

Genetic variability of Cape buffalo populations in South Africa

Lené van der Westhuizen,

Prof Frederick WC Neser & Dr Roan Louw

OUTLINE

1. Terminology
2. Genetic diversity
3. Data collection
4. Previous studies
5. Current study
6. Additional measurements
7. Advantages / Take home message

TERMINOLOGY

DNA Profile – microsatellite markers

ID	BM1824		BM3205		BM3517		BM4028		BM719	
L1	189	193	222	224	100	102	136	140	146	152
L2	185	189	222	222	92	102	136	138	142	148
L2	180	193	224	226	92	100	135	140	152	152

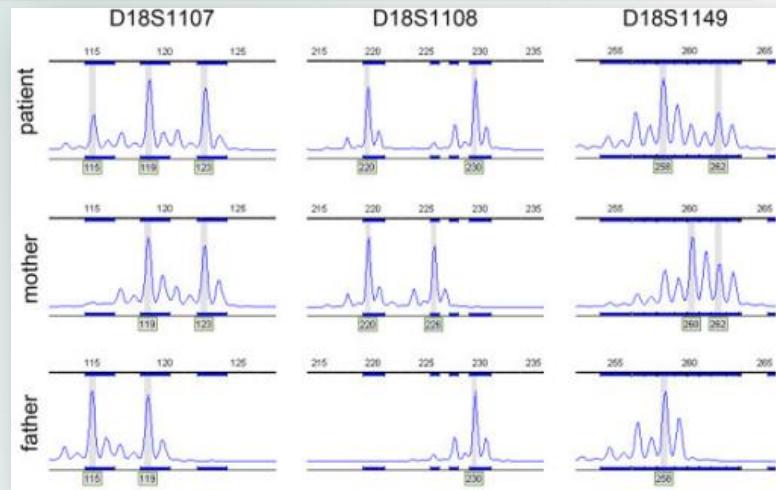
GENETIC DIVERSITY

- Variation of alleles and genotypes present in a population
- If variation is present, animals can respond to environmental changes



