Population Structure of *G. pallidipes* Tsetse Flies in Northwestern Kenya _ Towards Effective Vector Control

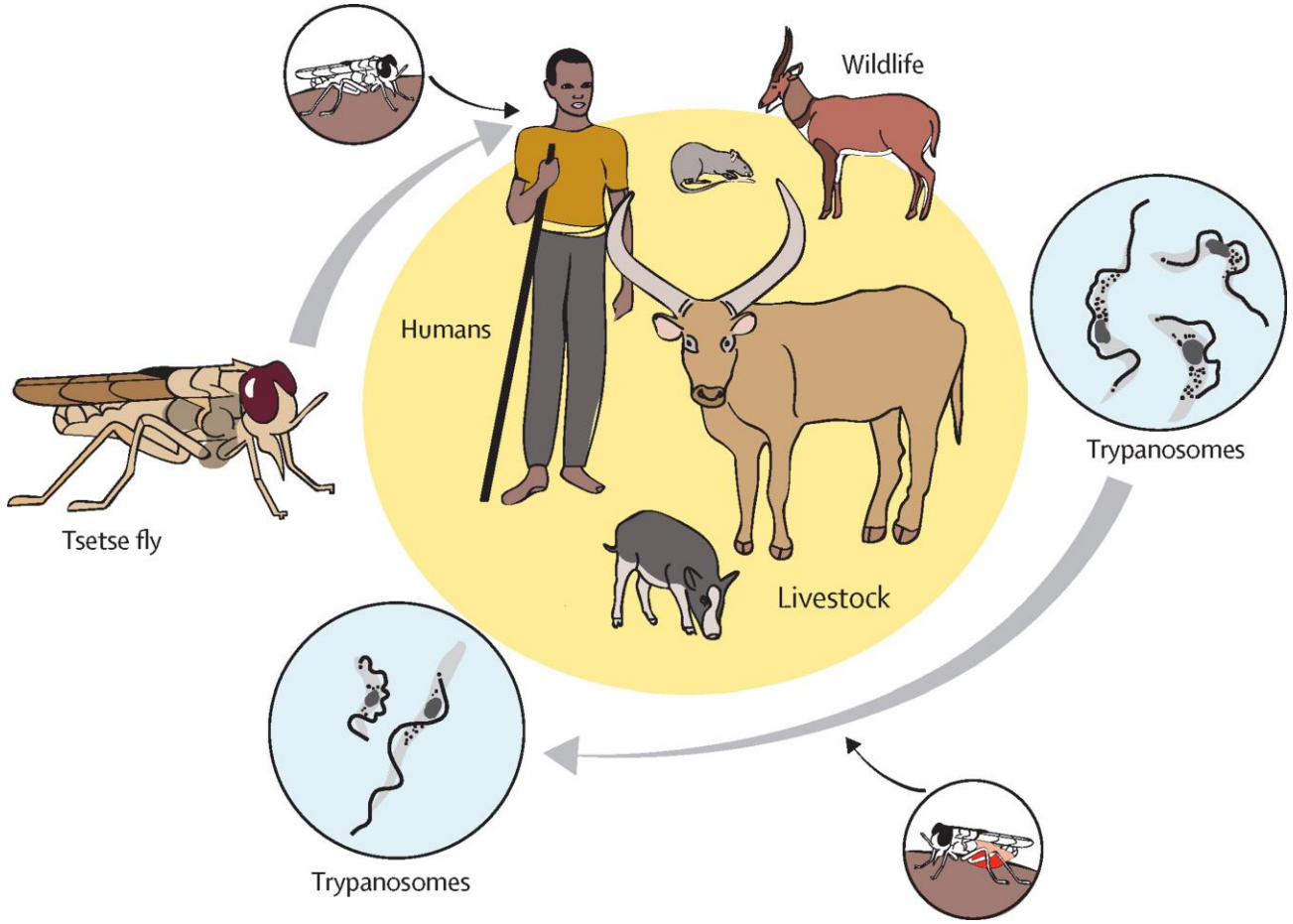
Winnie A. Okeyo*[a], Sylvia Korir[b], Daniel Ochieng' Gamba[b], Miriam Jemutai[a], Samuel Onyoyo Guya[c], David N. Ndung'u[d], Paul Mireji Odhiambo[a,e], Rosemary Bateta[a]

