

# Geographical patterns of cattle, sheep and goat diversity

Clines, clusters, introgression, and a conservation dilemma

*Towards a strategy for the conservation of  
the genetic diversity of European cattle*

EU project ResGen CT98-118

*Sheep and goat genetic  
resources in marginal rural*

*areas* [sirs.epfl.ch/projets/econogene/](http://sirs.epfl.ch/projets/econogene/)



## Utrecht

J.A. Lenstra  
I.J. Nijman

## Malle

G. Mommens

## Berne

G. Dolf

## Roslin

J.L. Williams

P. Wiener

D. Burton

## Dublin

D. Bradley

D.E. MacHugh

R.A. Freeman

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Josas

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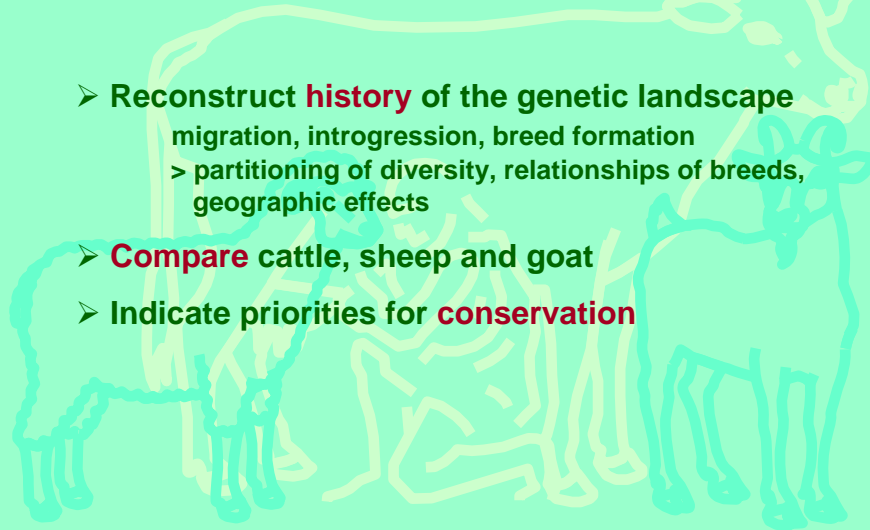
C. Maudet



# Geographical patterns of cattle, sheep and goat diversity

Clines, clusters, introgression, and a conservation dilemma

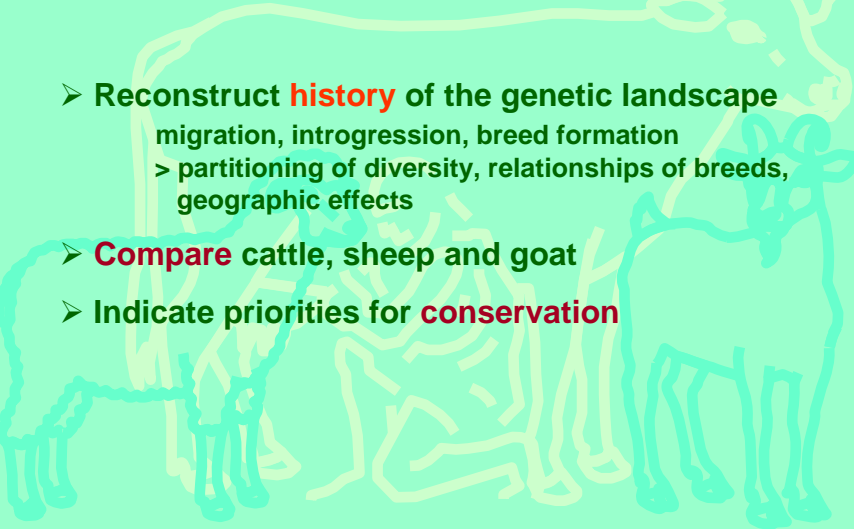
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  - migration, introgression, breed formation
  - > partitioning of diversity, relationships of breeds, geographic effects
- **Compare** cattle, sheep and goat
- Indicate priorities for **conservation**