MEASURING GENETIC DIVERSITY

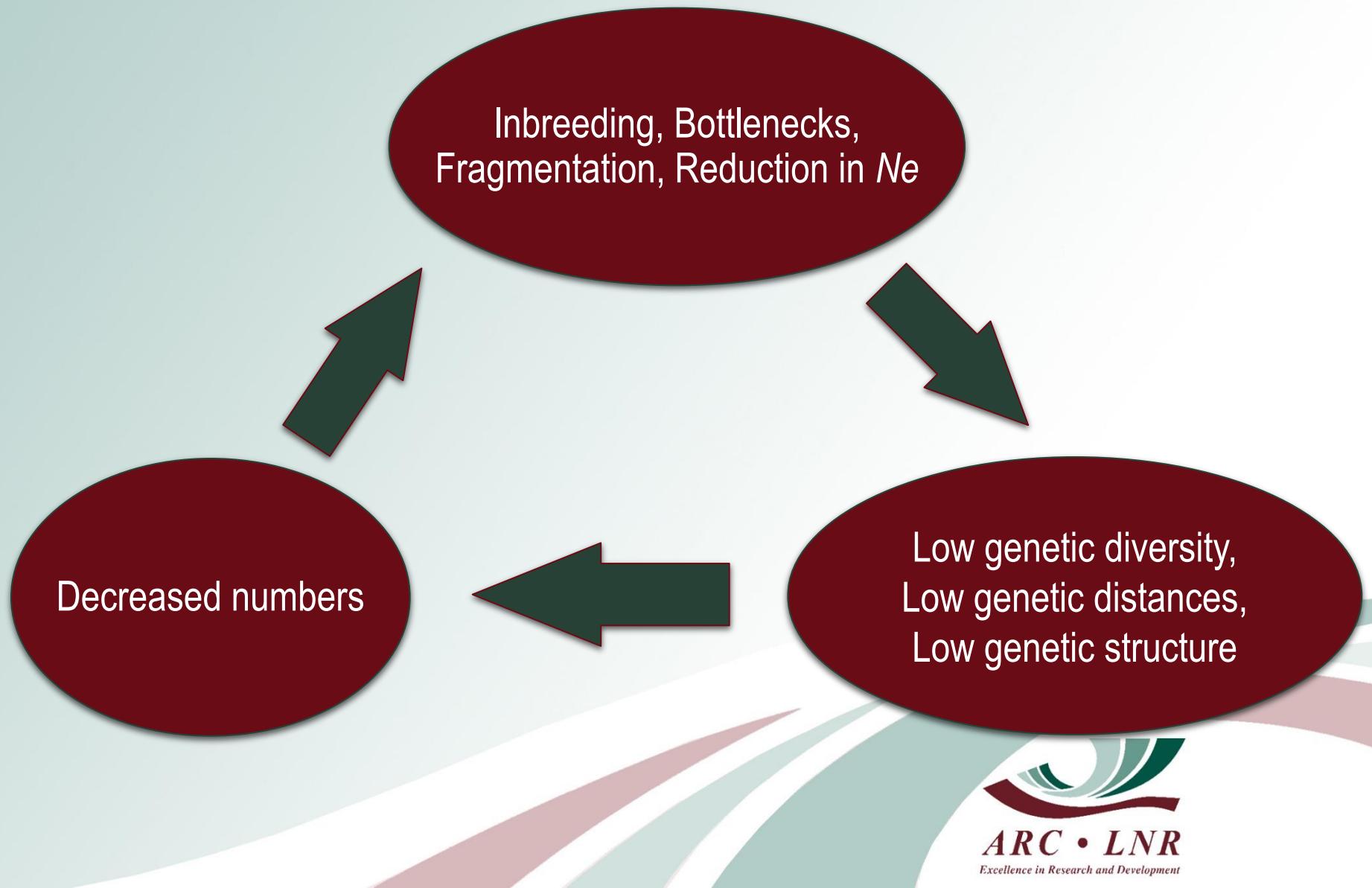
- Microsatellite markers



- SNPs



GENETIC DIVERSITY





Hair, blood,
semen,
biopsy



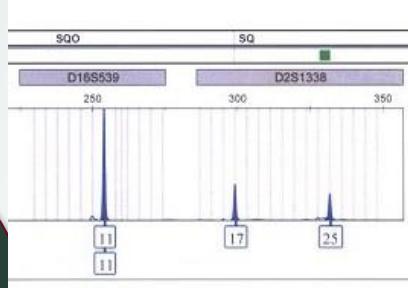
Populations

DATA COLLECTION



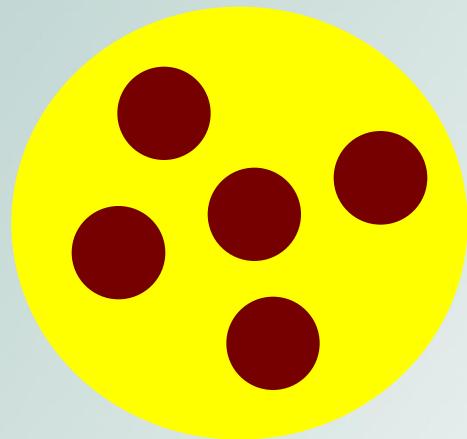
DNA

DNA
Profiles



Microsatellite
analysis

