



A water buffalo with large, curved horns is standing in a field of tall grass. The buffalo is the central focus of the image, and its body is dark with some lighter patches on its legs. The background is a soft-focus field of green and yellow grass.

The buffalo of HIP and KNP: A comparative study

Ben Greyling and Armanda Bastos

Introduction and background

- **KNP & HUP house SA's largest buffalo populations**
 - **KNP: 2000 000 ha / 28500 buffalo**
 - **HUP: 89 000 ha / 3000 buffalo**
- **KNP: average herd size = 245**
- **HUP: average herd size = 170**
- **Parks have been separated and fenced for a number of years, restricting gene flow and fragmenting the two populations**
- **Differential infection rates (BTB)**
- **Differences in behaviour ecology between two population?**



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Opportunity to draw comparisons:

Evaluate the effect of different driving forces that maintain or erode genetic variation (fragmentation, dispersal, genetic drift, founder effect (post bottleneck) etc.

Premise:

Insight into buffalo population genetics will contribute to effective management and protection of the species

Specific objectives

- **Determine current degree of genetic diversity in HUP and KNP**
 - **(genetic status inventory)**
- **Are KNP and HUP two differentiated populations?**
- **Are the two populations structured?**
- **-sex biased structure**
- **Isolation by distance?**
- **Sex biased dispersal?**
- **Effective population sizes**
- **Genetic relatedness between KNP and HUP populations?**

Materials and Methods

- **mtDNA sequence analysis: HV 1 domain of D-loop area (455 bp)**
- **Microsatellites: Panel of 17 (3 multiplexes – single injection) unlinked bovine Msats**
 - **KNP: n=486 (Msats); n=162 (mtDNA)**
 - **HUP: n=401 (Msats); n=97 (mtDNA)**

Results and discussion

Genetic diversity and structure (Msat analysis)

KNP: $H_e = 0.65$ (moderate to high variation)

HUP: $H_e = 0.54$ (low level of variation)

Y-chromosomal diversity (van Hooft) :

- **KNP: $D = 0.741$, $NH = 15$**
- **HUP: $D = 0.475$, $NH = 5$**

Garza & Williamson's "M"

- **HUP = 0.742 (variance = 0.039)**
- **KNP = 0.860 (variance = 0.015)**

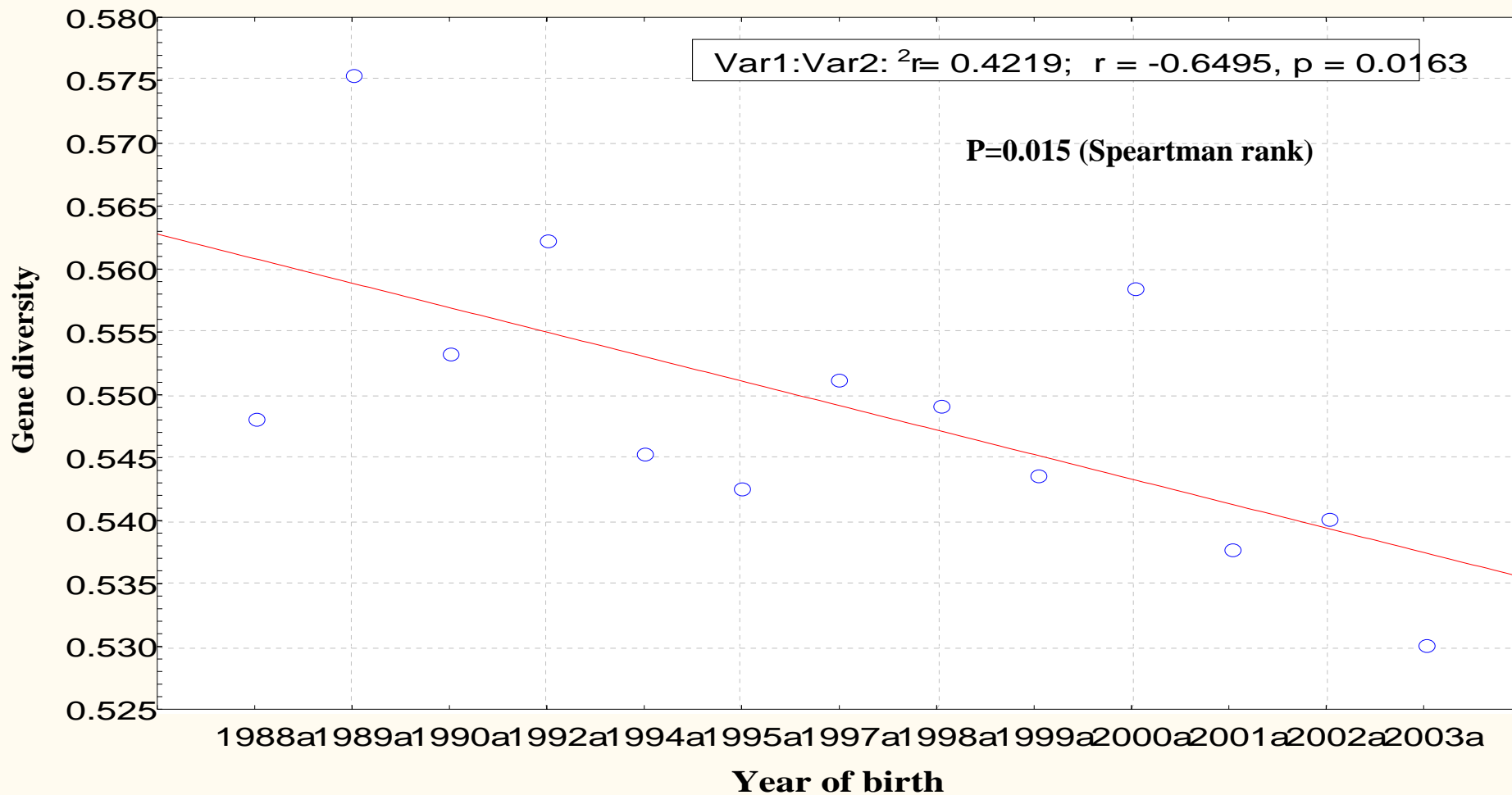
KNP = outbred, HUP shows remnants of bottleneck