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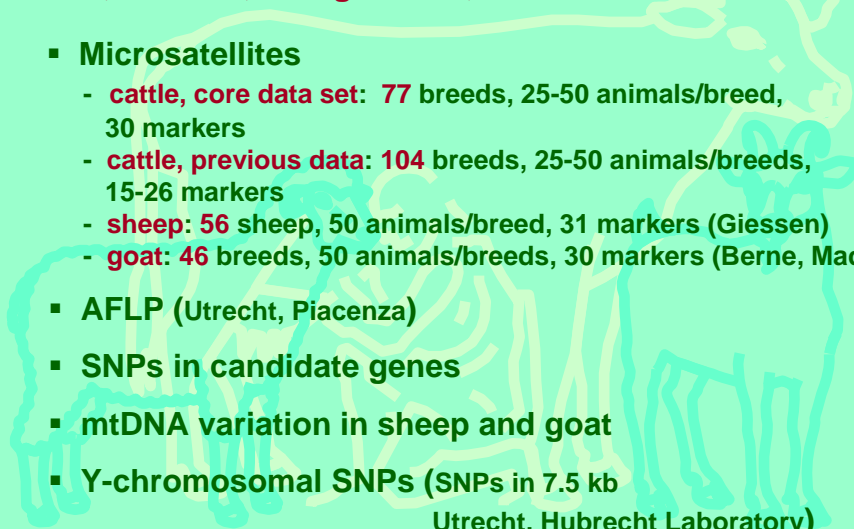
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## Geographical patterns of cattle, sheep and goat diversity

Clines, clusters, introgression, and a conservation dilemma

- **Microsatellites**
  - **cattle, core data set:** 77 breeds, 25-50 animals/breed, 30 markers
  - **cattle, previous data:** 104 breeds, 25-50 animals/breeds, 15-26 markers
  - **sheep:** 56 sheep, 50 animals/breed, 31 markers (Giessen)
  - **goat:** 46 breeds, 50 animals/breeds, 30 markers (Berne, Madrid)
- **AFLP** (Utrecht, Piacenza)
- **SNPs in candidate genes**
- **mtDNA variation in sheep and goat**
- **Y-chromosomal SNPs** (SNPs in 7.5 kb  
Utrecht, Hubrecht Laboratory)