PREVIOUS STUDY



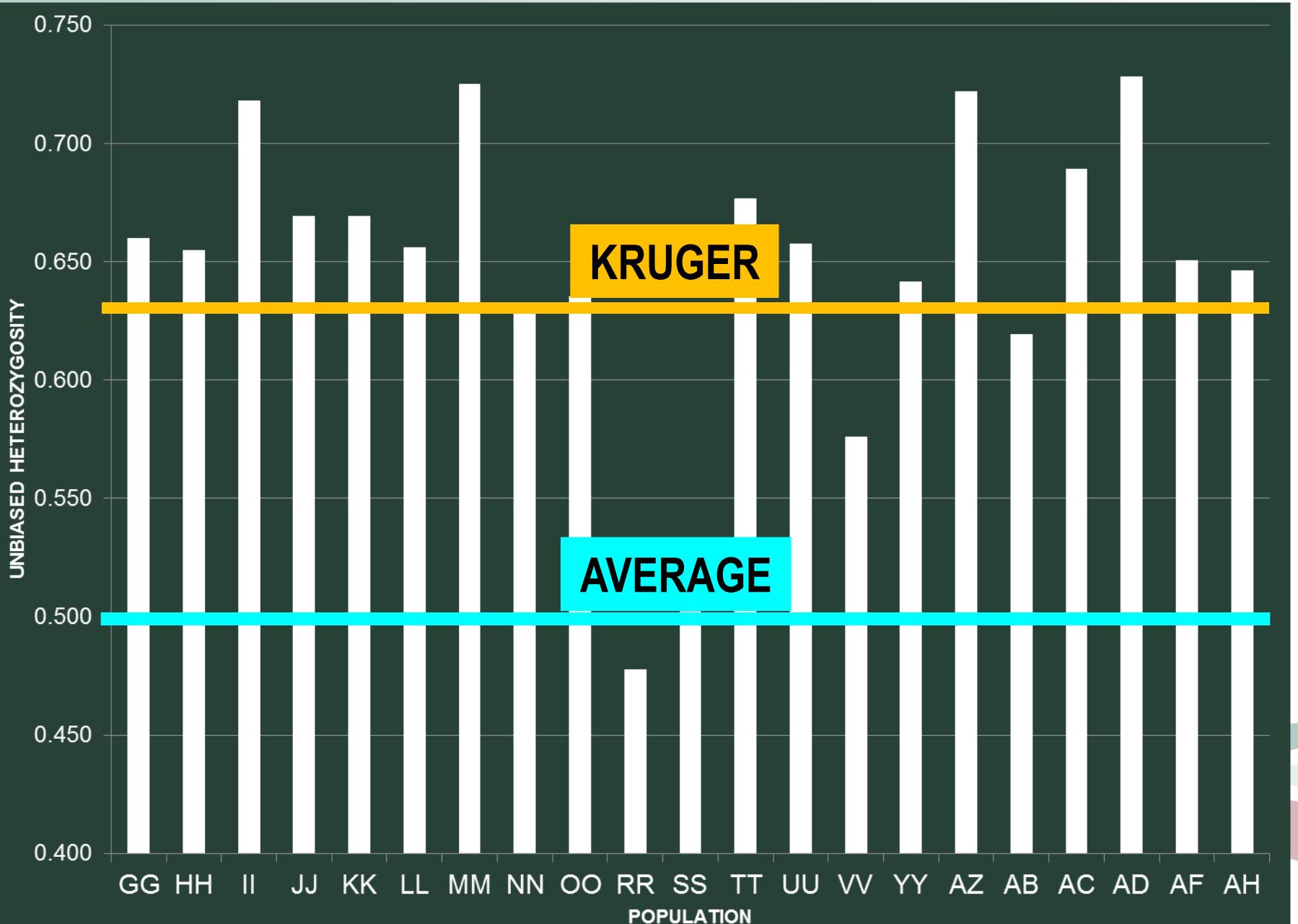
KRUGER AND HiP

METHODOLOGY

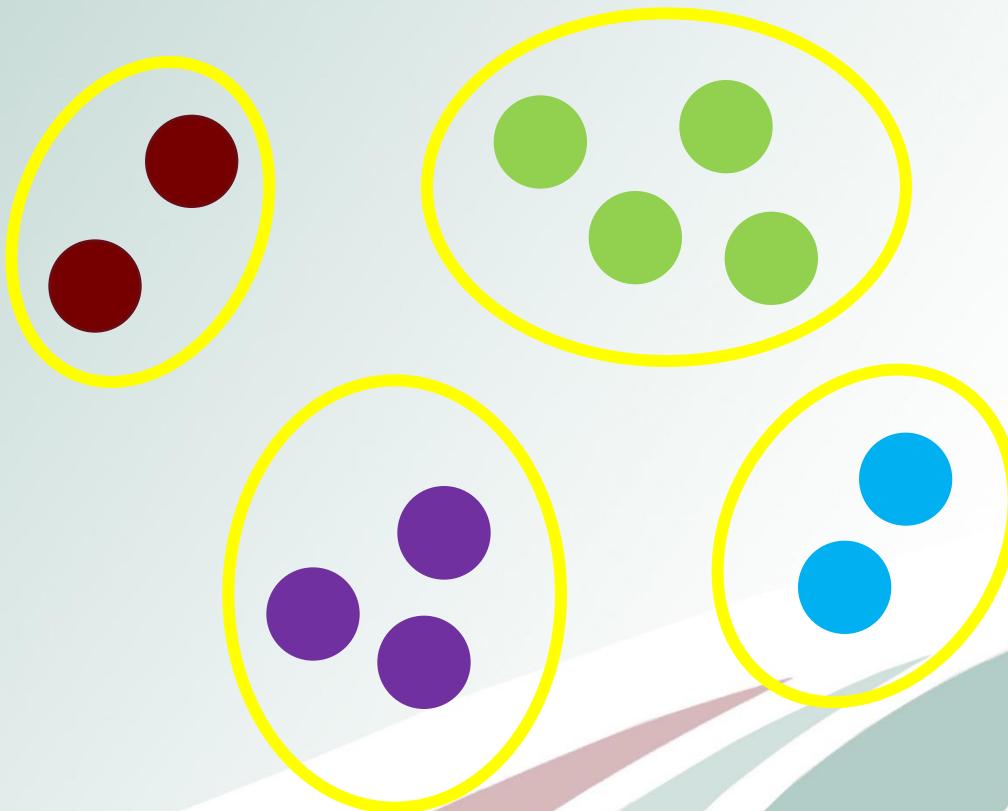
- Existing microsatellite marker data of buffalo populations
- Number of populations = 21 populations
- Min number of animals per population = 30 animals
- Amount of microsatellite markers = 14 markers