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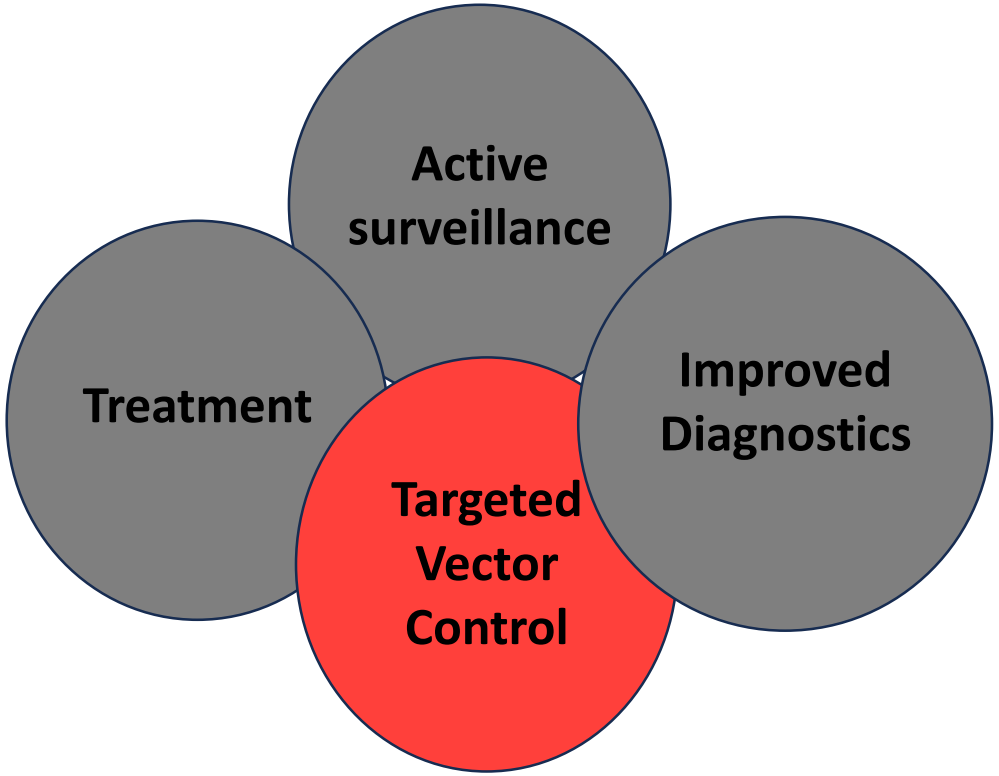
37TH ISCTRC CONFERENCE

