

The genetic structure of pastoralists in Northern Kenya

Angela M. Taravella^{1,2}, Carla Handley³, Emma K. Howell^{1,2}, Anne C. Stone^{1,2,3}, Sarah Mathew³, and Melissa A. Wilson^{1,2}

¹School of Life Sciences, Arizona State University, Tempe, AZ 85281, USA

²Center for Evolution and Medicine, Arizona State University, Tempe, AZ 85281, USA

³School of Human Evolution and Social Change, Arizona State University, Tempe, AZ 85281, USA



amtarave@asu.edu



Background

Genetic analyses across human populations in Africa have shed light onto the details of major population movements and migrations within Africa. However, the genetic history and how it relates to cultural practices and social organization among human populations in Africa on a local geographic scale remain relatively unexplored. The **Borana**, **Rendille**, **Samburu**, and **Turkana** are neighboring pastoral populations inhabiting Northern Kenya (**Figure 1**). They have male clan descent, are partially or fully patrilocal, and practice exogamy at either the clan or moiety kinship level. Further, when a female marries, they become culturally affiliated with their husbands clan. Linguistically, the Turkana and Samburu speak Eastern Nilotic languages while the Borana and Rendille speak Cushitic languages. **The aim of this project is to characterize the genetic relationships within and among Northern Kenyan human populations in light of cultural relationships and marital practices.**

Methods

Sampling
378 individuals
(Table 1)
Illumina's Multi Ethnic
Global Array

Quality control

Population genetic analyses

Visualization of genetic
structure

Principal
components
analysis
(Figure 1)

ADMIXTURE
(Figure 2)

Calculation of genetic
differentiation

Sex stratified clan based F_{st}
across autosomes and X
Chromosome
(Figure 3)

Population	Cultural Clan Affiliation	Total	# Males	# Females
Borana (87)	Nonituu	32	18	14
	Warjidda	35	20	15
Rendille (61)	Ldupsai	23	11	12
	Saale	27	13	14
Samburu (48)	Lpsikishu	21	12	9
	Lukumai	18	11	7
Turkana (167)	Ngidoca	46	30	16
	Ngipongaa	41	27	14
	Ngisiger	46	26	20

Table 1. Sample information. We sampled individuals from at least 2 clans in each population characterize culturally informed clan based genetic differentiation.