KNP - north pop.: $H_e = 0.66$ while south pop.: $H_e = 0.62$ ($p = 0.008$)

HUP: Significant correlation between age (year of birth) and gene diversity

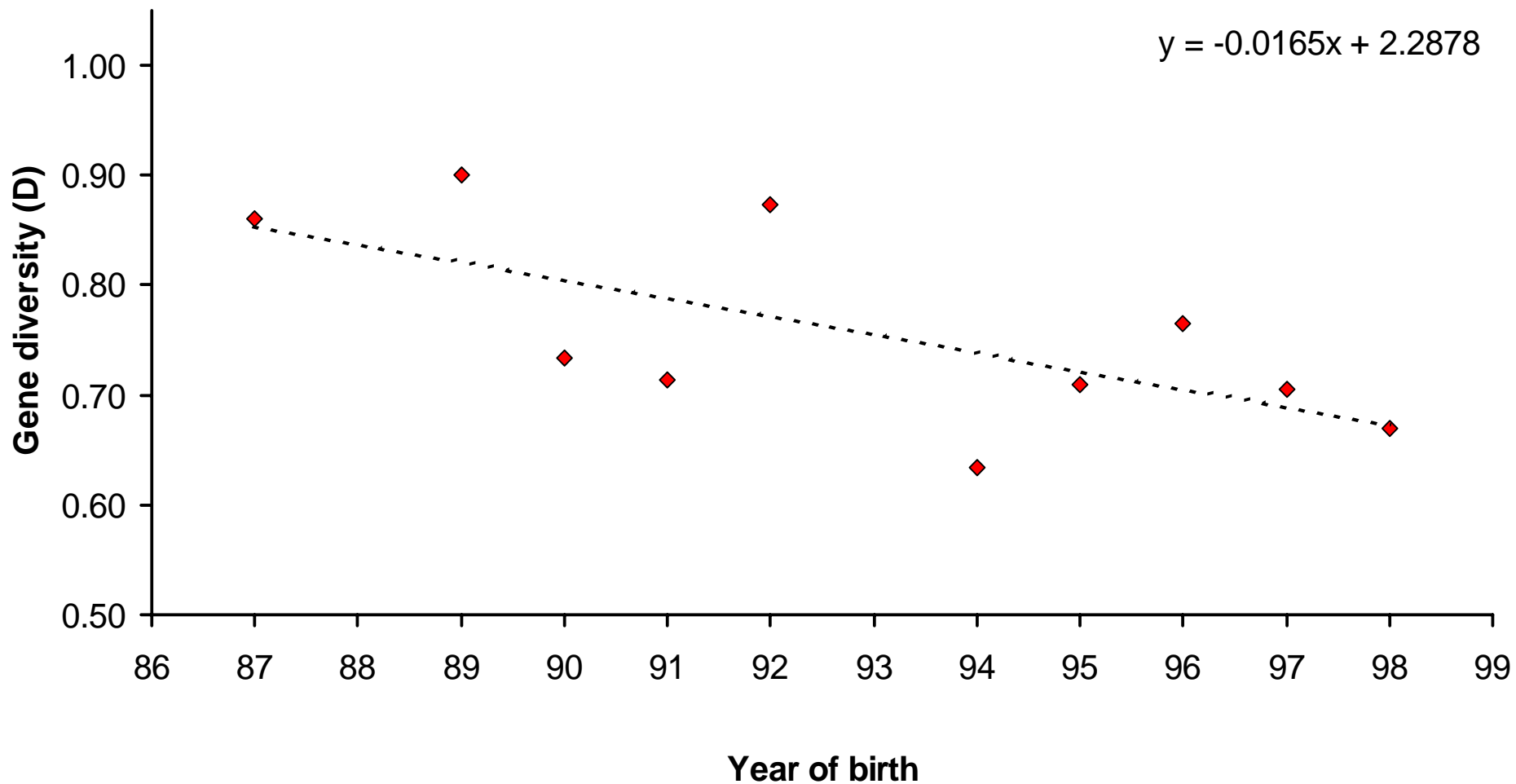
Gene diversity as a function of year of birth in HUP

Var2 = 0.7574-0.0019



Y chromosomal data (Pim van Hooft):

KNP, correlation between year of birth and gene diversity (P=0.038)



KNP:

Among all herds: $F_{st} = 0.012$ ($p = 0.01$) – little structure among herds

- **males $F_{st} = 0.008$**
- **females $F_{st} = 0.013$**

HUP:

Among all herds: $F_{st} = 0.014$

Isolation over distance *or* do long distance love affairs actually exist (and work)?

North *vs* South KNP: $F_{st} = 0.0123$ ($p=0.01$) – small but significant isolation by distance

KNP: F_{st} (males) of north and south pops. = 0.017

- “substantial” long distance dispersal

Cow's secret weapons to attract bulls.....



For HUP – no significant isolation over distance!