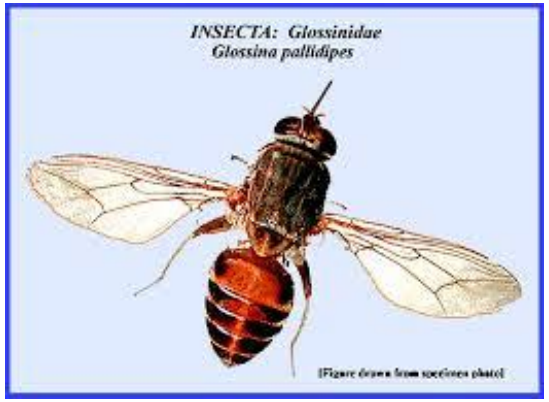
NAIROBI, KENYA, 15TH TO 19TH SEPTEMBER

Background

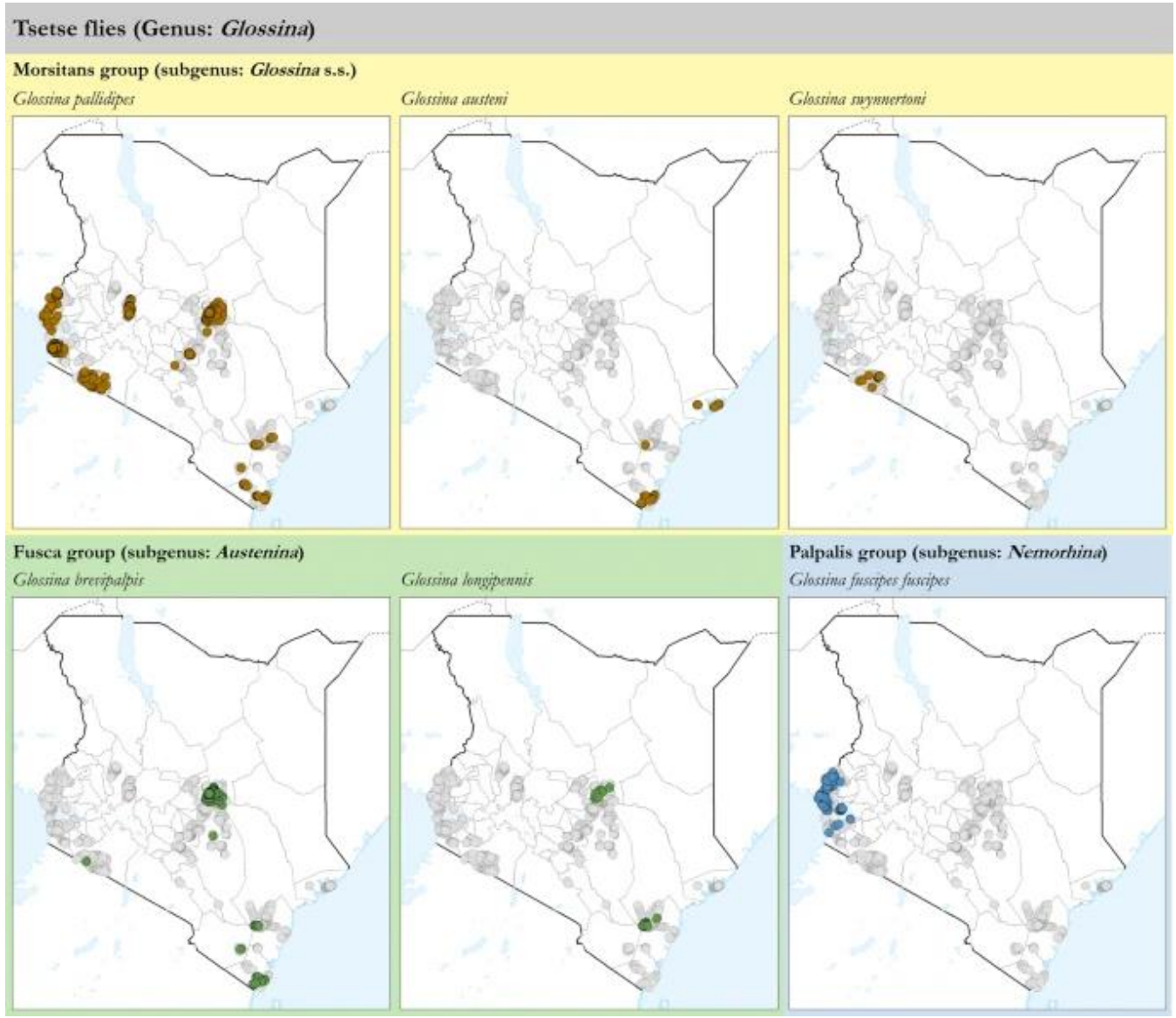


Lejon, Veerle et al., 2025

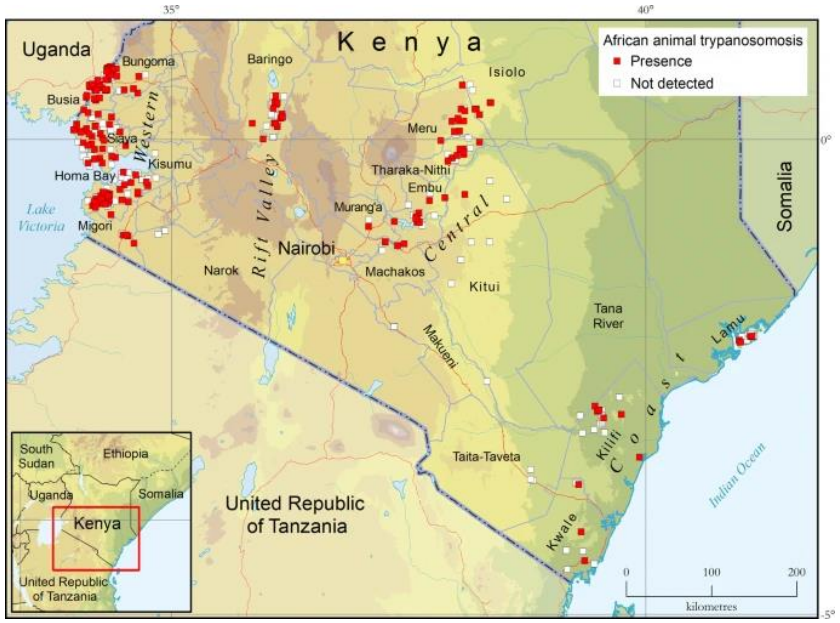




Current tsetse fly/trypanosomiasis distribution



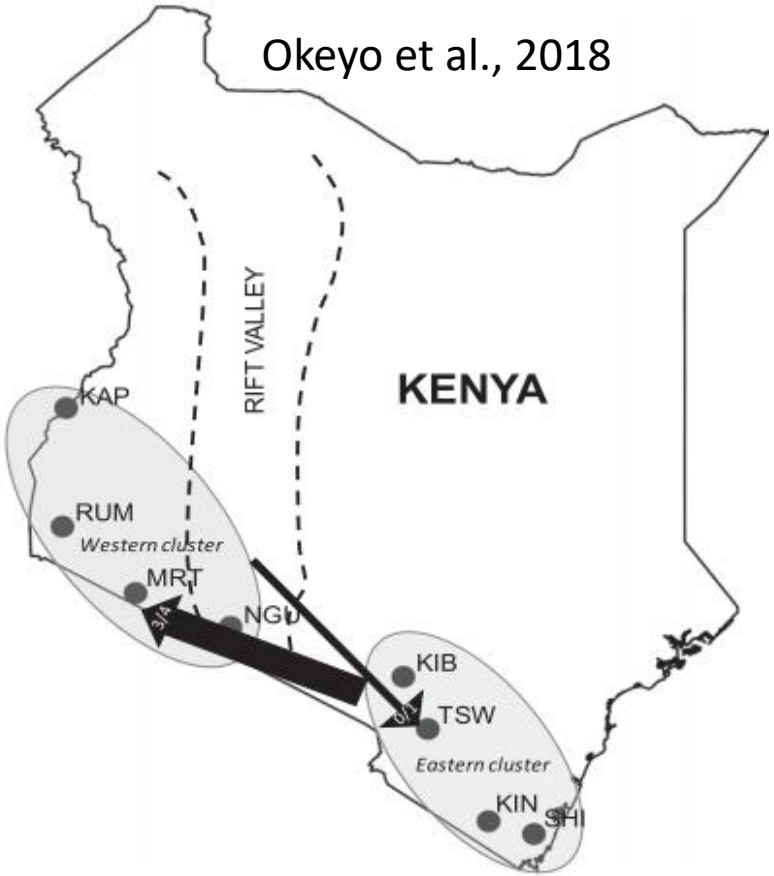
Animals screened for AAT



Ngari et al., 2020

Previous work

Okeyo et al., 2018



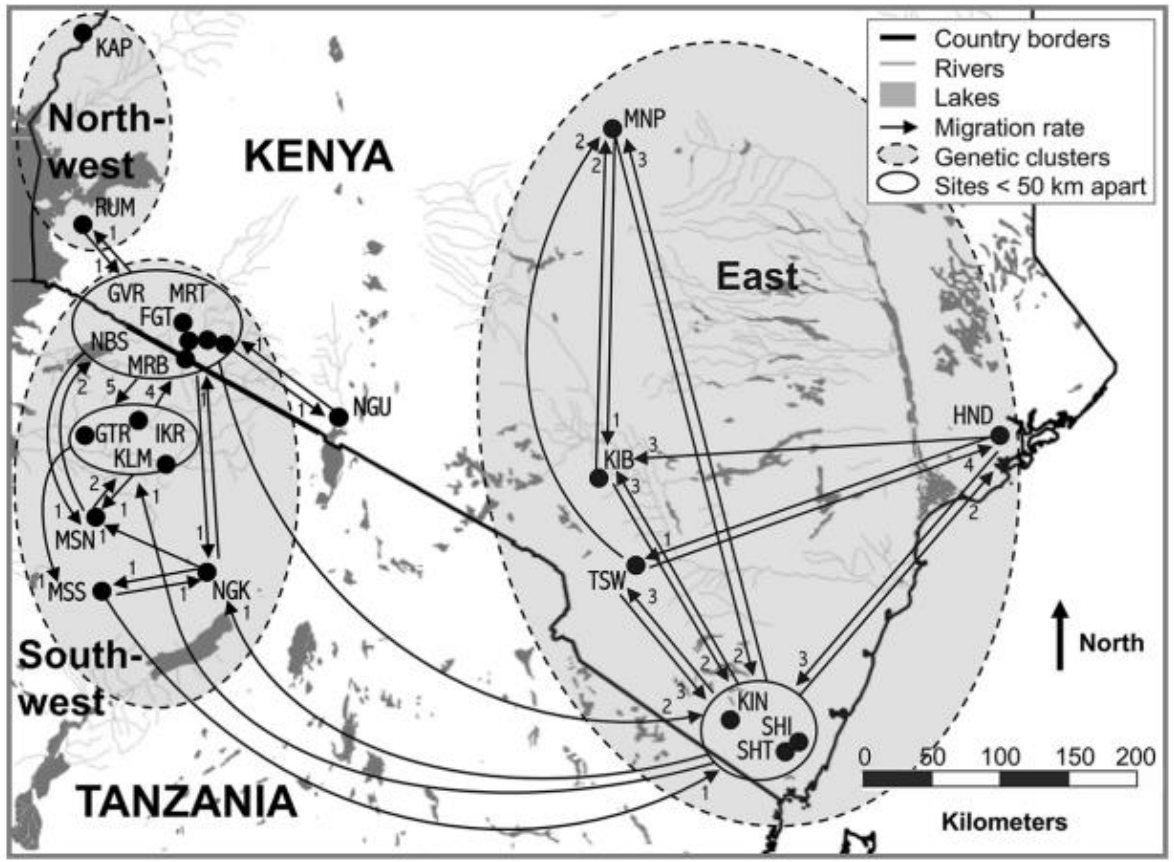
Genetic Differentiation of *Glossina pallidipes* Tsetse Flies in Southern Kenya

Winnie A. Okeyo,[1,2,3]*† Norah P. Saarman,[4]† Rosemary Bateta,[2] Kirstin Dion,[4] Michael Mengual,[4] Paul O. Mireji,[2,3,5] Collins Ouma,[1] Sylvance Okoth,[2] Grace Murilla,[2,3] Serap Aksoy,[3] and Adalgisa Caccone[3,4]

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Abstract. The tsetse fly *Glossina pallidipes*, the major vector of the parasite that causes animal African trypanosomiasis in Kenya, has been subject to intense control measures with only limited success. The *G. pallidipes* population dynamics and dispersal patterns that underlie limited success in vector control campaigns remain unresolved, and knowledge on genetic connectivity can provide insights, and thereby improve control and monitoring efforts. We therefore investigated the population structure and estimated migration and demographic parameters in *G. pallidipes* using genotypic data from 11 microsatellite loci scored in 250 tsetse flies collected from eight localities in Kenya. Clustering analysis identified two genetically distinct eastern and western clusters (mean between-cluster $F_{ST} = 0.202$) separated by the Great Rift Valley. We also found evidence of admixture and migration between the eastern and western clusters, isolation by distance, and a widespread signal of inbreeding. We detected differences in population dynamics and dispersal patterns between the western and eastern clusters. These included lower genetic diversity (allelic richness; 7.48 versus 10.99), higher relatedness (percent related individuals; 21.4% versus 9.1%), and greater genetic differentiation

