



A Century of Conservation Genetics

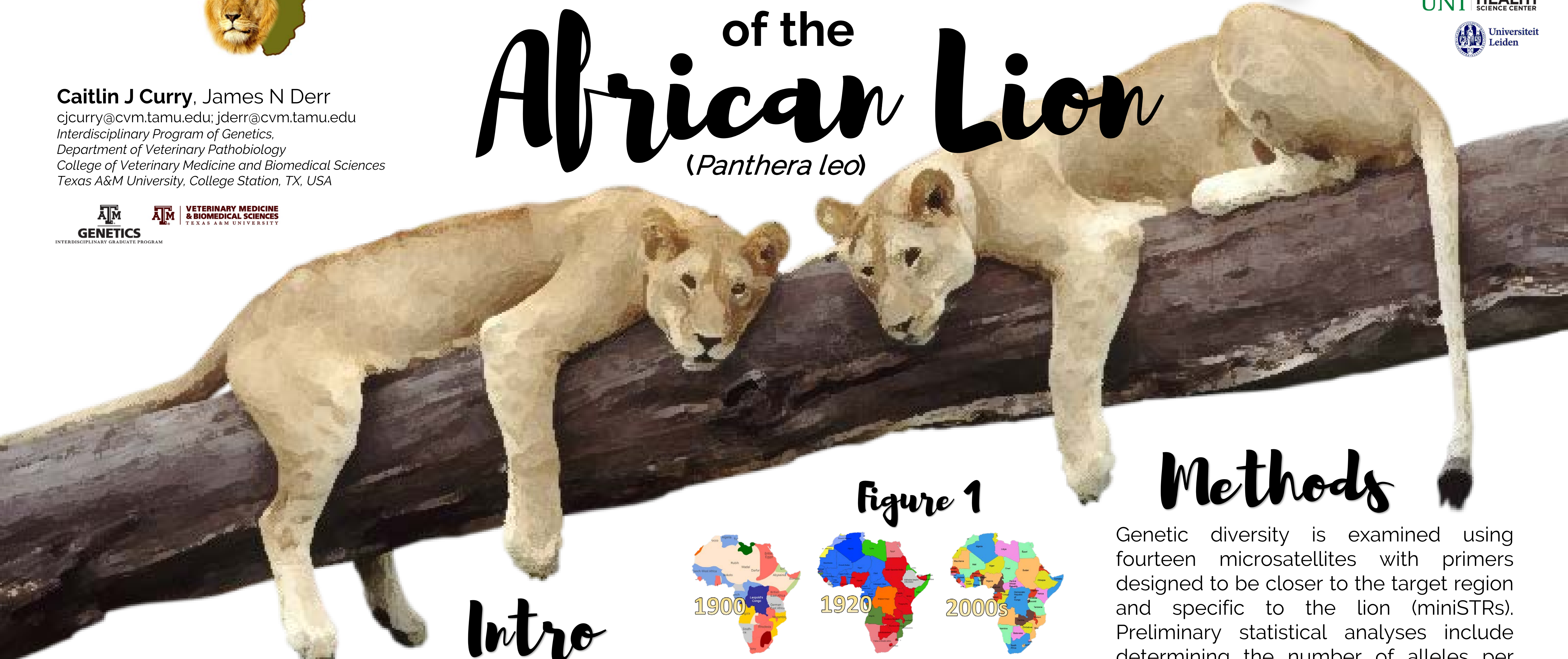


Thank you to:



of the African Lion (*Panthera leo*)