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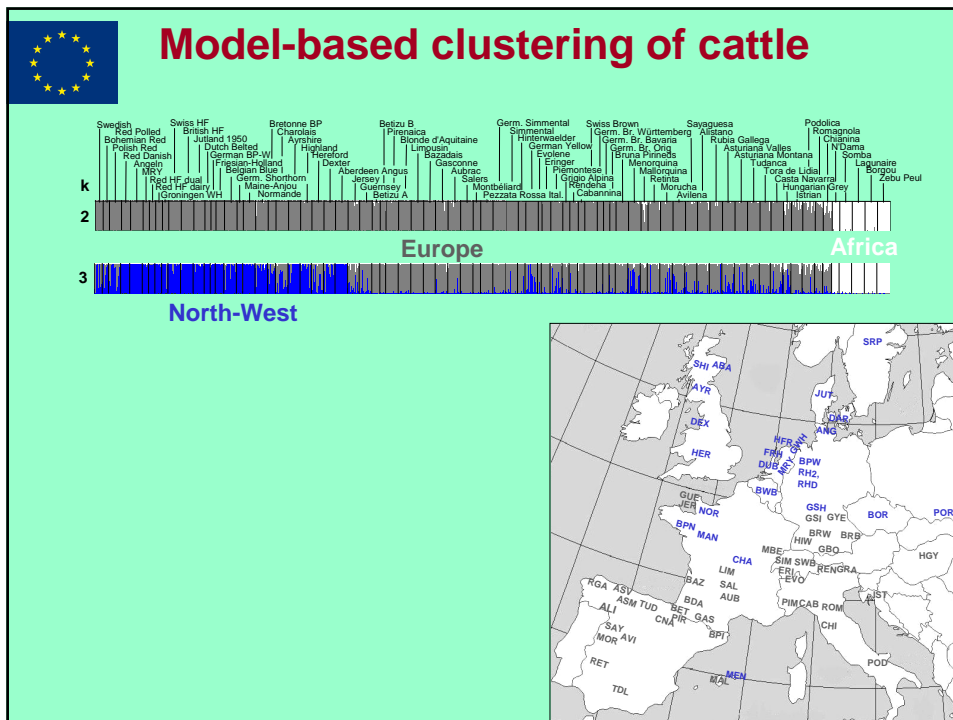
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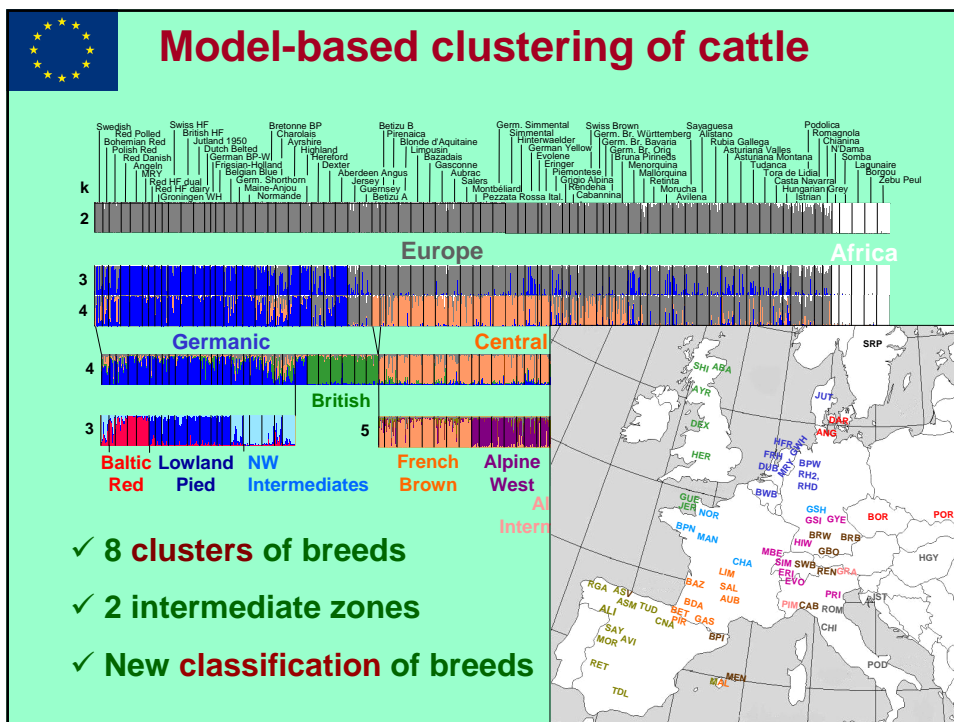
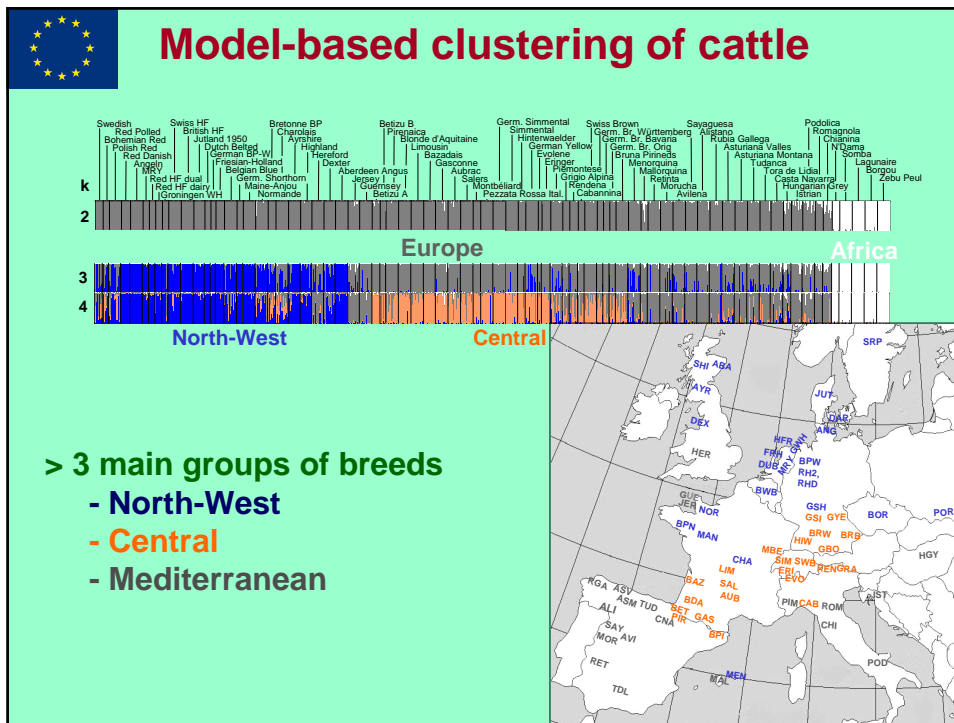
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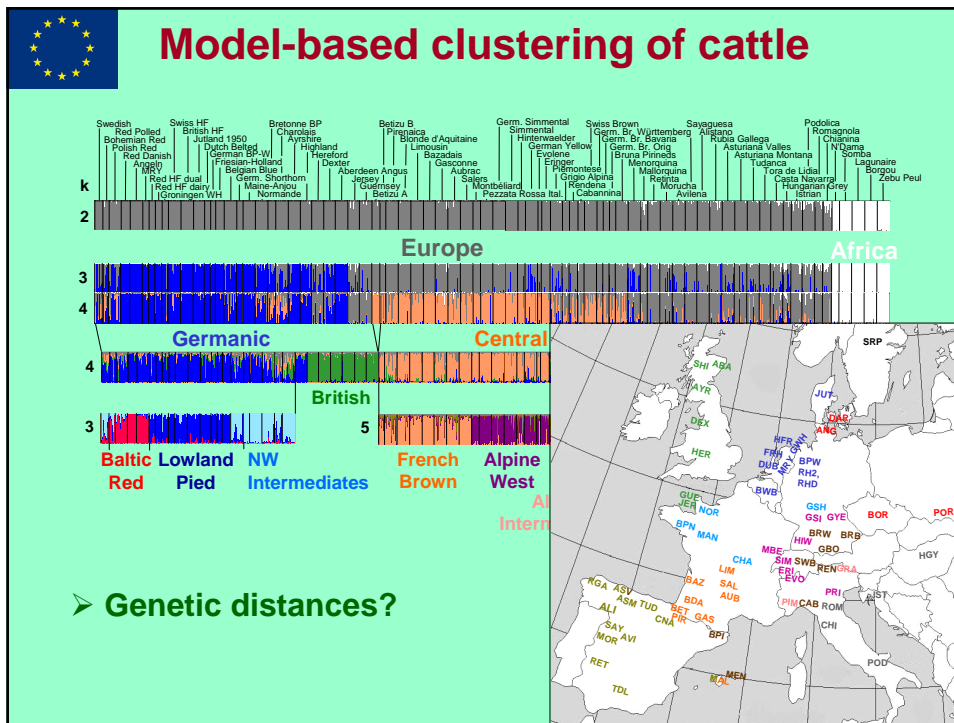
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- **Analysis**
  - **Model based-clustering** of multilocus genotypes
  - **Network** representation of genetic distances
- **Y-chromosomal SNPs (7.5 kb, 800 animals, Utrecht, Hubrecht Laboratory)**