Bateta et al., 2020



PLOS | NEGLECTED TROPICAL DISEASES

RESEARCH ARTICLE

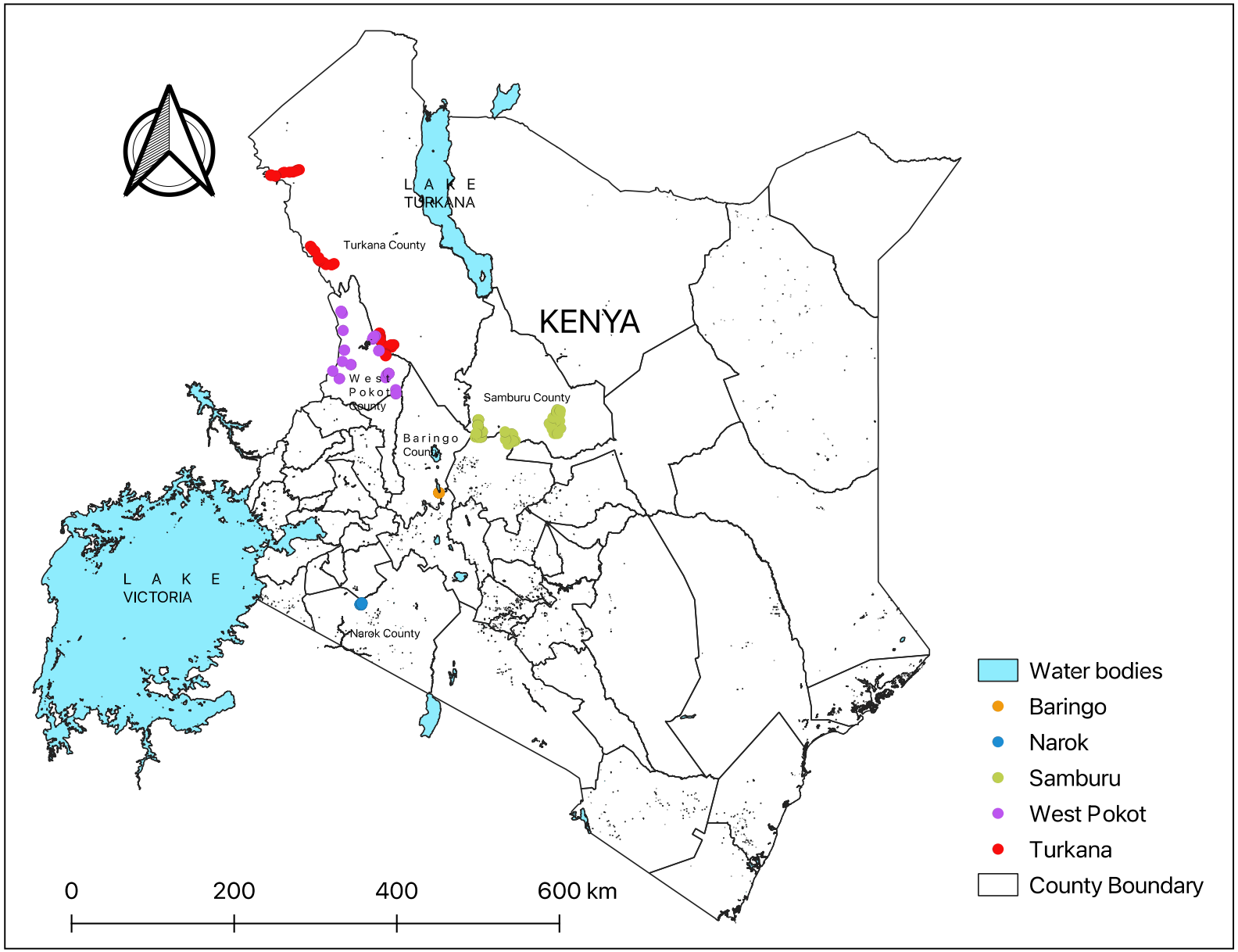
Phylogeography and population structure of the tsetse fly *Glossina pallidipes* in Kenya and the Serengeti ecosystem

Rosemary Bateta[1☯], Norah P. Saarman[2☯*], Winnie A. Okeyo[1,3], Kirstin Dion[2], Thomas Johnson[2], Paul O. Mireji[1,4], Sylvance Okoth[1], Imna Malele[5], Grace Murilla[1], Serap Aksoy[6], Adalgisa Caccone[2]

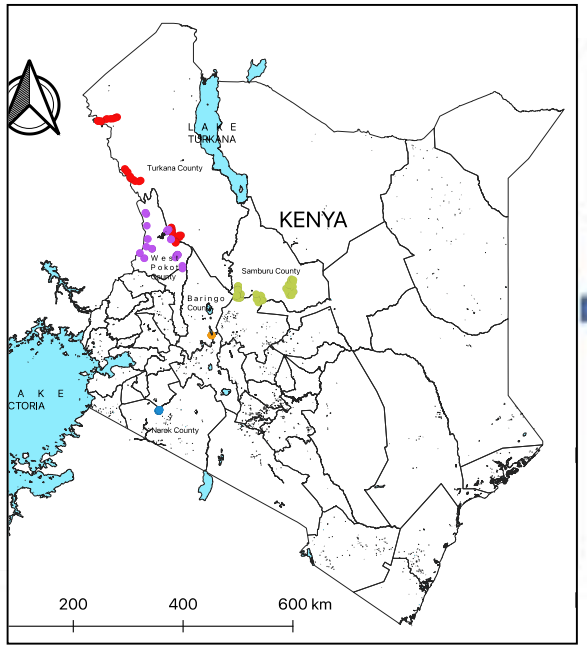
1 Biotechnology Research Institute, Kenya Agricultural and Livestock Research Organization, Kikuyu,