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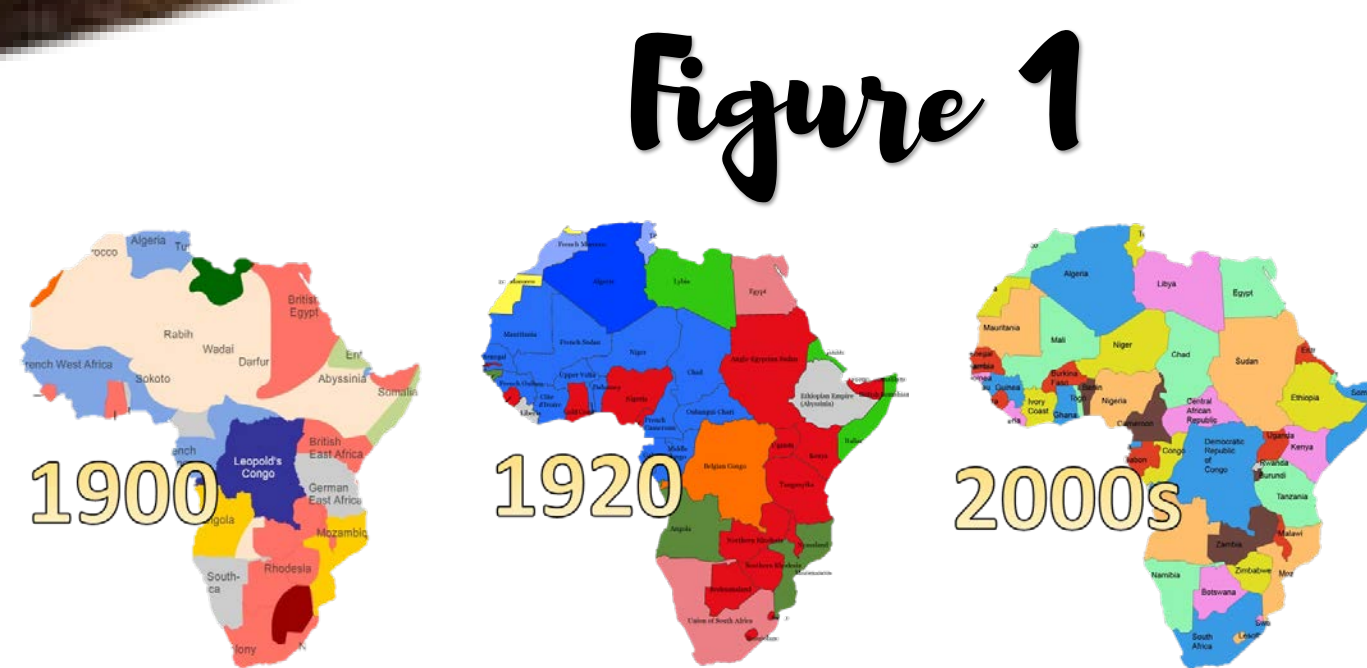


Methods

Genetic diversity is examined using fourteen microsatellites with primers designed to be closer to the target region and specific to the lion (miniSTRs). Preliminary statistical analyses include determining the number of alleles per locus and calculation of expected heterozygosity (*GenAEx*), structural analysis (*Structure*) and determining the most likely number of clusters following the ΔK method (*Structure Harvester*).

Intro

We determined the genetic architecture of both historical (>100 years ago; n=155) and contemporary (2000 to present; n=557) African lion populations across the traditional range states in Africa (*Figure 1*). Both datasets were analyzed using the same methods allowing for a more direct comparison over time than has previously been employed. The historical lion dataset is DNA isolated from high quality and well-documented museum specimens while the contemporary lion dataset is from modern material and data from several recently published studies. Combining the datasets of historical as well as contemporary populations provides quantitative measures on the extent of change in the genetic diversity of lions over the past 100 years and provides a basis for assessing the genetic health of the African lion.



