



THE UNIVERSITY
of EDINBURGH



Biotechnology and
Biological Sciences
Research Council

Genetic diversity and population structure of the endangered Tanzanian Mpwapwa cattle breed

Isidore Houaga, Z. Nziku, A. Nguluma, G. Msuta, O. Opoola, M. Okeyo, R. Mrode, A. Djikeng, G. Gorjanc, **Christina Marie Rochus**

EAAP 2024-09-02

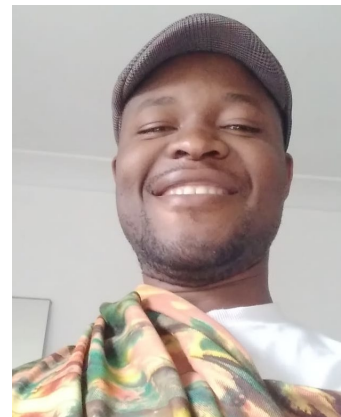
Isidore.Houaga@roslin.ed.ac.uk



[dr-isidore-houaga](https://www.linkedin.com/in/dr-isidore-houaga)



Centre for
Tropical Livestock
Genetics and Health



Tanzanian Mpwapwa cattle

Dual purpose (beef and dairy)

Developed during colonial time ~1930s

Well adapted to various agro-ecological zones

Faced development and maintenance challenges



Tanzanian Mpwapwa cattle

National research centres (TALIRI) +
few smallholder farmers

Less than 1500 head (1997 declared at
risk, FAO)

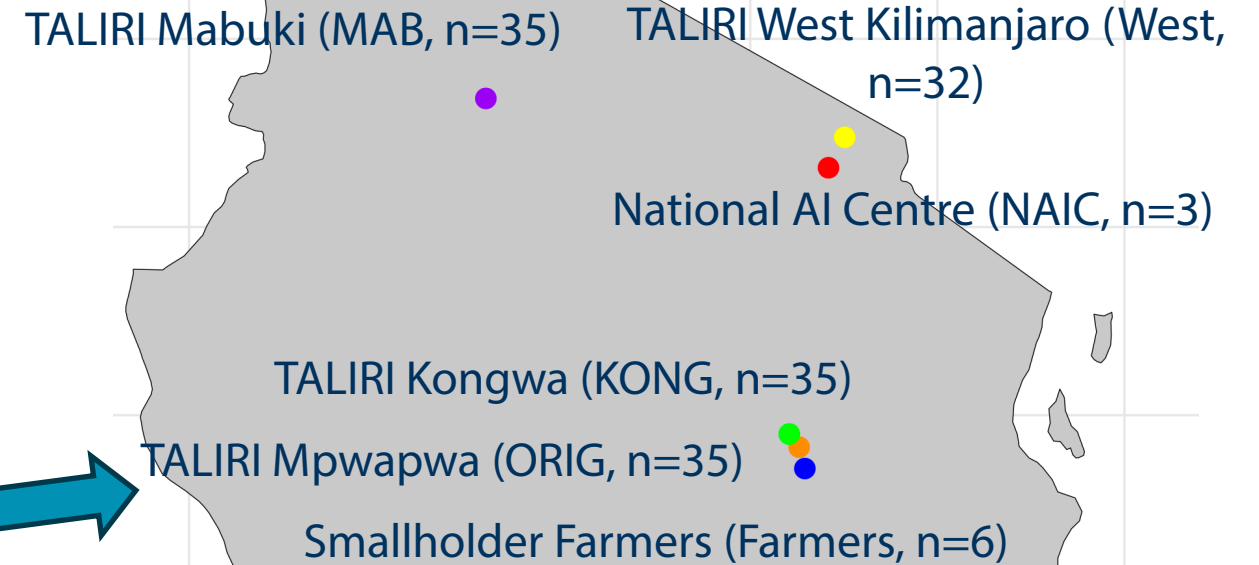
~600 animals in January 2023 (TALIRI
Centres)

No genomic characterisation at the
country level



***Aim: Assess the current diversity to guide conservation
and improvement decisions***

Sampling areas in Tanzania



Sampling areas in Tanzania



252 samples

SNP quality control and analysis

100K SNP array (GGP, Geneseek® Neogen)

95,256 SNPs

PLINK 1.9 (Purcell et al., 2007)