Methodology

Study sites



Data collection









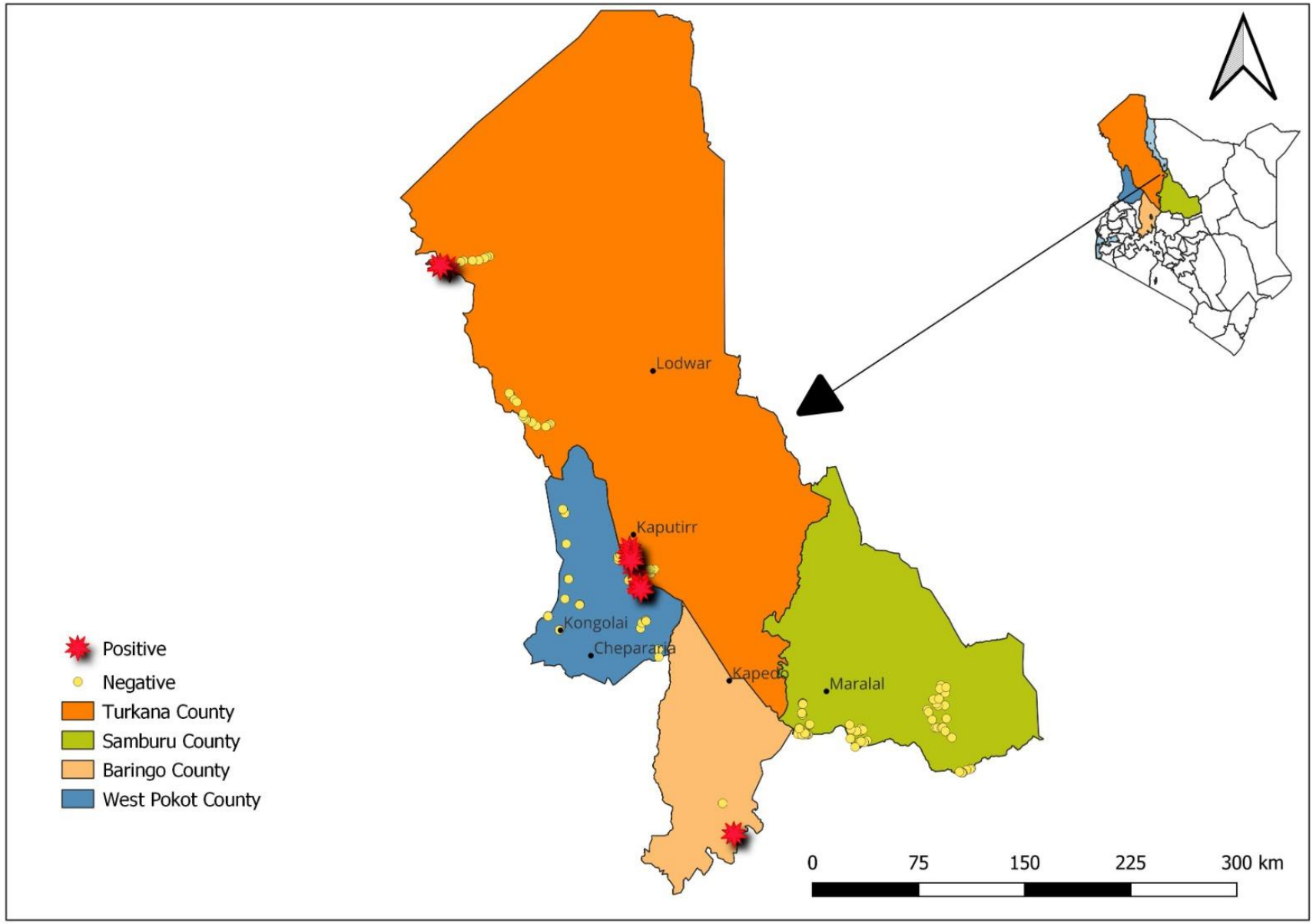






Results

Presence/absence



Genetic Diversity

Site Name	ID	Lat	Long	N	Year	AR	H_O	H_E	F_{IS}	F_{IS} p-value
Kapesur	KAP	0.733	34.316	30	2016	3.271	0.386	0.512	0.25	**0.0004**
Ruma	RUM	-0.608	34.307	30	2016	2.701	0.348	0.413	0.16	**0.0012**
Maasai Mara	MMR	1.435	35.065	30	2015	4.065	0.491	0.571	0.143	**0.0004**
Nguruman	NGU	-1.977	36.117	48	2015	3.078	0.488	0.505	0.035	0.1746
Meru National Park	MNP	0.077	38.064	30	2016	5.373	0.553	0.666	0.172	**0.0004**
Kibwezi	KIB	-2.416	37.954	30	2015	5.369	0.561	0.654	0.144	**0.0004**
Tsavo West	TSW	-3.027	38.218	30	2015	5.267	0.519	0.647	0.199	**0.0004**
Kinango	KIN	-4.108	38.874	30	2015	5.406	0.434	0.693	0.377	**0.0004**
Shimba Hills NP	SHI	-4.152	39.420	30	2015	5.217	0.535	0.650	0.179	**0.0004**
Hindi	HND	-2.117	40.791	30	2016	4.802	0.545	0.634	0.143	**0.0004**
Kainuk	KAI	1.962	35.459	16	2020	3.680	0.378	0.501	0.252	**0.0004**
Oropoi	ORO	3.781	34.242	14	2020	4.291	0.535	0.606	0.124	**0.0135**

Study site identity (ID), Latitude and Longitude (Lat, Long), samples per site (N), year of collection (Year), AR (Allelic Richness), Observed and expected heterozygosity (H_o and H_e), coefficient of inbreeding (F_{is}) and its corresponding p-value

