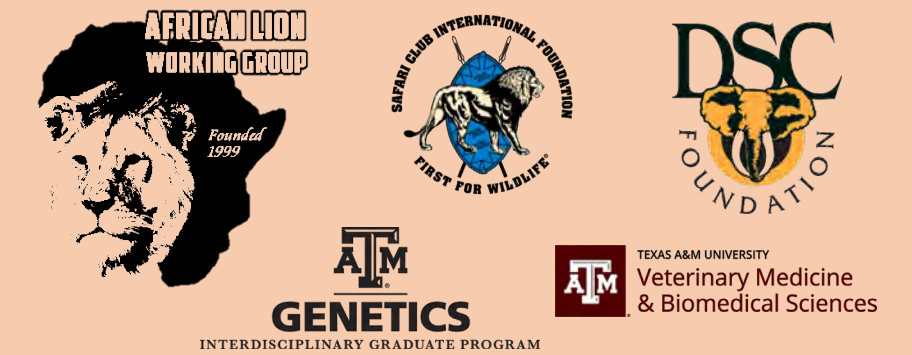


# A DETAILED ANALYSIS OF POPULATION SUBSTRUCTURE AND GENE FLOW IN ZAMBIAN LIONS (*Panthera leo*)

Caitlin J. Curry, Texas A&M University; Paula A. White, Zambia Lion Project; James N. Derr, Texas A&M University

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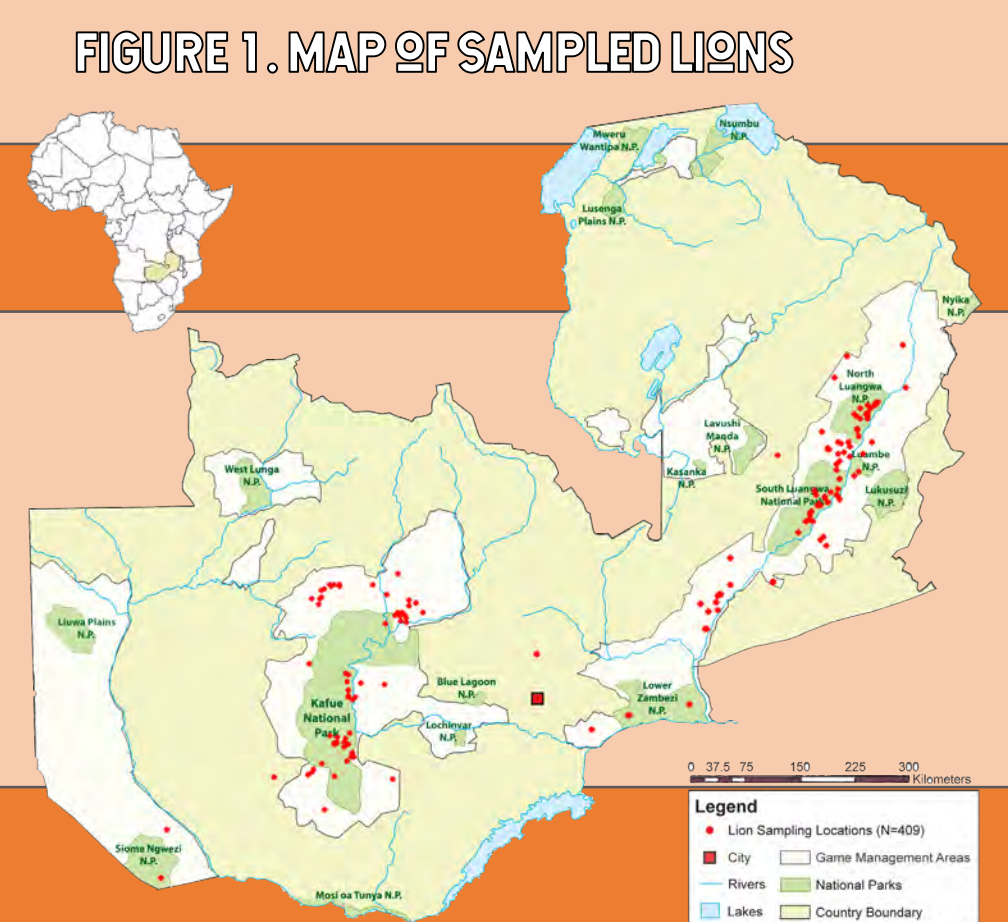


## INTRODUCTION

Zambia has one of the largest lion populations with an estimated census of around 1,200 individuals and range measuring more than 200,000 km<sup>2</sup>. Lions are found throughout the country but can generally be divided into two regions geographical separated by a rift valley and anthropologically separated by the absence of official land management through the central part of the country. The Luangwa Valley in eastern Zambia is a transverse offshoot of the Great Rift Valley system and appears to have an isolating effect as evidenced by speculated endemic subspecies, such as the Cookson's wildebeest and Thornicraft giraffe. Recent mtDNA studies have shown lions in Zambia to consist of two highly diverse eastern and western sub-populations. This study supports this population substructure across Zambia but proposes only partial isolation of the Luangwa Valley with more movement between the populations than previously thought.