71,055 SNPs and 251 animals after QC

PLINK QC

- - autosome
- - geno 0.10
- - maf 0.05
- - hwe 0.0000000001
- - mind 0.10

Heterozygosity and homozygosity

Expected and observed heterozygosity

detectRUNS package in R

Homozygosity islands (and functional analysis (GALLO))

$$F_{ROH} = \frac{L_{ROH}}{L_{aut}}$$

detectRUNS

Sliding window method

Window size : 15

Minimum ROH length: 40 SNPs

Minimum density: 1 SNP in 1000kb

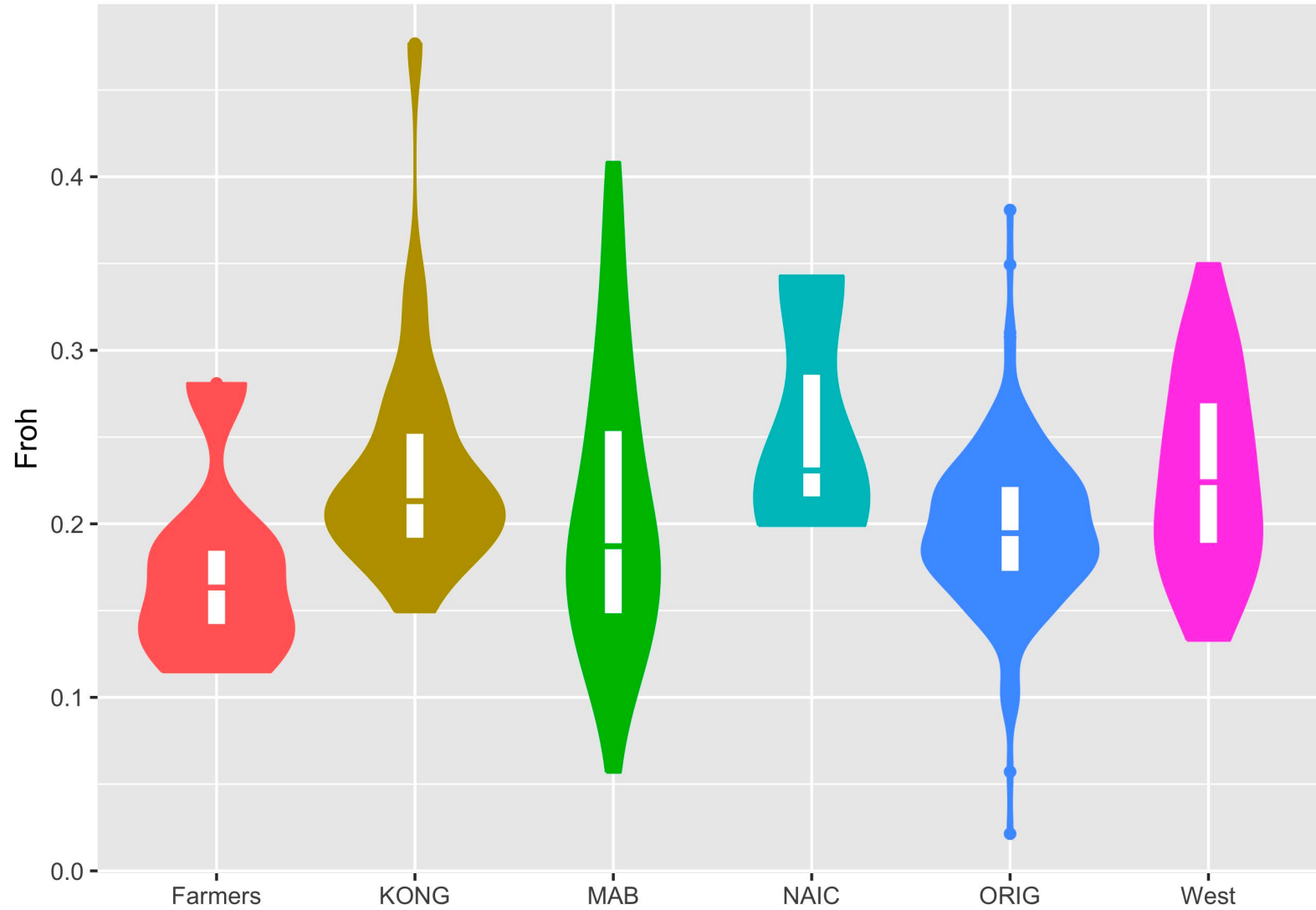
Maximum gap: 1Mb

Observed and expected heterozygosity

Population	n	Ho	He
Farmers	6	0.34	0.31
Kongwa	28	0.32	0.30
Mabuki	35	0.34	0.32
NAIC	3	0.30	0.25
ORIG	147	0.33	0.33
West	32	0.32	0.30