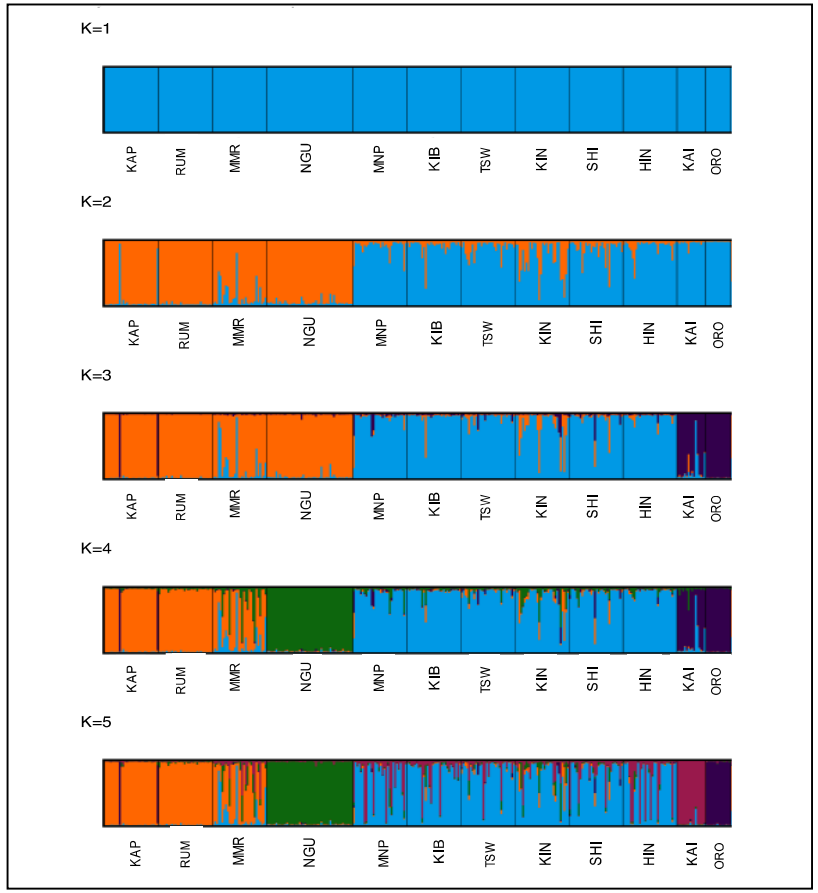
Effective Population size and Bottlenecks

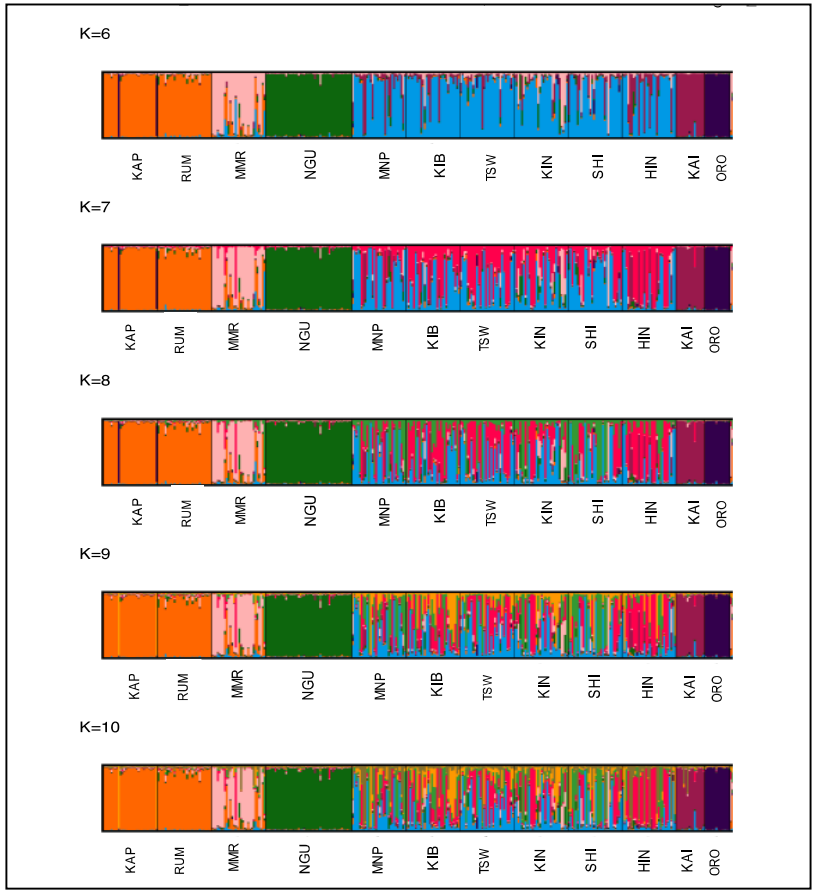
Site Name	Ne	Ne CI	Bottleneck Analysis		
			IAM	TPM	SMM
Kapesur	2.3	1.9 - 2.9	**0.020**	0.121	0.346
Ruma	214.6	30.9 - ∞	**0.024**	0.131	0.635
Maasai Mara	110.1	42.1 - ∞	**0.015**	**0.024**	0.325
Nguruman	1852.8	94.3 - ∞	0.056	0.088	0.251
Meru National Park	45.3	28.0 - 95.9	**0.002**	**0.034**	0.587
Kibwezi	71.0	43.2 - 165.0	**0.002**	**0.004**	0.592
Tsavo West	n/a	168.2 - ∞	**0.024**	0.315	0.400
Kinango	n/a	183.7 - ∞	**0.024**	0.324	0.195
Shimba Hills	336.6	83.0 - ∞	**0.022**	0.125	0.405
Hindi	n/a	156.7 - ∞	**0.003**	**0.037**	0.165
Kainuk	129.0	18.8 - ∞	**0.002**	**0.003**	**0.004**
Oropoi	50.4	14.1 - ∞	**0.014**	**0.017**	**0.028**

Infinite Allele Model (IAM), Two-Phase Model (TPM), and Stepwise Mutation Model (SMM)