Effective population size:

KNP: 4292/2238

HUP: 2354/1469

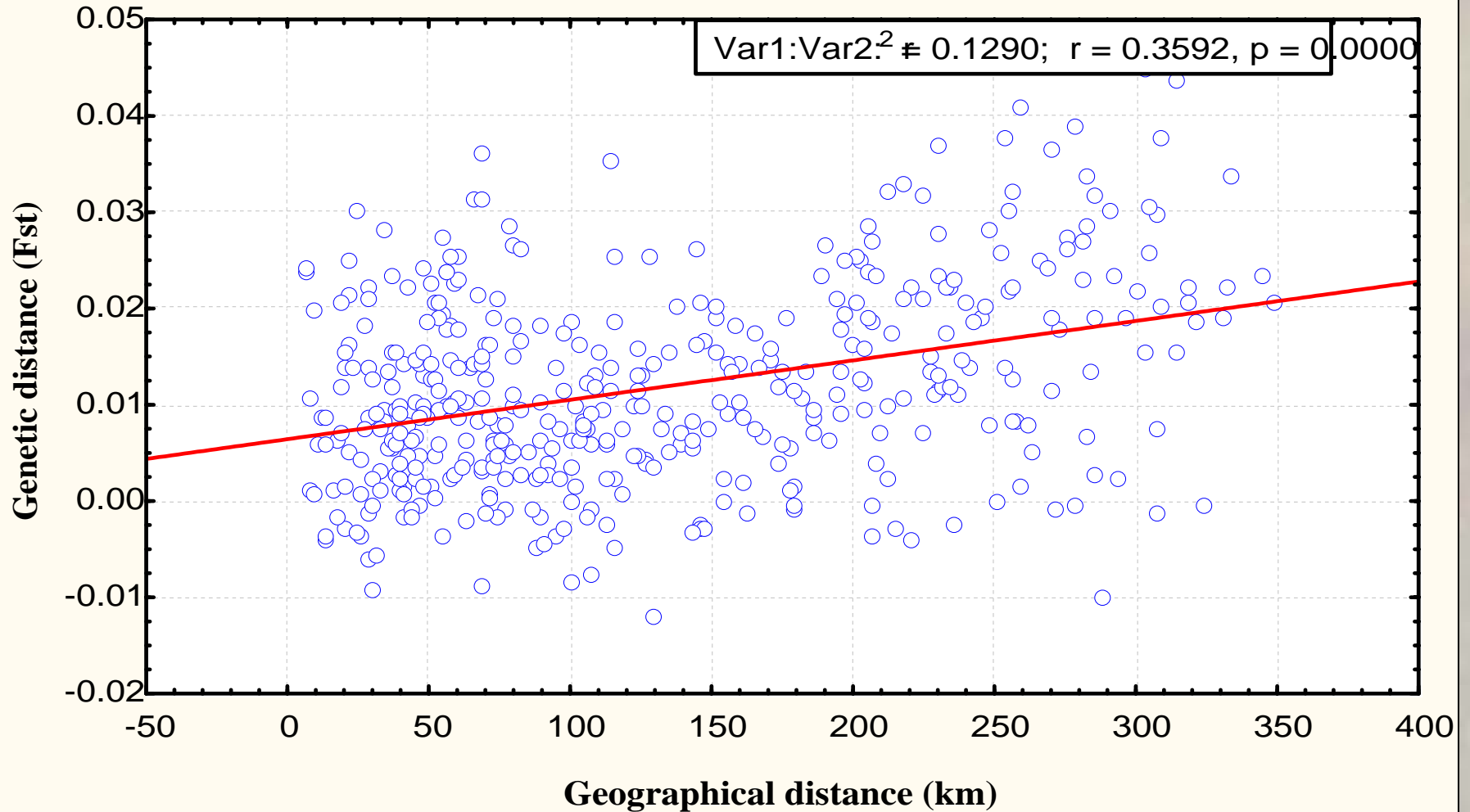
(SMM/IAM; mutation rate = $2.05E-4$)

D-loop:

- **Among herd structure in KNP: $F_{st} = 0.06739$ ($p=0.0063$)**
 - **stronger structure among females (phylopatric)**
- **Both males and females in KNP (all ages included) show isolation by distance (small however)**