- MSToolkit (Park, 2001) = **unbiased heterozygosity (Hz);**
= **mean number of alleles (MNA)**
- FSTAT (Goudet, 2002) = **allelic richness (Rs)**

Population Statistics			
Pop	Hz ± SD	MNA ± SD	Rs ± SD
GG	0,660 ± 0,051	8,71 ± 3,43	6.354 ± 2.390
HH	0,655 ± 0,062	7,43 ± 3,30	6.651 ± 2.792
II	0,718 ± 0,048	8,93 ± 4,07	7.366 ± 2.963
JJ	0,669 ± 0,054	7,21 ± 2,39	6.734 ± 2.217
KK	0,669 ± 0,044	6,14 ± 2,41	6.026 ± 2.354
LL	0,656 ± 0,056	8,07 ± 3,29	6.507 ± 2.533
MM	0,725 ± 0,041	6,93 ± 2,40	6.816 ± 2.363
NN	0,630 ± 0,066	7,36 ± 2,65	6.337 ± 2.316
OO	0,635 ± 0,052	6,50 ± 2,93	5.907 ± 2.442
RR	0,478 ± 0,058	6,07 ± 2,30	4.779 ± 1.628
SS	0,502 ± 0,064	3,50 ± 1,56	3.478 ± 1.537
TT	0,677 ± 0,053	7,57 ± 3,48	6.401 ± 2.879
UU	0,658 ± 0,056	8,00 ± 3,19	6.462 ± 2.667
VV	0,576 ± 0,064	5,71 ± 2,27	5.293 ± 2.047
YY	0,642 ± 0,055	6,64 ± 2,68	6.196 ± 2.498
AZ	0,722 ± 0,044	7,36 ± 2,65	7.069 ± 2.502
AB	0,619 ± 0,068	7,36 ± 2,76	6.356 ± 2.411
AC	0,689 ± 0,040	8,93 ± 3,10	6.642 ± 2.218
AD	0,728 ± 0,040	7,86 ± 2,66	6.860 ± 2.195
AF	0,651 ± 0,053	6,86 ± 2,28	6.334 ± 2.231
AH	0,646 ± 0,059	6,57 ± 2,93	6.370 ± 2.775



CURRENT STUDY



METHODOLOGY

- Existing microsatellite marker data of buffalo populations
- Number of herds = 5