Results

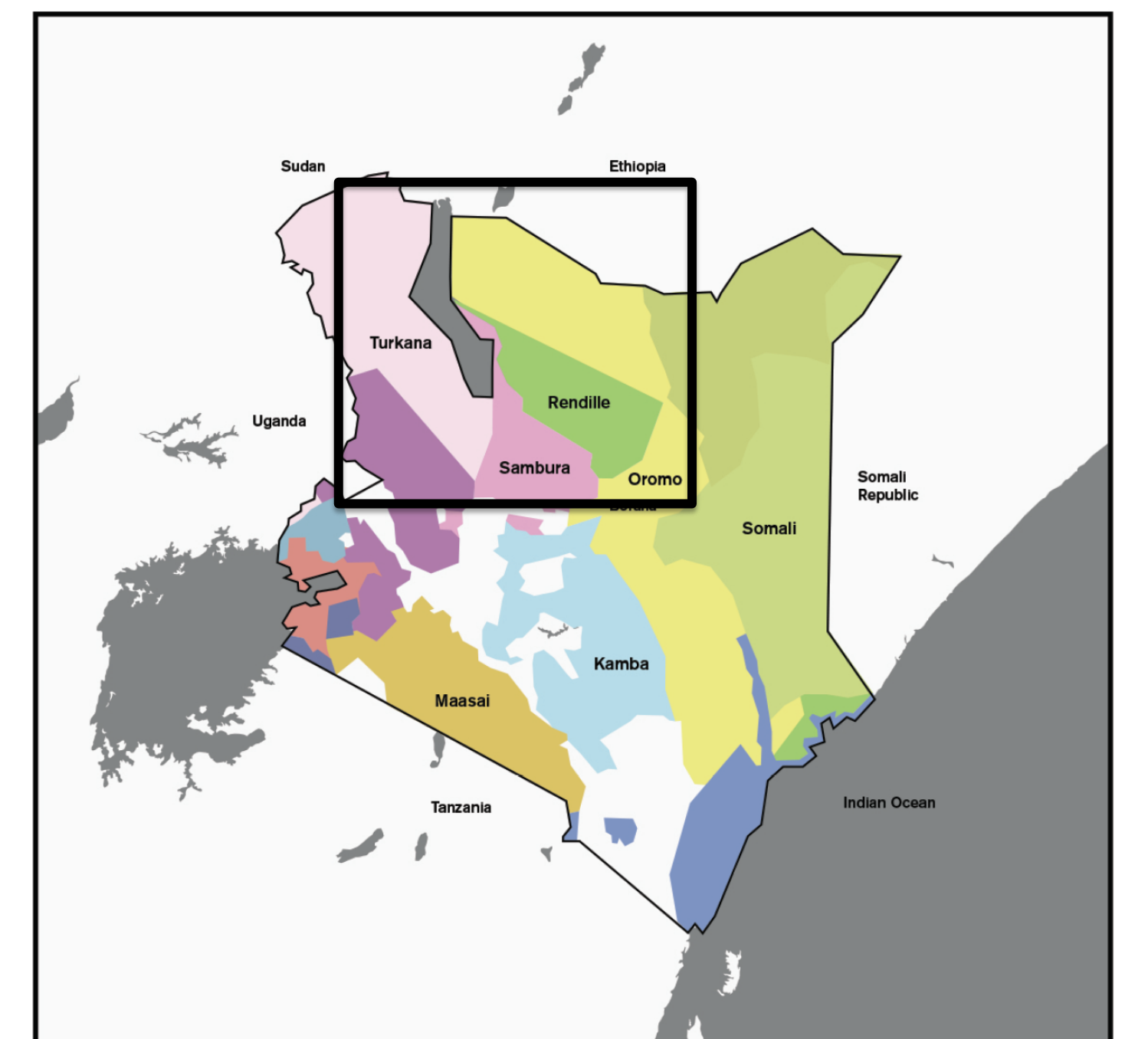
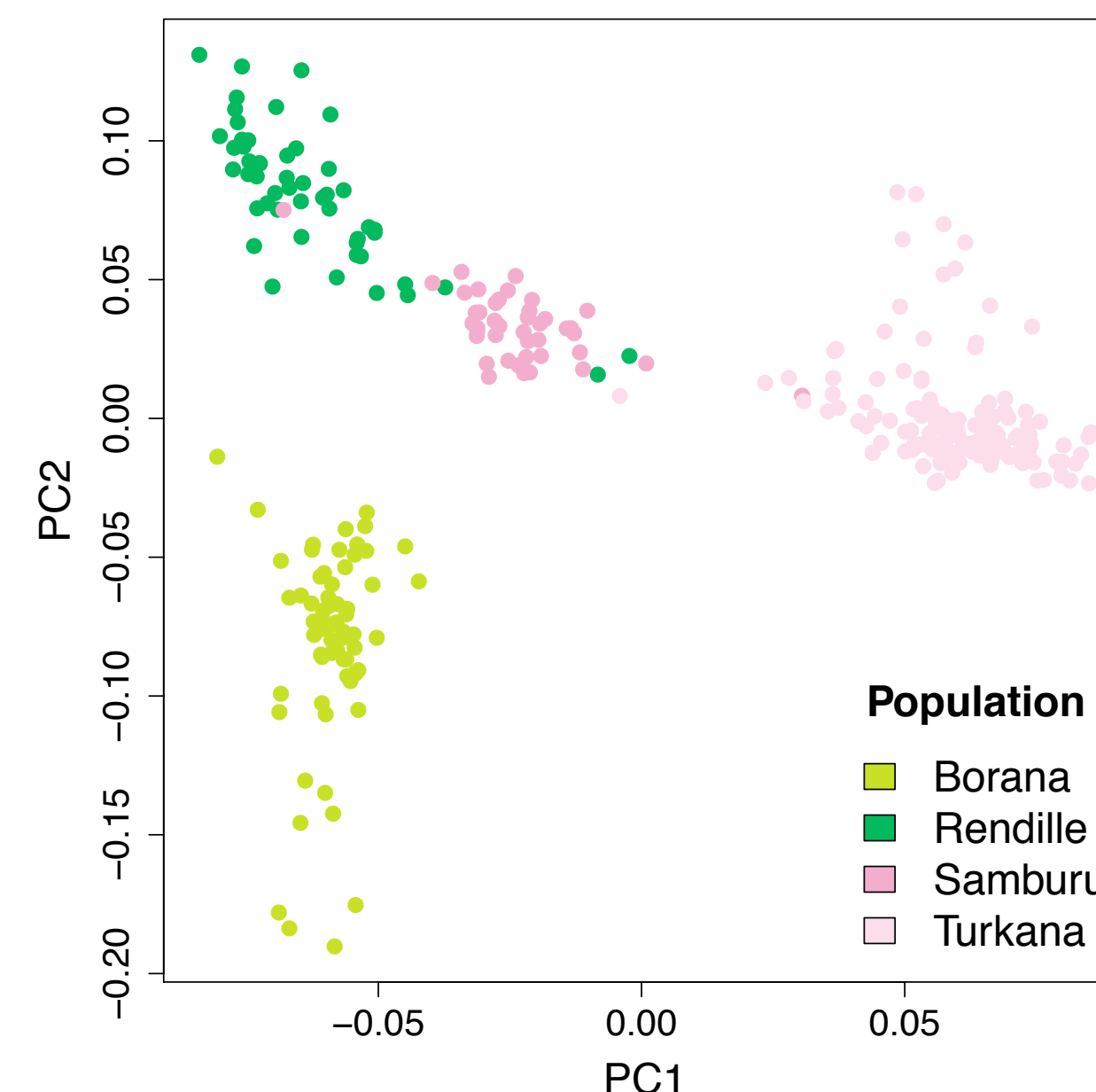