Isolation by distance: All KNP individuals

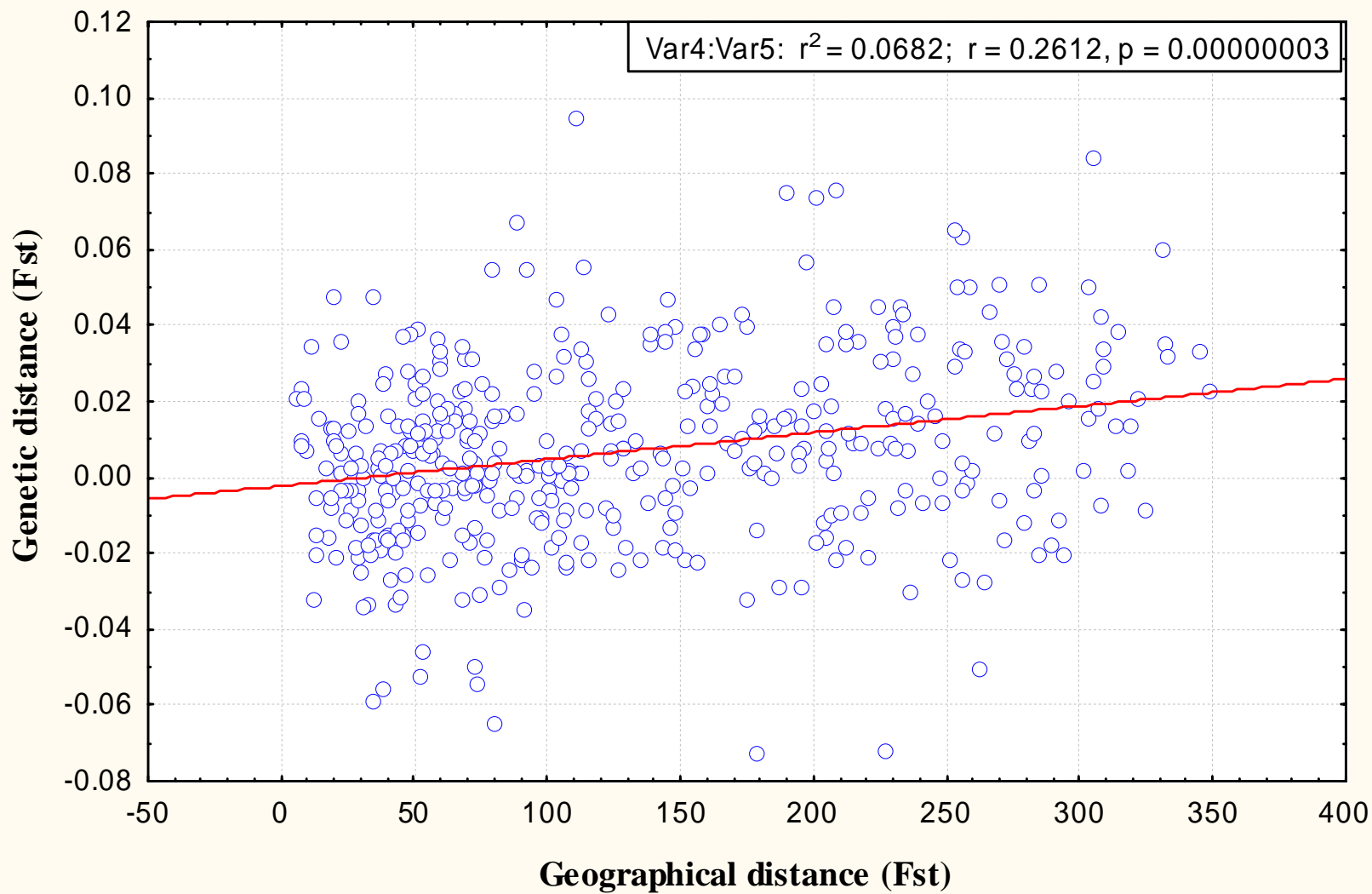
Var2 = 0.0064+4.0932E



Isolation by distance: Males from KNP

$$\text{Var5} = -0.0022 + 7.0184\text{E-}5 * x$$

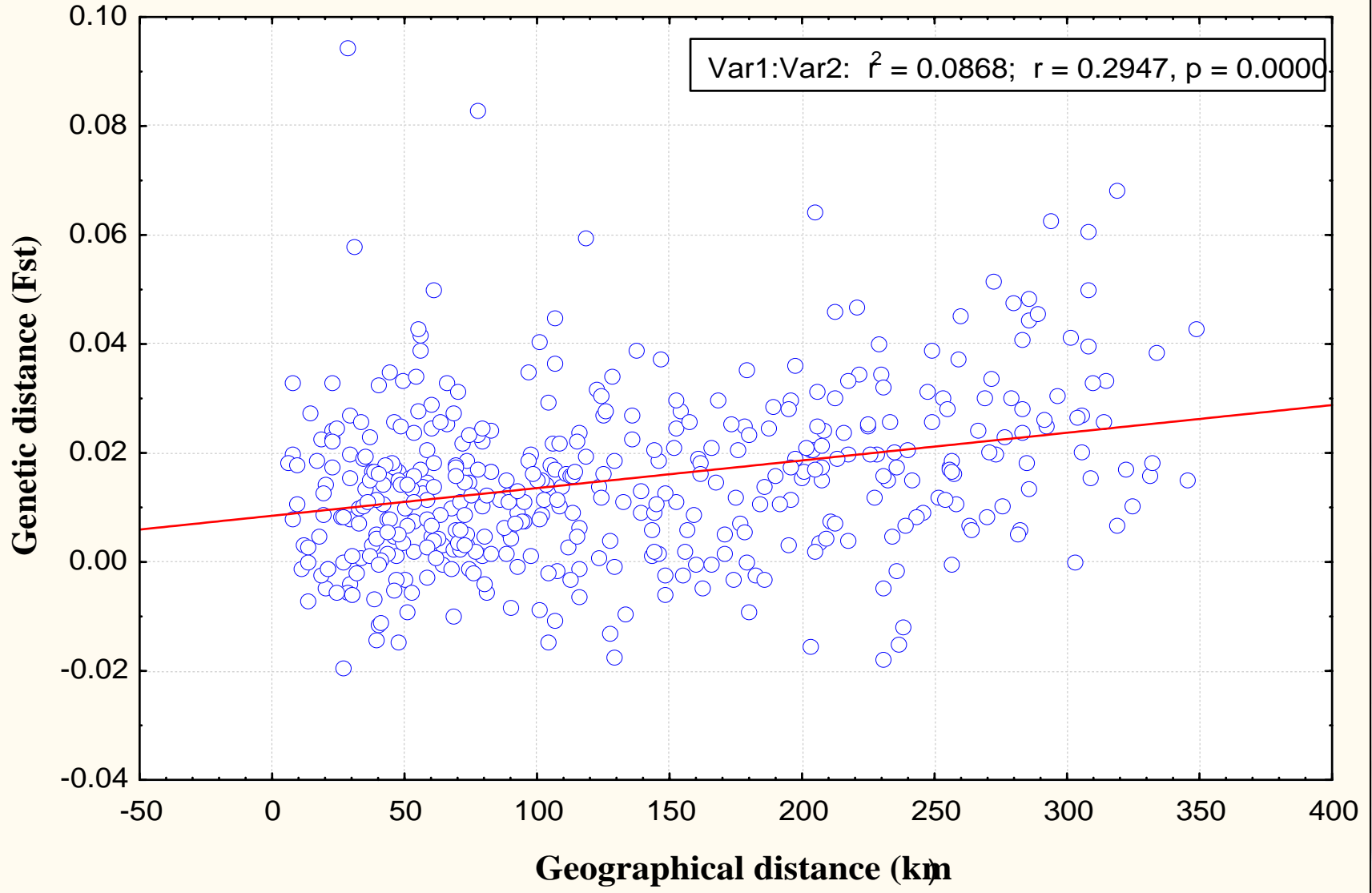
Var4:Var5: $r^2 = 0.0682$; $r = 0.2612$, $p = 0.00000003$