All samples are categorized into 6 conventionally recognized regions:

- North (Historical Only)
- West
- Central
- East
- Southeast
- Southern

Additional sample categories:

- India (Asiatic Lion – *Panthera leo persica*)
- Unknown (Historical Only – Date Provide, No Location)

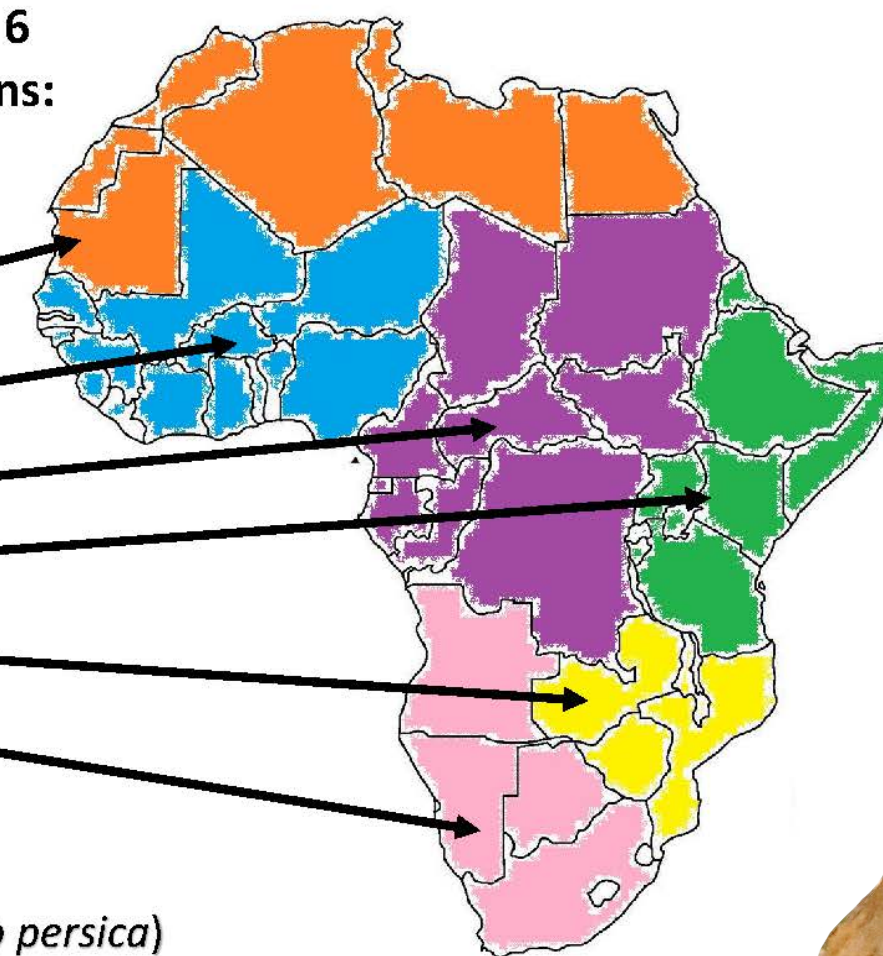


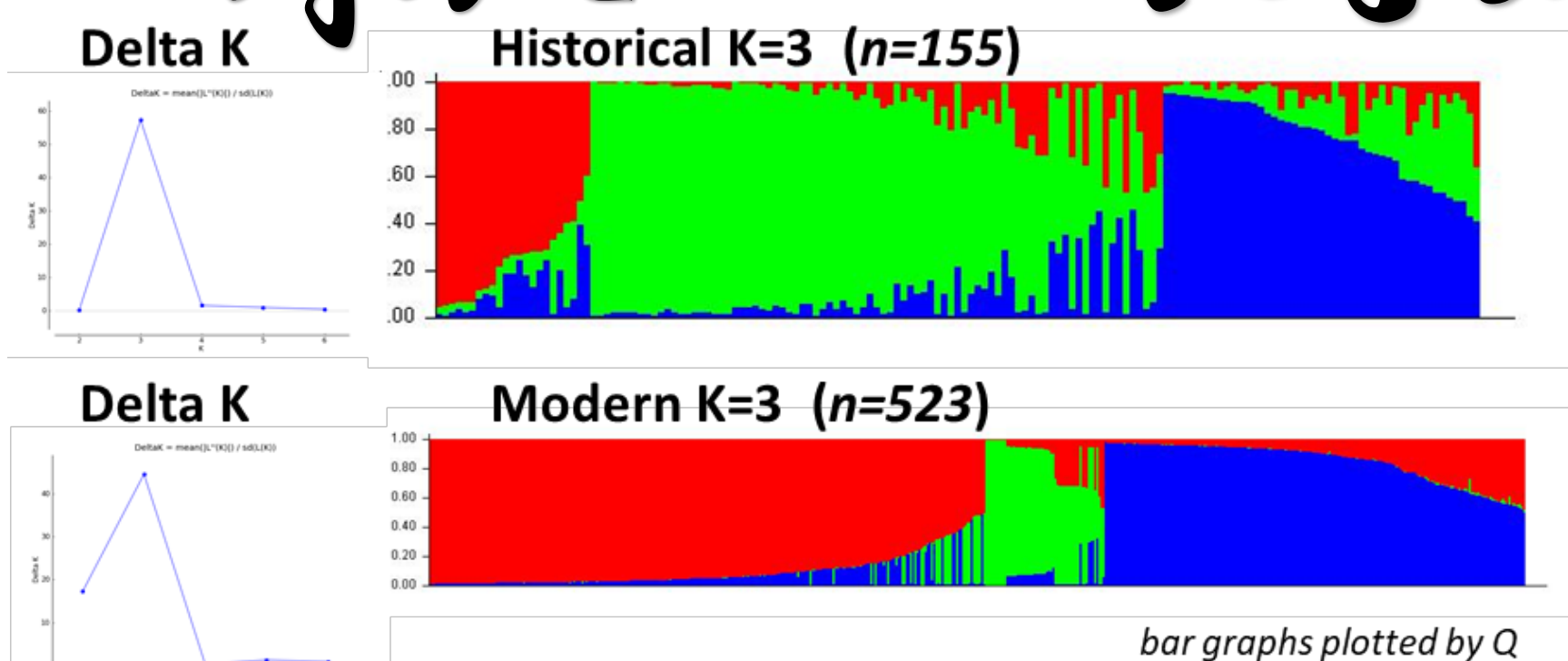
Table 1 Genetic Diversity Overall and By Locus

	Overall	Leo006	Leo008	Leo031	Leo045	Leo077	Leo085	Leo098	Leo126	Leo224	Leo230	Leo247	Leo281	Leo391	Leo506	
%AS	97.5%	98.1%	100.0%	98.5%	92.5%	100.0%	100.0%	99.8%	97.8%	99.0%	86.6%	99.5%	98.3%	99.3%	95.6%	Modern
N	455	476	470	405	410	441	499	469	501	504	415	508	464	408	393	
Na	12	20	8	8	11	9	12	9	16	10	13	10	19	9	10	
He	0.71	0.84	0.75	0.40	0.39	0.75	0.65	0.72	0.78	0.77	0.82	0.82	0.72	0.74	0.81	Historical
%AS	83.3%	87.1%	97.4%	76.8%	88.4%	85.2%	98.1%	95.5%	91.6%	99.4%	77.4%	94.2%	76.8%	60.6%	38.1%	
N	129	135	151	119	137	132	152	148	142	154	120	146	119	94	59	
Na	16	24	15	12	21	10	16	11	24	13	11	18	22	10	16	
He	0.81	0.90	0.81	0.73	0.59	0.83	0.80	0.82	0.86	0.84	0.85	0.83	0.84	0.84	0.82	

