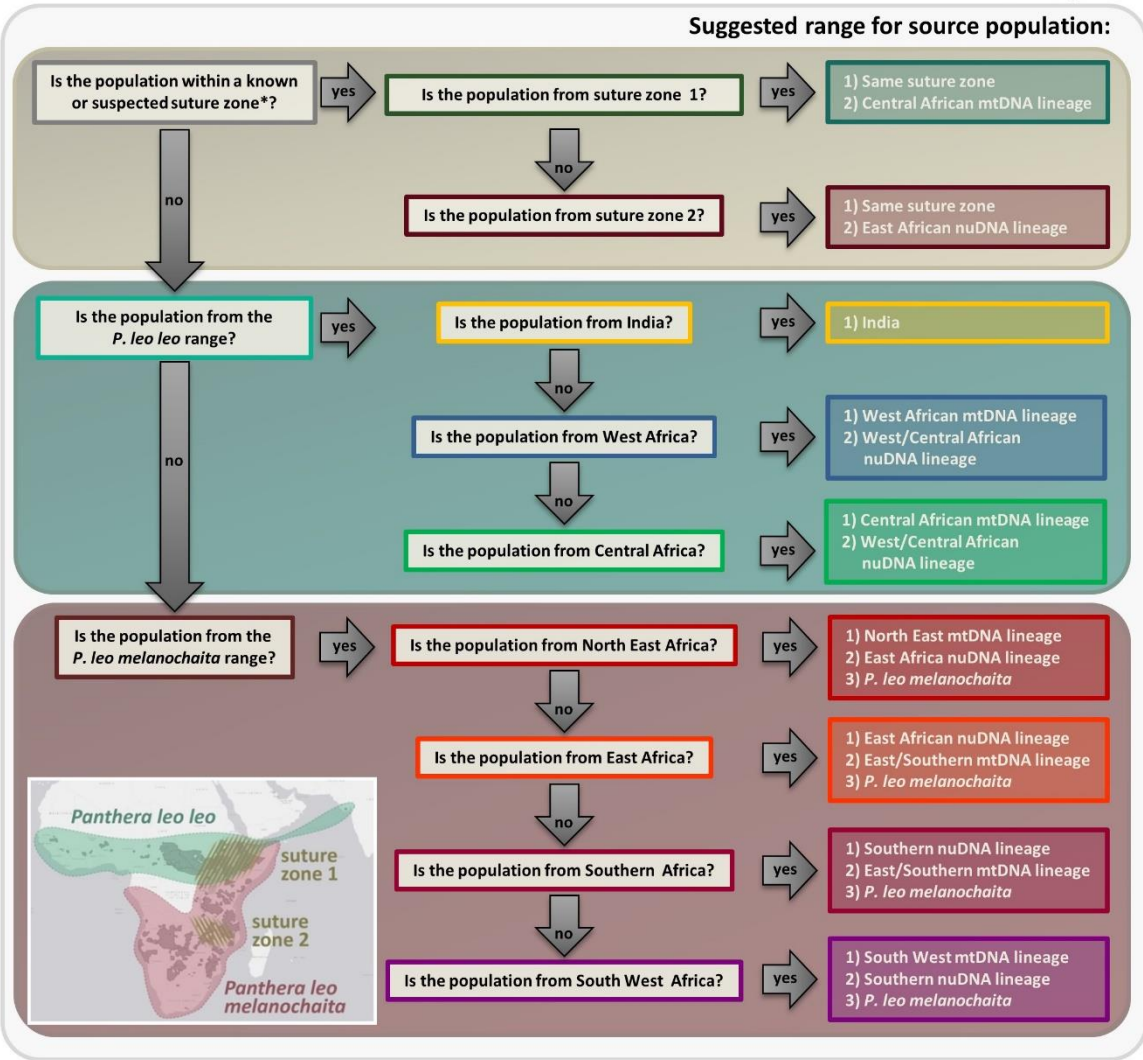
- First choice:** same nuDNA + same mtDNA clade
- Second choice:** same nuDNA, different mtDNA clade
- Third choice:** different nuDNA clade, same subspecies
- No option:** different subspecies + Indian population

We provide a decision making tool (next page) and a matrix (Bertola et al., 2022, Evol. Appl.) in which the score for each possible source/target combination for each of the 132 lion populations is shown.

Current and long term recommendations

The recommendations in our publication and this Decisions Guide are based on data currently available and the current on the ground situation for lion populations. These can be subject to change if new insights are gained or the situation regarding these populations changes (e.g. no suitable source populations available). Please feel free to contact us for up to date information. Contact details below.

Questions refer to the target population  
for a potential lion conservation translocation



\* Known/inferred suture zones:  
1) Sudan, South Sudan and Ethiopia (suture *P. leo leo* and *P. leo melanochoita*);  
2) Zambia, Malawi, Mozambique (suture East and Southern African nuDNA lineages)

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Contact

For more information, please read our paper (Open Access): Bertola L.D., Miller S.M., Williams V.L., Naude V.N., Coals P., Dures S.G., Henschel P., Chege M., Sogbohossou E.A., Ndiaye A., Kiki M., Gaylard A., Ikanda D.K., Becker M.S., Lindsey P. (2022) Genetic guidelines for translocations: Maintaining intraspecific diversity in the lion (*Panthera leo*). Evolutionary Applications , 15(1), 22-39. DOI: 10.1111/eva.13318, or contact us. Laura Bertola:

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