Isolation by distance: Females of KNI

$$\text{Var2} = 0.0085 + 5.0763\text{E-}5^*$$

$$\text{Var1:Var2: } r^2 = 0.0868; r = 0.2947, p = 0.0000$$



HUP female structure (D-loop) among all herds :

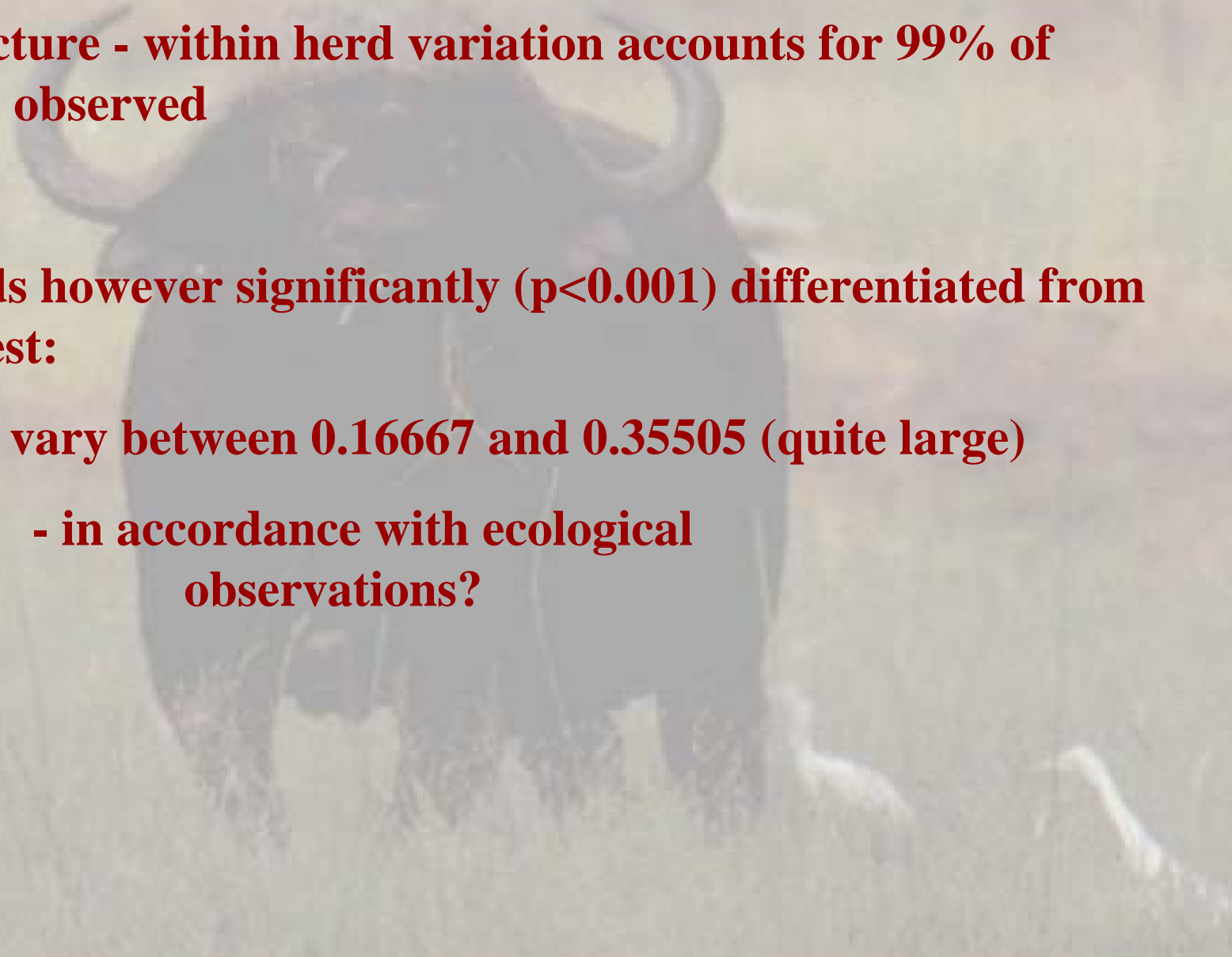
Fst: 0.00564, p=0.42326

- no structure - within herd variation accounts for 99% of variation observed**

Certain herds however significantly ($p < 0.001$) differentiated from the rest:

Fst's vary between 0.16667 and 0.35505 (quite large)

- in accordance with ecological observations?**



Population differentiation: KNP vs HUP

Msats

- **Fst: 0.1586 (p=0.05) = two very diverse populations!**
- **Assignment tests: 99.4% accuracy (GeneClass), 100% (Agarst)**

(can thus identify the population of origin of individual animals)