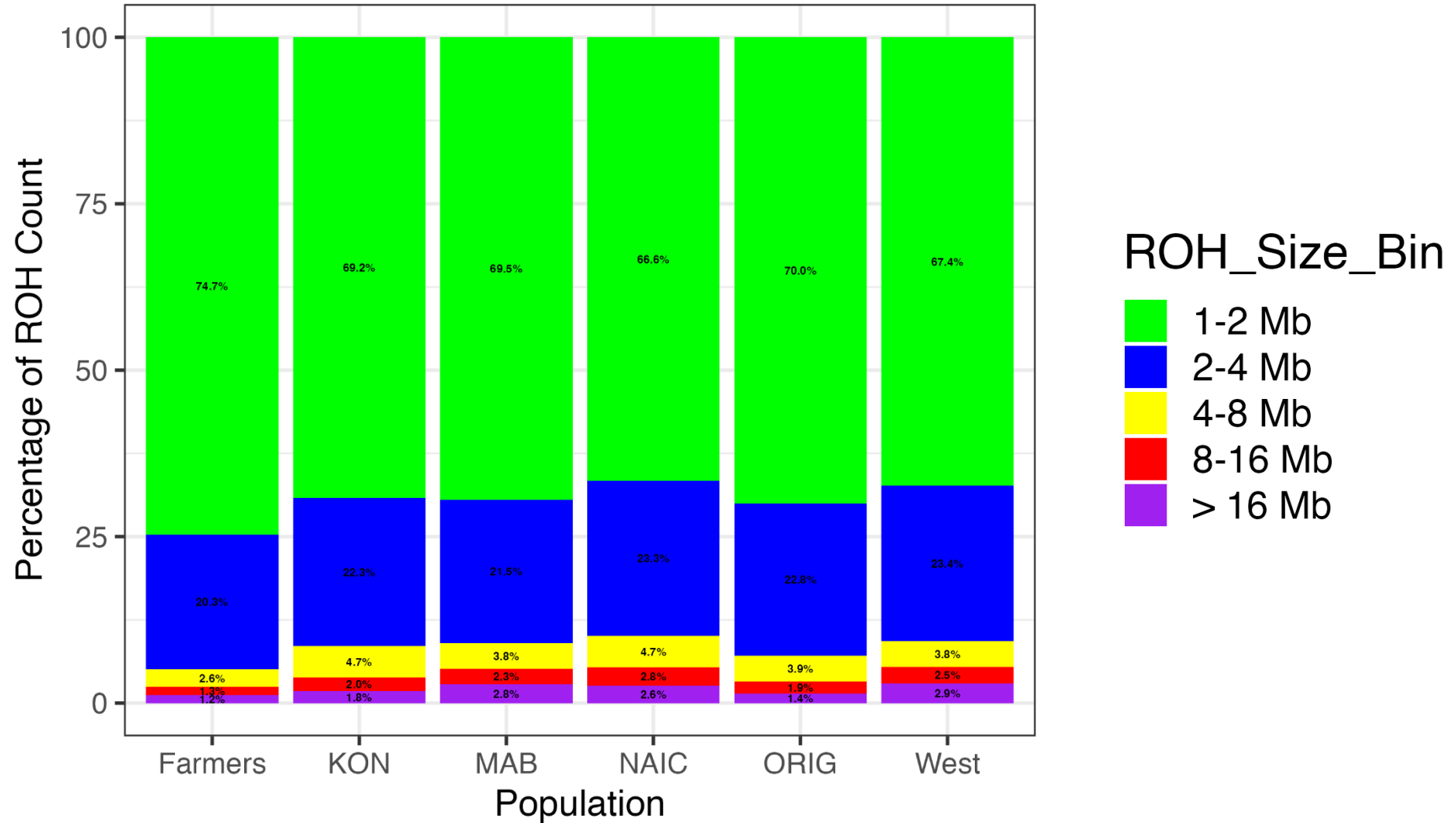
n= sample size, **Ho**=Observed heterozygosity, **He**=Expected heterozygosity

