

Clinal variation and genetic diversity loss in a genetically distinct subpopulation of
Southern African lions (*Panthera leo*)

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While African lions (*Panthera leo*) as a whole are listed as threatened by the International Union for Conservation of Nature (Bauer et al., 2018), and despite restrictions of gene flow due to anthropogenic pressures such as habitat fragmentation, a new study by the Zoological Society of London reveals that ecological factors can also cause genetic diversity loss. This was found to be the case with a distinct lion subpopulation in Southern Africa.

Dures et al. (2020) of the Institute of Zoology and Imperial College London performed a genetic analysis of a population of 149 lions located in the Kavango-Zambezi Transfrontier Conservation Area (KAZA) in northern Botswana. By examining and analyzing allele frequencies from blood and tissue samples, researchers discovered that clinal variations were causing population fragmentation via gene flow restriction, resulting in a decrease in heterozygosity. In other words, the loss in genetic diversity is being caused by adaptation needs by lions as they adapt to different habitats (Dures et al., 2020).

In this case, researchers identified two populations of lions in KAZA, both of which were found to be slightly genetically different from one another, and both of which were adapted to two different habitats. The small population of wetland lions were located in the wetlands of Botswana's Okavango Delta, while the larger population of dryland lions were observed in the country's semi-arid Kalahari Desert (Dures et al., 2020). While the small wetland lion population has adapted to the Okavango's many waterways, using them as navigational points from which to hunt prey, dryland lions exist along a different spatial gradient, known as a cline, similar to lions found elsewhere on the African continent. Put simply, a cline can be viewed as an ecological and evolutionary consequence to local adaptation when selection and migration act accordingly (Manel et al., 2003).

It should be stressed that despite the fact that the wetland lion population are not genetically different enough to be considered a distinct lion subspecies, there are still enough genetic differences that led to phenotypic plasticity, or certain changes in the behavior, physiology, and morphology of an organism responding to a new environment (Price, Qvarnström & Irwin, 2003; Dures et al., 2020).

Recall that larger species populations are more strongly associated with greater genetic diversity, while smaller populations are more closely associated with less genetic diversity, leading to deleterious mutations that can negatively impact individual fitness (Makino et al., 2018). At the same time, both lion populations—despite being of the same species—are specifically adapted to two very different habitats. Dures et al. (2020) posit that these two different adaptations by two populations of the same species (wetland vs. dryland) means that ecological factors are restricting gene flow, thus dividing them, “into two genetically distinct clusters.” Dures et al. (2020) elaborate on this in the following statement:

The partitioning of the wetland lions into a separate genetic cluster, with no obvious restrictions to movement into the dryland areas, strongly suggests the need to consider lions from Okavango Delta as a somewhat isolated subpopulation.

Consider not only how local adaptations and gene flow correlate with the ability of heterogeneous landscape to structuring species populations (Manel et al., 2003), but also think about the implications for conservation science and wildlife management strategies.

Hypothetically, if wildlife managers were to relocate a sample population of the lion population from the wetland habitat to the dryland habitat to improve genetic diversity, the wetland lions might not be able to successfully adapt to their new, semi-arid surroundings.

One could argue that the historical emigration of lions from the Kalahari population into the wetland habitat of KAZA is an example of the founder effect, where a loss in genetic variation is the result of a new, colonizing population separating from a larger population, leading to genotypic differences (Joly, 2011). Thinking about the wetland lion population, this could lead to a decrease in heterozygosity.

To promote genetic diversity and protect the species from genetic drift, conservation biologists should consider translocating sample populations of *P. leo* to lion populations that utilize similar habitats. For example, Liuwa Plains National Park in western Zambia is a part of the larger Barotse Floodplain, which is ecologically similar to the Okavango Delta, and is considered high in conservation value (UNESCO World Heritage Centre, n.d.). This could potentially enable lions from the KAZA wetlands to more easily transition to the Barotse Floodplain. Further assessments of the ecological similarities of these two habitats and lion population carrying capacities (i.e. density and abundance) in the Barotse Floodplain and Liuwa Plains National Park should be performed to assess the suitability and success for such a translocation.

References

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