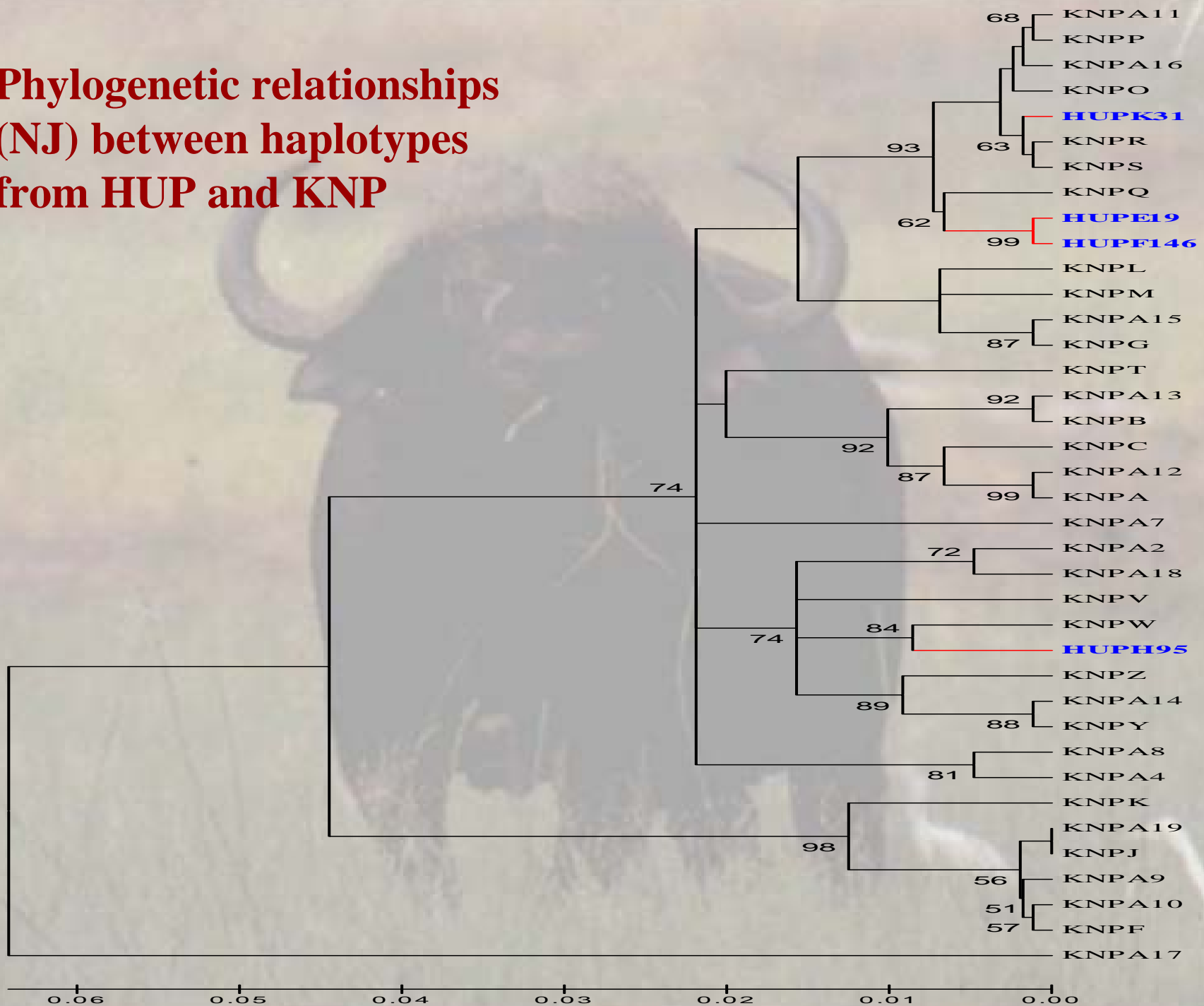
mtDNA

- **Fst = 0.27538 (p < 0.001)**

Parameters of mtDNA genetic diversity

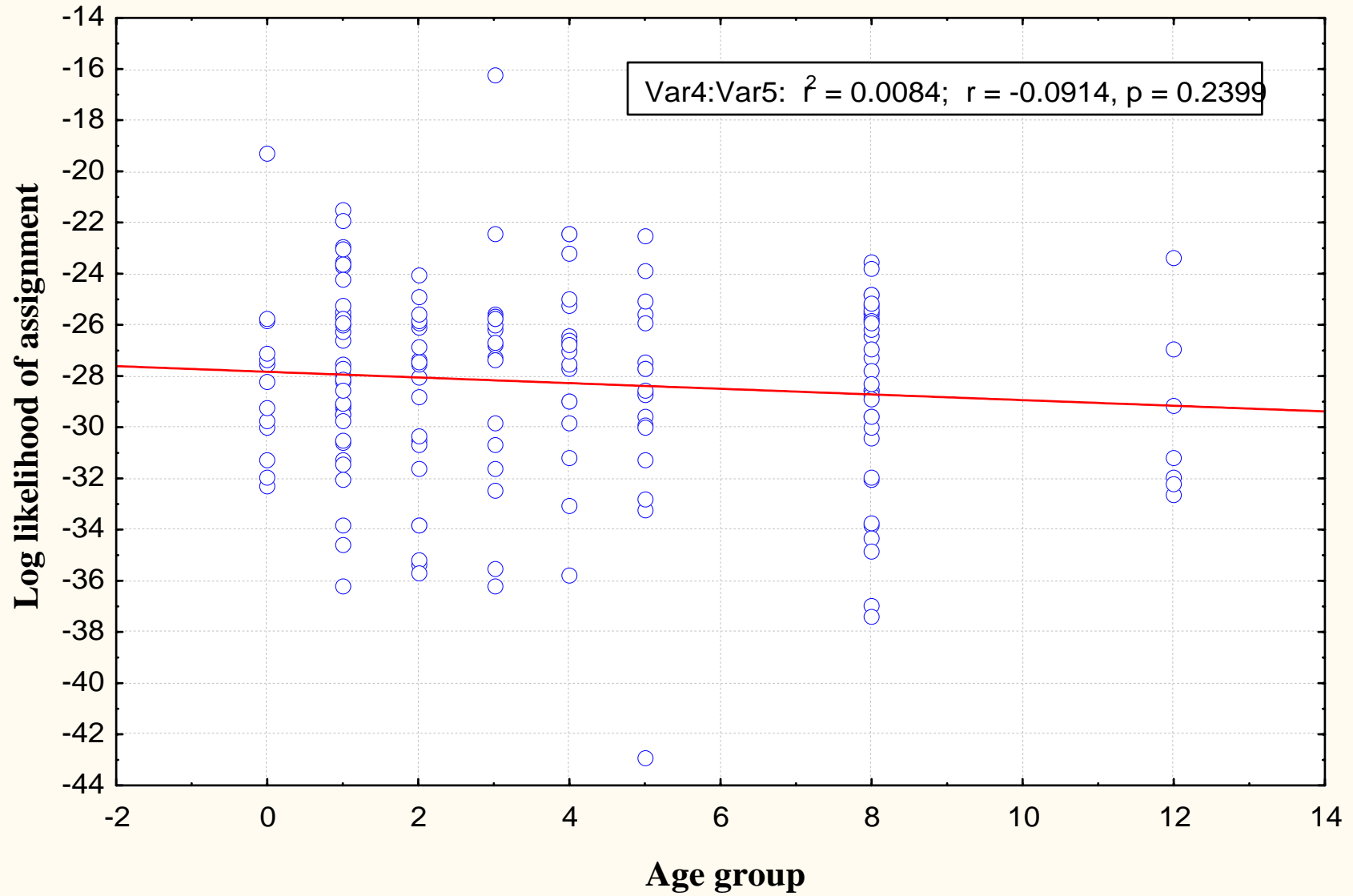
Diversity indices	KNP n=161	HUP n=97	HUP vs KNP
Number of haplotypes	34	4	
Gene diversity	0.9279	0.4899	
Nucleotide diversity (Pi)	0.049	0.030	
Ave no. of nucleotide differences (k)	20.5	12.6	
Fu's Fs statistic (neutrality test)	-10.64	0.607	
Tajimas D test of neutrality	-0.16, p>0.1	-0.33, p>0.1	
Mean genetic Kimura 2 corrected distance between all haplo's	0.06 (0.008SE)	0.035 (0.008se)	0.055 (0.008 SE)