Figure 1. Genetic variation mirrors geography among Northern Kenyan pastoralists. The map (right), adapted from³, highlights the major populations in Kenya, a country in east Africa. We performed principal components analysis (left) to visualize the genetic structure among these groups. Each point represents an individual, colored by population affiliation.

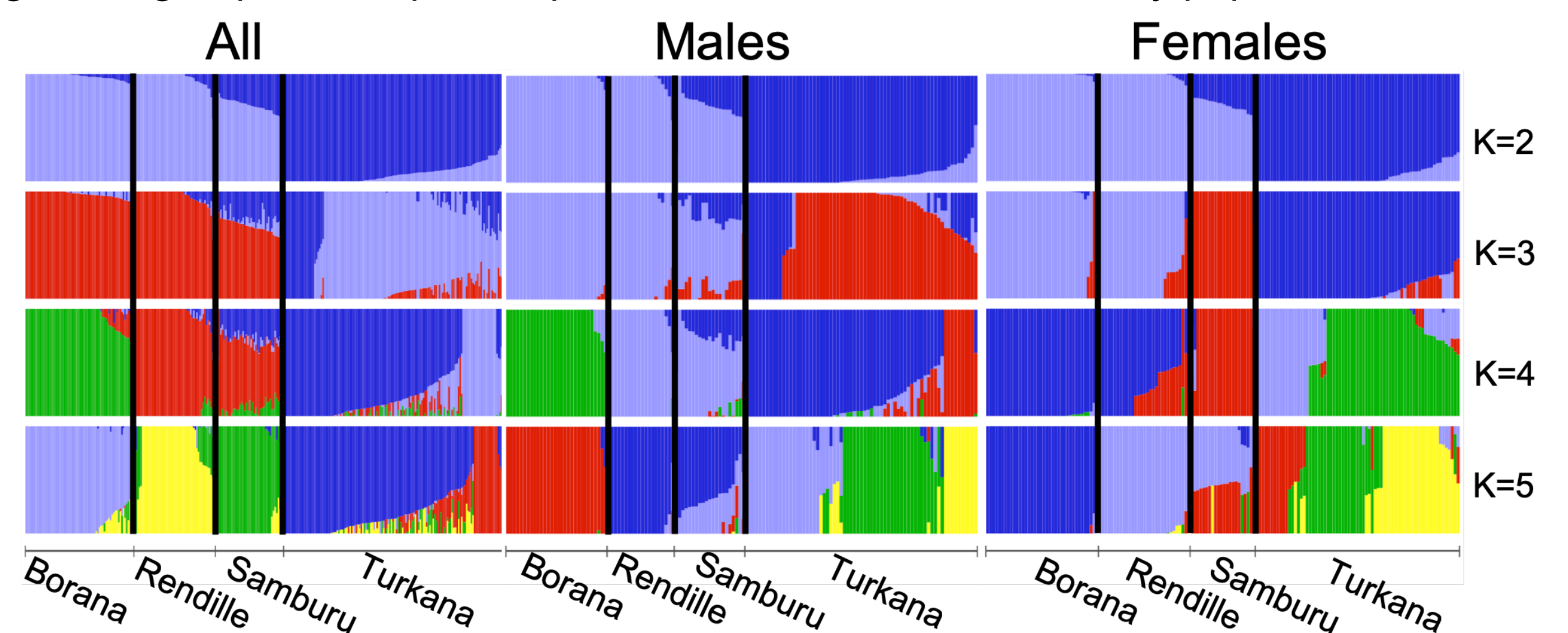


Figure 2. ADMIXTURE analysis shows evidence for a shared genetic ancestry between the Rendille and Samburu, populations from different language families. To explore the genetic structure of Northern Kenyan populations, we ran ADMIXTURE² for K = 2-5 for the all samples (left), males (middle) and females (right). Each vertical bar represents an individual, the colors represent the proportion of ancestry corresponding K.