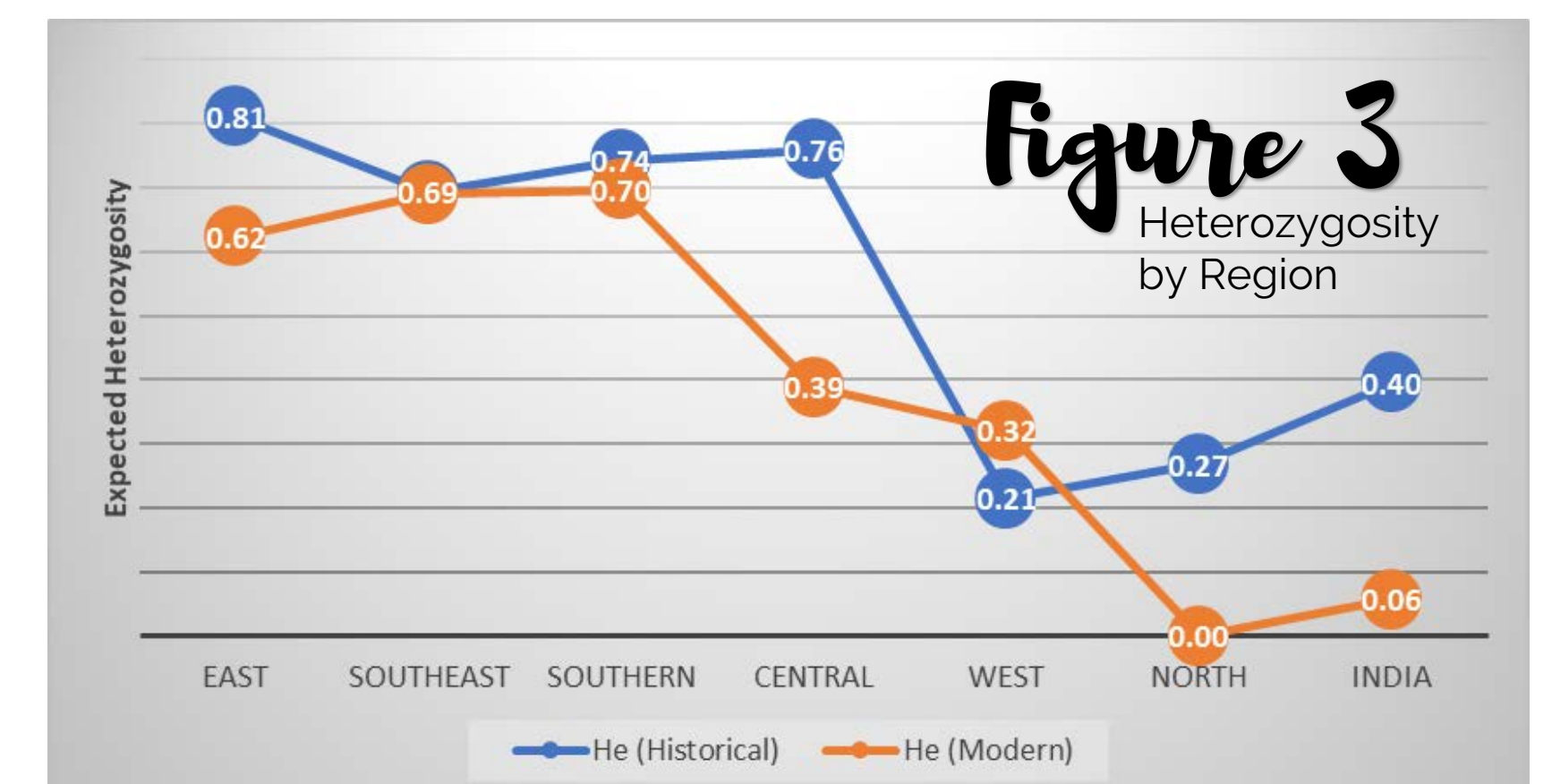
%AS = Amplification Success; Na = No. of Different Alleles; He = Expected Heterozygosity

Results

Figure 2



The historical and modern populations both have high levels of overall genetic diversity (*Table 1*). They also exhibit similar trends in population structure (*Figure 2*). Heterozygosity by region (*Figure 3*) supports observations from recent studies of a precipitous decline in population size occurring in West and Central Africa.



Further analysis will include the addition of mtDNA haplotypes. A phylogeographic analysis will be performed along with estimation of effective population size (N_e) and calculation of genetic differentiation between regions (F_{st}).