Phylogenetic relationships (NJ) between haplotypes from HUP and KNP

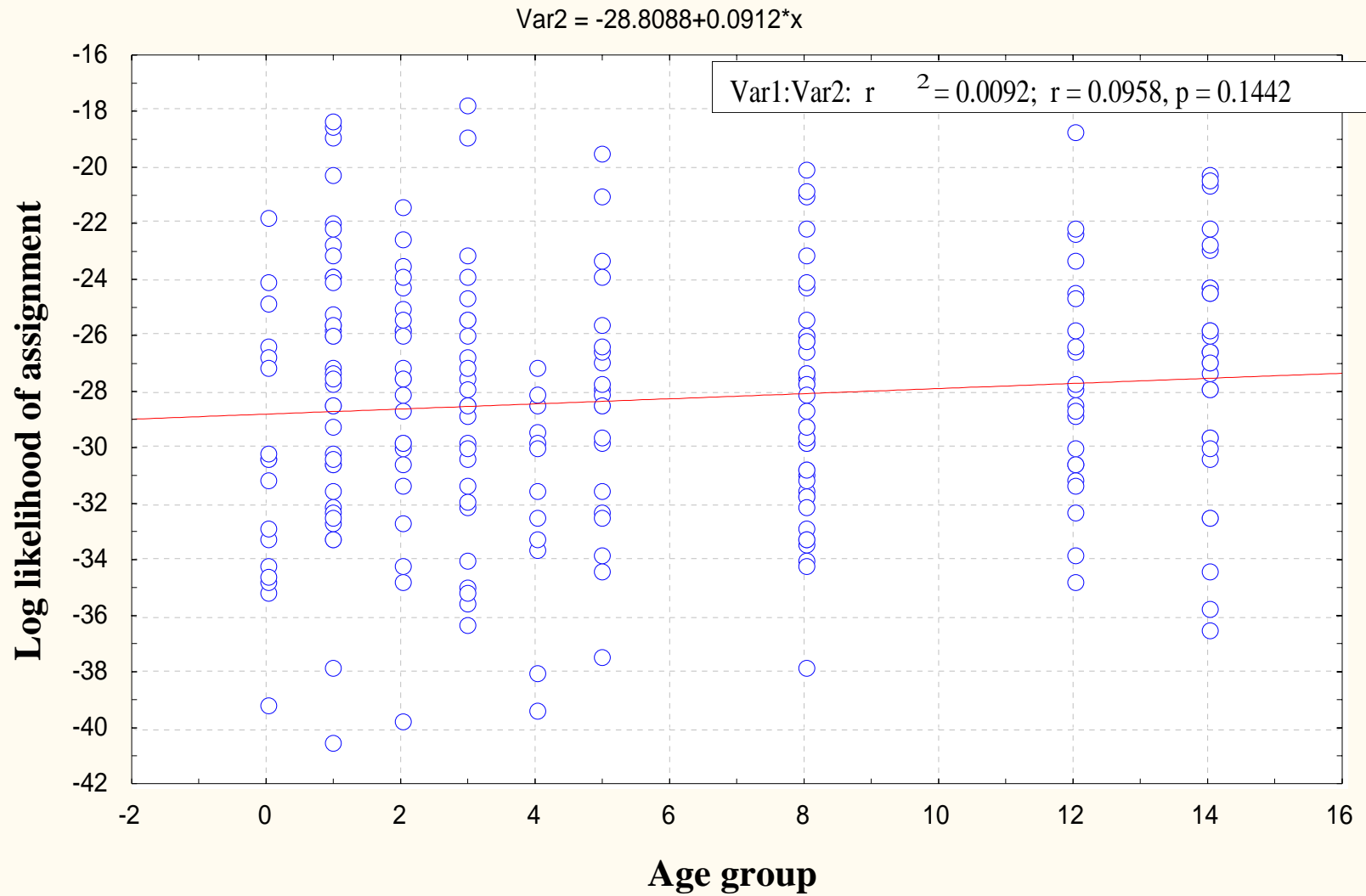


Log likelihoods of assignment of individual male buffalo in HUF

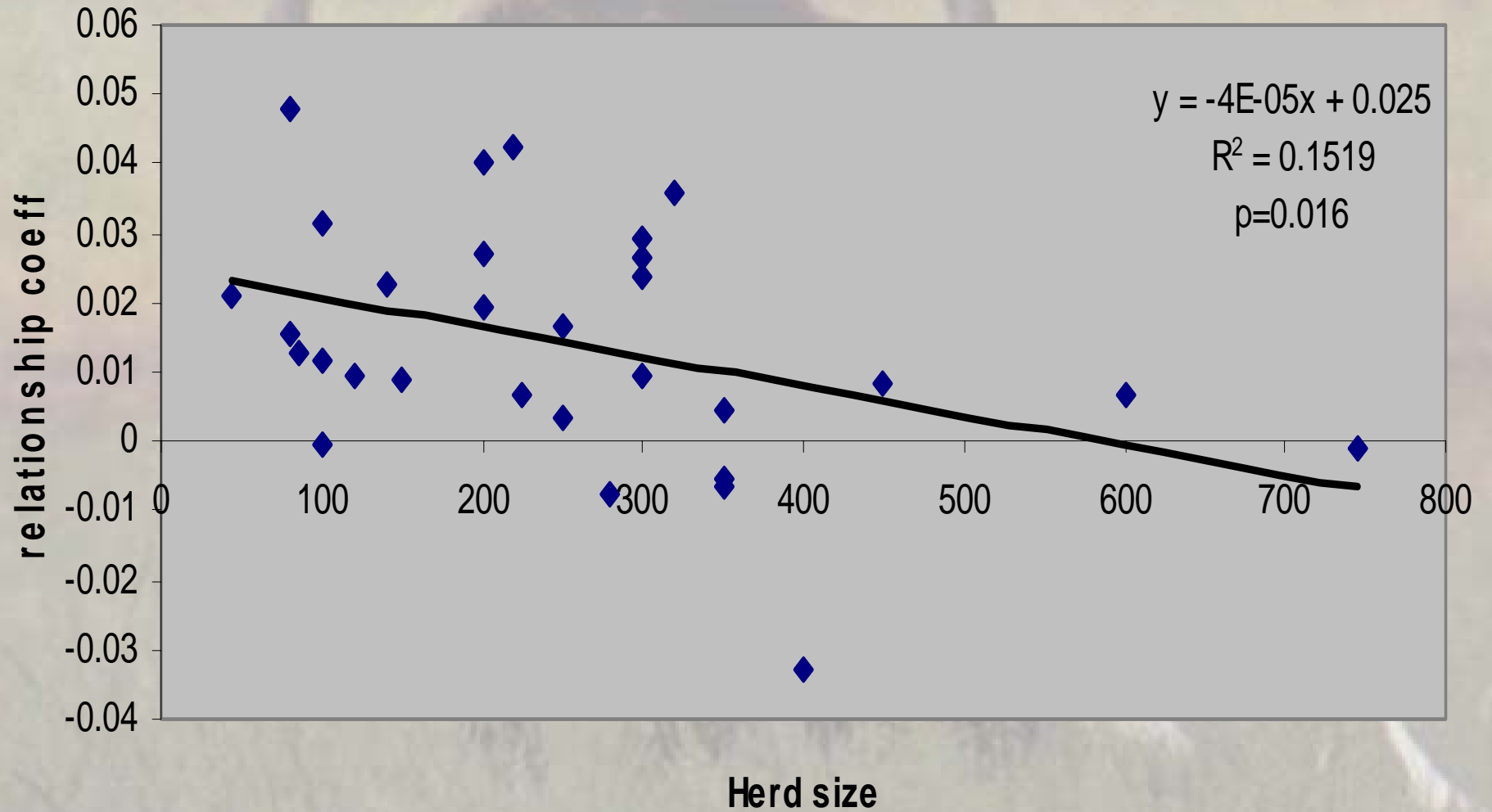
$$\text{Var5} = -27.8313 - 0.1106^* \text{Age group}$$



Log likelihoods of assignment of individual female buffalo in HUP



Relatedness among herd members as a function of herd size in KNP



Conclusions

- **KNP has “retained” much of its genetic diversity, while HUP diversity is relatively low and quickly declining**
 - founder effect or genetic drift (small pops. prone to drift) – or both?
- **Little diversity among female lineages in HUP**
 - small founder female population (remnant of bottleneck?) or genetic drift?
- **Very little structure in HUP, except for particular herds**
 - Little female dispersal taking place among certain herds within HUP (large F_{st} values)
- **Male biased dispersal :Relat. for F.: 0.0352 Relat. for M.: 0.0155 (P= 0.05)**

•Bottleneck impacted more severely on HUP

•Low degree of variation

• genetic drift taking place?

- also shown for Y-chromosomal data (van Hooft)

• drift may lead to inbreeding = may compromise the buffalo's ability to adapt to future environmental changes in the future

Based on Y-chromosomal data:

•Many populations not sustainable and susceptible for inbreeding depression

($N_e < 50$, $> 1\%$ genetic erosion per generation)

•Dominant males may have a large role in disease transmission

Current genetic status of parks may call for different genetic management practices?

A water buffalo with large, curved horns is grazing in a field of tall grass. The image is slightly faded and serves as a background for the text.

Acknowledgements

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