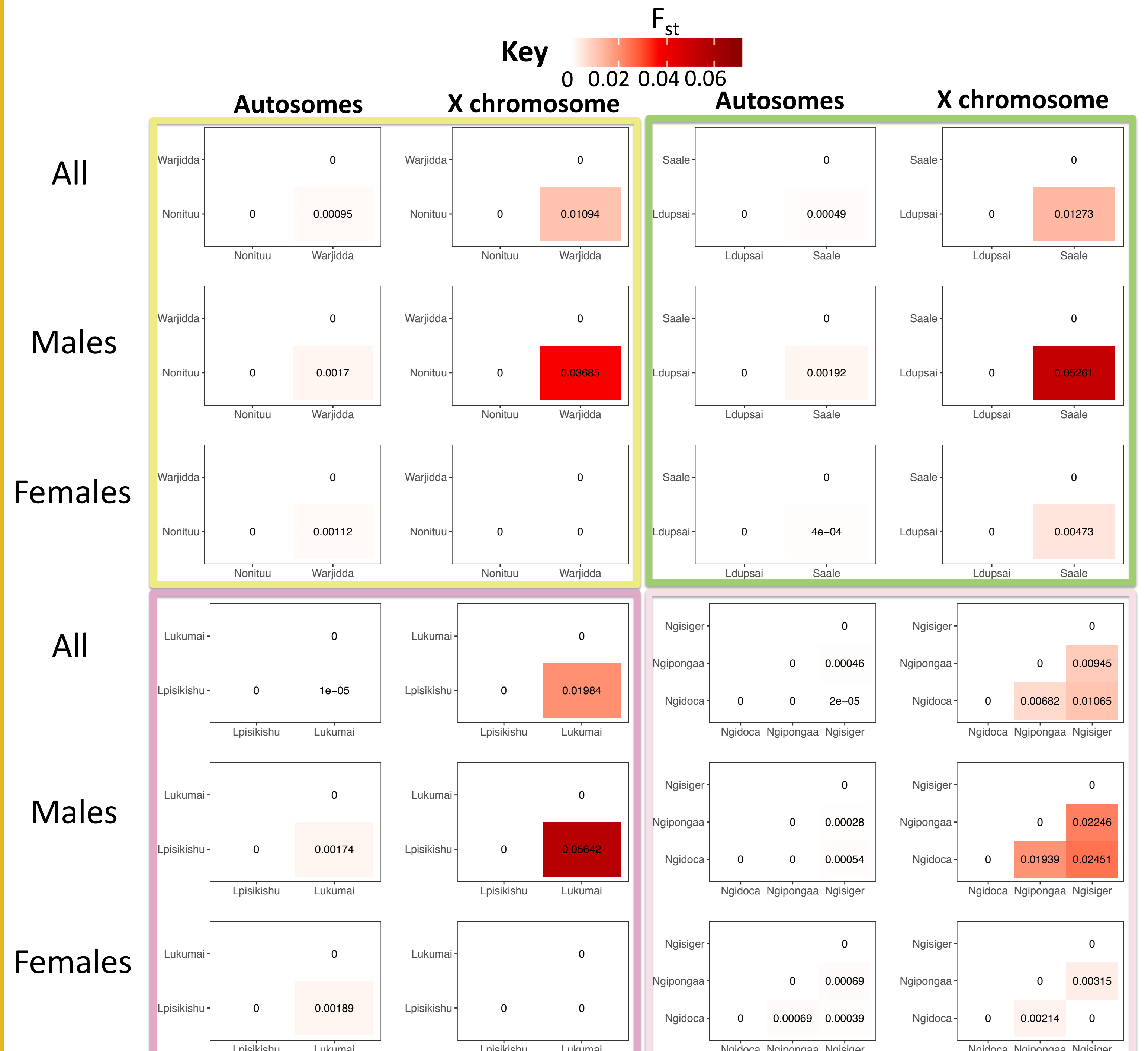


Figure 3. Inconsistent patterns of clan-based genetic F_{st} and cultural practices. To understand how cultural patterns relate to genetic variation, we calculated genetic differentiation as F_{st} across the autosomes and X chromosome among clans for each population – colored boxes corresponding to populations in figure 1. In a patrilocal society we expect more genetic differentiation for males and less for females. Although X chromosome F_{st} is consistent with these expectations, autosomal F_{st} is variable.

Conclusions and Future Directions

- Genetic variation mirrors geography in Northern Kenya
- Shared genetic relationship between Rendille and Samburu
- Future analyses: 1) analyzing genetic variation of uniparental markers – Y chromosome and mitochondrial DNA – within and among Northern Kenyan populations, and 2) evaluate the correspondence between genetic, cultural, geographic, and linguistic relationships

References

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