Genetic differentiation

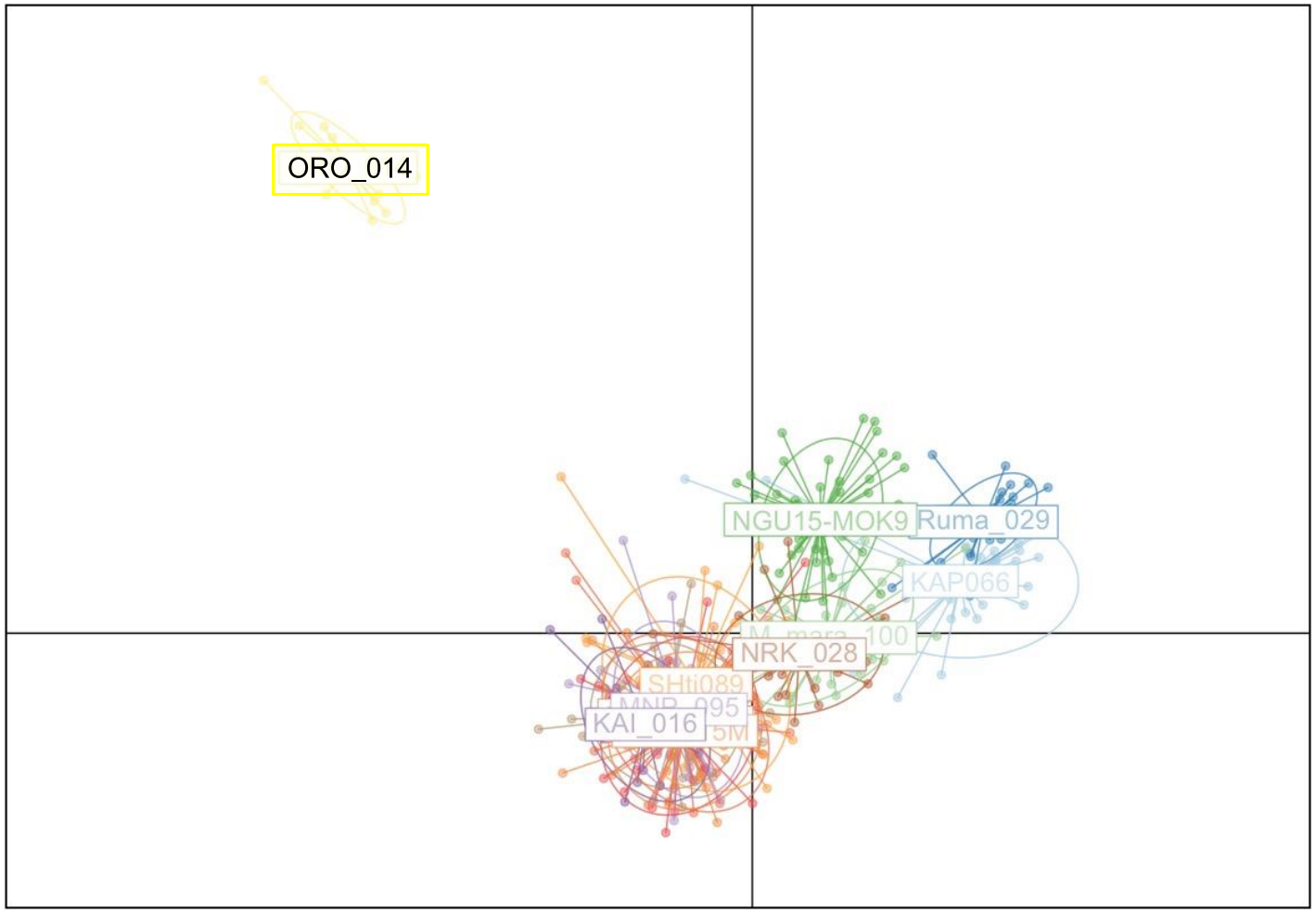
STRUCTURE





STRUCTURE estimated Ln likelihood of the data for K values 1-10 for Kenyan samples including Turkana (KAI and ORO). Each bar represents the composite genotype of one individual, the colors within the bar reflect the assignment probability (q-value) of that individual to one of K genetic clusters

Discriminant analysis of Principle Component (DAPC)



Discriminant analysis of Principle Component (DAPC) showing *G. pallidipes* sampling sties from Kenya including Turkana sites and Narok. Ellipses represent 95% confidence interval.

FST (Pairwise genetic distances)

	KAP	RUM	MMR	NGU	MNP	KIB	TSW	KIN	SHI	HIN	KAI	ORO
RUM	0.145											
MMR	0.143	0.158										
NGU	0.293	0.279	0.177									
MNP	0.236	0.3	0.129	0.176								
KIB	0.23	0.299	0.128	0.198	0.021							
TSW	0.209	0.275	0.104	0.195	0.016	0.022						
KIN	0.206	0.251	0.098	0.155	0.015	0.03	0.014					
SHI	0.22	0.279	0.105	0.182	0.002	0.018	-0.002	0.008				
HIN	0.244	0.305	0.116	0.18	0.015	0.015	0.031	0.027	0.024			
KAI	0.377	0.471	0.283	0.298	0.135	0.118	0.167	0.17	0.16	0.134		
ORO	0.455	0.552	0.38	0.437	0.296	0.307	0.307	0.291	0.307	0.317	0.393	

Western Kenya samples

Western vs Eastern Kenya samples

Eastern Kenya samples

Oropoi and all Kenyan samples

Table showing the pairwise genetic distances between samples from Kenya

Conclusions

Presence and absence

- *G. pallidipes* samples collected from Oropoi (far north), and in Kainuk (along Turkana West Pokot border).
- Oropoi – Turkana-Uganda border (conflict between the Karamajong' in Uganda and the Turkana over cattle and resources).

Genetic structure of Western Kenya

- Kenyan samples divided into eastern and western clusters (Okeyo et al., 2018, Bateta et al., 2020)
- Kainuk (southern Turkana) clustered with samples from the eastern cluster
- Oropoi sub-cluster to form a different population

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DNA Analysis Facility on Science Hill

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