Average F_{ROH}



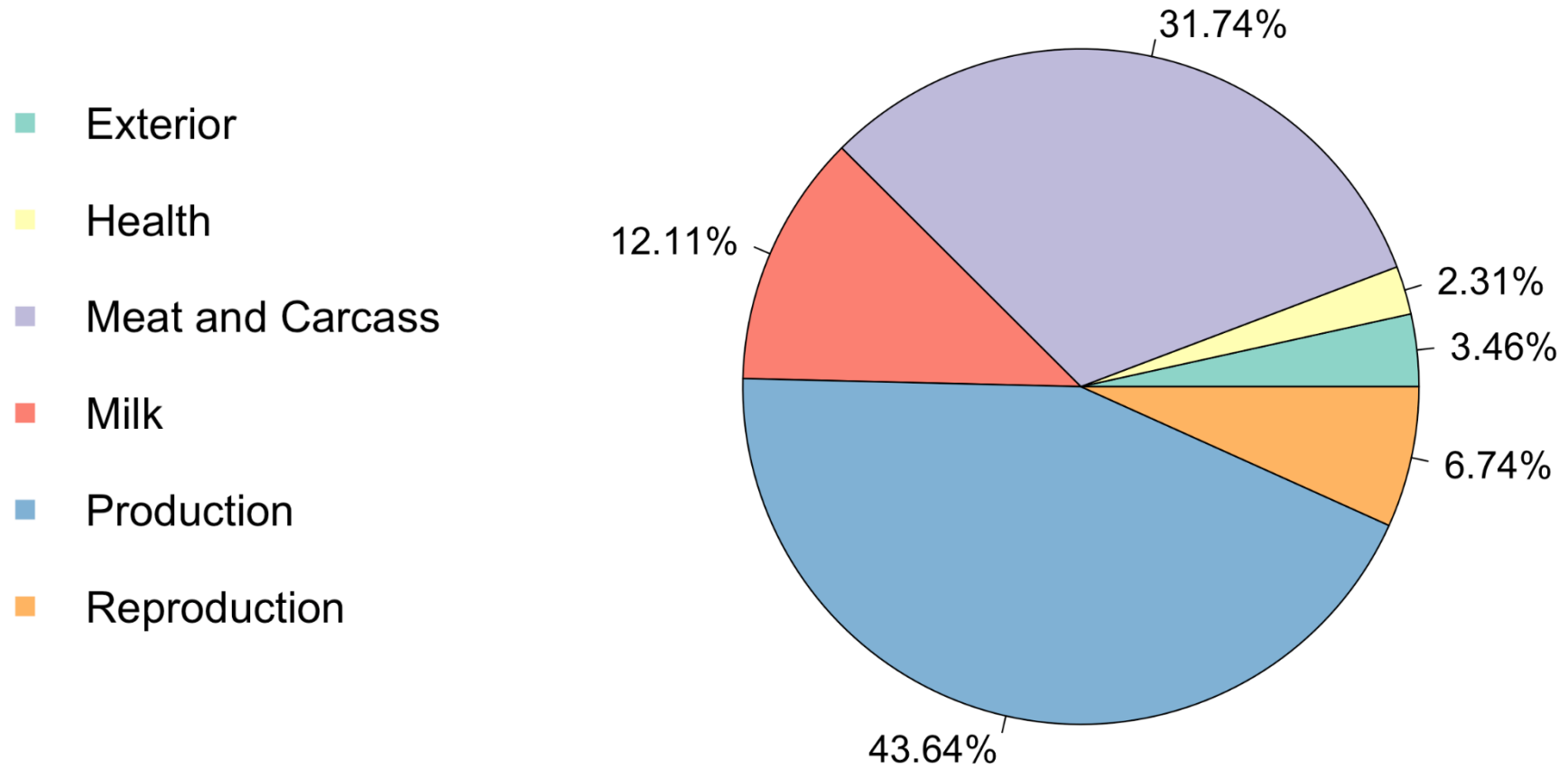
Mean $F_{ROH} = 0.21 \pm 0.06$

ROH by population and bin size



~70% of ROH with size up to 2 Mb

Homozygosity islands



CHR	Start pos (bp)	End pos (bp)
8	52,676,049	73,389,421
11	37,668,186	41,008,850

Future directions

Mpwapwa relationship to other African and global breeds

Develop conservation and inbreeding management strategies

Genomic selection

Build a high-quality reference genome of the breed

Conclusions

First genomic characterisation of
Tanzanian Mpwapwa

Genetic diversity not well
managed

More than 50% of sampled
individuals showed $F_{ROH} > 20\%$





THE UNIVERSITY
of EDINBURGH



Biotechnology and
Biological Sciences
Research Council

Genetic diversity and population structure of the endangered Tanzanian Mpwapwa cattle breed

Isidore Houaga, Z. Nziku, A. Nguluma, G. Msuta, O. Opoola, M. Okeyo, R. Mrode, A. Djikeng, G. Gorjanc, **Christina Marie Rochus**

EAAP 2024-09-01

Isidore.Houaga@roslin.ed.ac.uk



[dr-isidore-houaga](#)



ADGG
African Dairy Genetic Gains
More productive and profitable dairy cows



Centre for
Tropical Livestock
Genetics and Health