## METHODS

We genotyped 14 microsatellites and sequenced the 12S-16S mtDNA genes of 409 lions across Zambia (**Figure 1**) to assess genetic diversity, population structure, and the potential for movement of lions across the country.



## RESULTS

STRUCTURE analysis identifies two populations with little evidence of admixture assigning lions to either the eastern or western sub-populations (**Figure 2**). A high occurrence of private alleles and clear evidence for a Wahlund effect further justify the presence of a highly structured population. But, while mtDNA analysis still shows little to no matrilineal gene flow ( $F_{ST}=0.53$ ) between sub-populations, microsatellite analysis suggests there is gene flow ( $F_{ST}=0.04$ ) with low but significant isolation-by-distance (IBD) and an average of 6 migrants per generation. Evidence of IBD is also found in factorial correspondence analysis (**Figure 3**) with the Lower Zambezi National Park and eastern corridor clusters overlapping isolated clusters of the Luangwa Valley and western sub-population. From this evidence, the Luangwa Valley appears separated from the western sub-population with some dispersal through the southern regions of the eastern sub-population. Both the eastern and western sub-populations have high heterozygosity (0.68 and 0.69, respectively) and genetic diversity (0.4 and 0.50, respectively) values, indicative of genetically healthy populations.

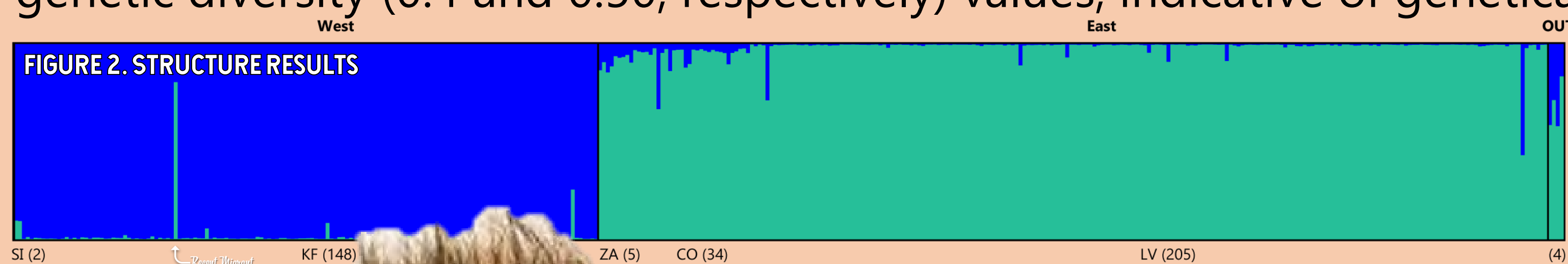


TABLE 1. MEAN MICROSATELLITE DIVERSITY.

	N <sub>Total</sub>	A	AR	PA	PAR	H <sub>O</sub>	H <sub>E</sub>	Signif
Zambia	398	9.79	9.68			0.665	0.701	*
East	150	8.79	8.22	2.21	1.81	0.657	0.682	ns
West	244	7.64	7.51	1.00	1.09	0.677	0.692	ns

N, Sample Size; A, Number of Alleles; AR, Allelic Richness; PA, Number of Private Alleles; PAR, Private Allelic Richness; H<sub>O</sub>, Observed Heterozygosity; H<sub>E</sub>, Expected Heterozygosity  
ns, not significant; \* p-value < 0.05; \*\* p-value < 0.01; \*\*\* p-value < 0.001

## CONCLUSIONS

In Zambia, human-lion conflict is the greatest threat to lions outside of protected areas. Much of the area between the Luangwa Valley in the east and Kafue National Park in the west is unprotected and considered to be uninhabited by lions. However, this study reveals there is movement across this area.

The best management strategy for Zambia is a more narrowed focus to prevent the loss of genetic diversity within sub-populations and, as long as there isn't an increase in human-lion conflict, maintenance of diversity across Zambia should still occur through migration of lions between sub-populations.