1 breeder; 3 herds

1 breeder; 2 herds

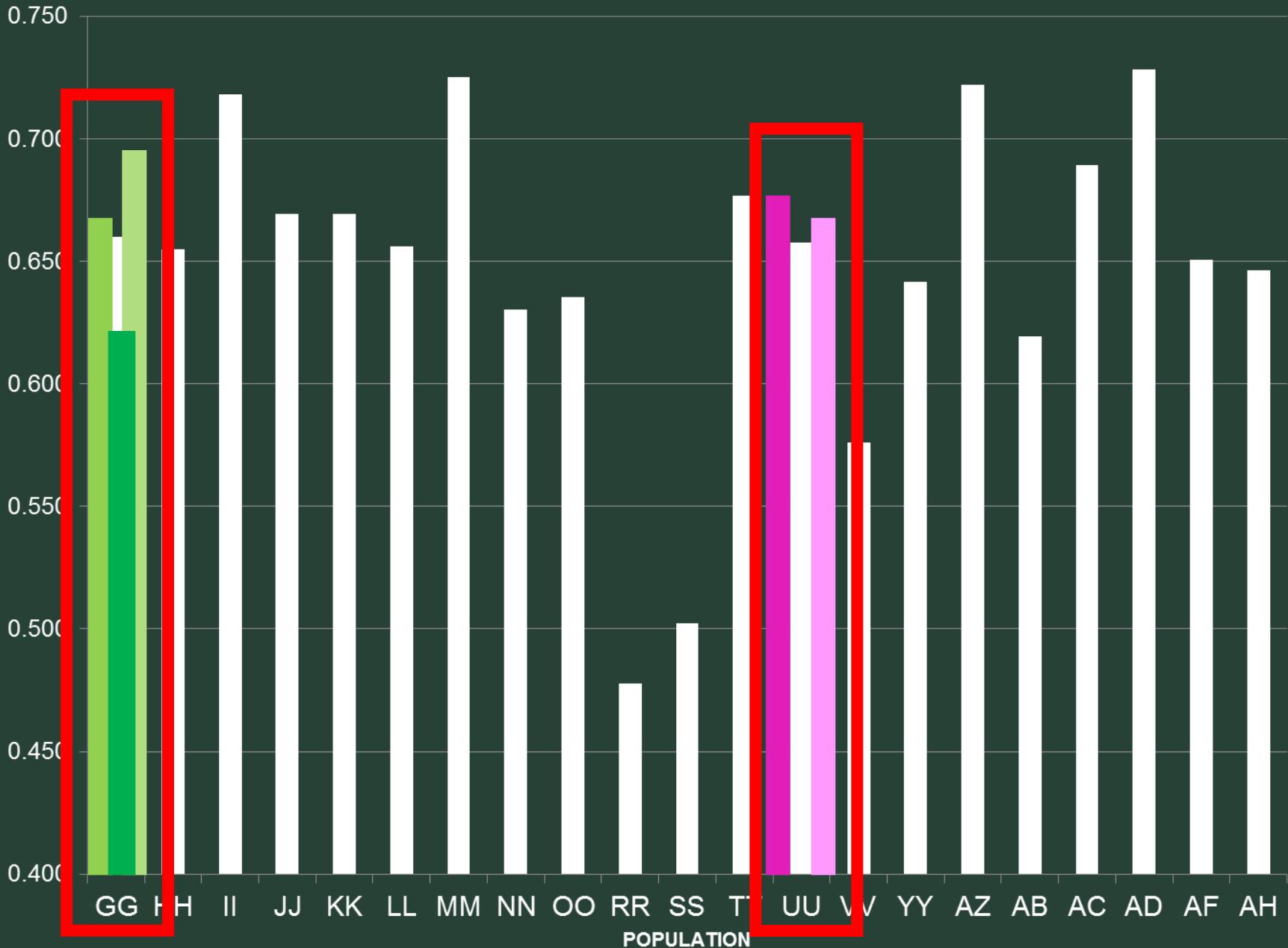
- Min number of animals per herds = 30 animals
- Amount of microsatellite markers = 14 markers

RESULTS

POPULATION STATISTICS

Herd	Hz ± SD	MNA ± SD	Rs ± SD	Fis
1	0,668 ± 0,048	7,00 ± 2,69	3,673 ± 1,080	-0,033
2	0,628 ± 0,065	6,57 ± 2,53	3,520 ± 1,185	-0,039
3	0,699 ± 0,072	4,71 ± 2,20	4,357 ± 1,932	0,076
4	0,664 ± 0,050	6,57 ± 2,93	3,701 ± 1,095	0,025
5	0,659 ± 0,057	6,07 ± 2,59	3,626 ± 1,148	-0,040
Total				
	0,664 ± 0,058	6,19 ± 2,59	3,776 ± 1,288	-0,024

UNBIASED HETEROZYGOSEITY



ADDITIONAL MEASUREMENTS

1. Inbreeding (Fis, Fit)

excess of heterozygotes = -1 to 0 to 1 = excess of homozygotes

2. Genetic Differentiation

3. Genetic Structure (DeltaK)

4. Principal Coordinate Analysis (PCoA)

ADVANTAGES / TAKE HOME MESSAGE

1. Important to measure genetic diversity – future adaptability
2. More accurate results
3. Methods provide useful tools for breeder (inbreeding)
4. Provides the breeder with genetic information



THANK YOU!!! DANKIE!!!



NORTH-WEST UNIVERSITY
YUNIBESITI YA BOKONE-BOPHIRIMA
NOORDWES-UNIVERSITEIT