## Model-based clustering Structure, J. Pritchard (2000)

- Originally designed for detection of stratification in genetic association studies
- Finding subdivision by optimization of Hardy-Weinberg and linkage equilibria via Monte-Carlo procedure
- Bayesian assignment of individuals to  $k$  clusters
- Application to **human genotypes** (Rosenberg *et al.*, 2002, Science 298, 2381-2385) praised by the *Lancet* as 'the most relevant biomedical publication in 2002' and already in textbooks



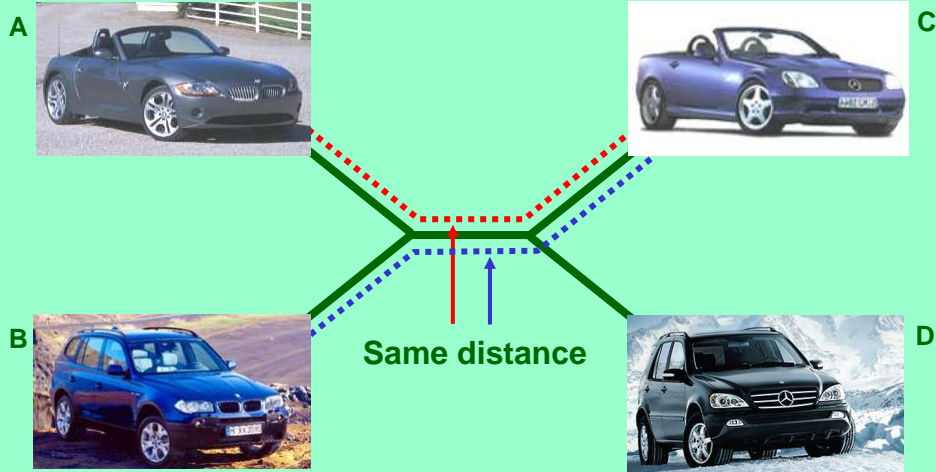




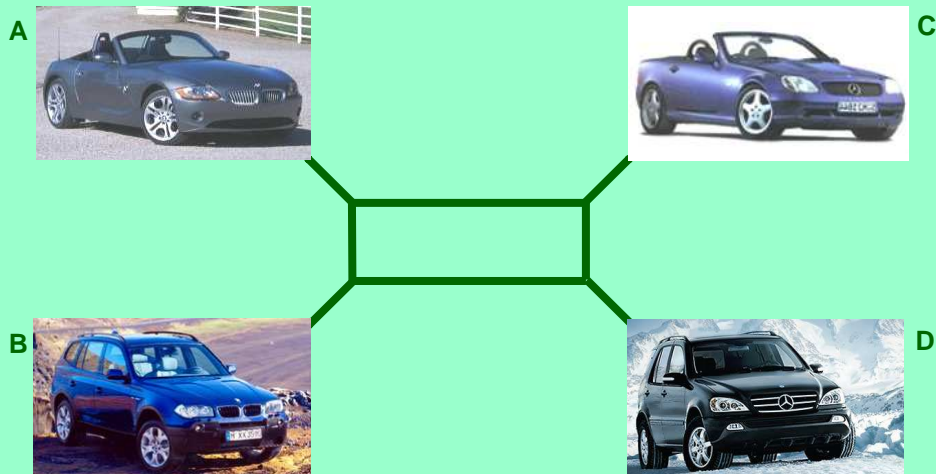
## Visualization of distance analysis

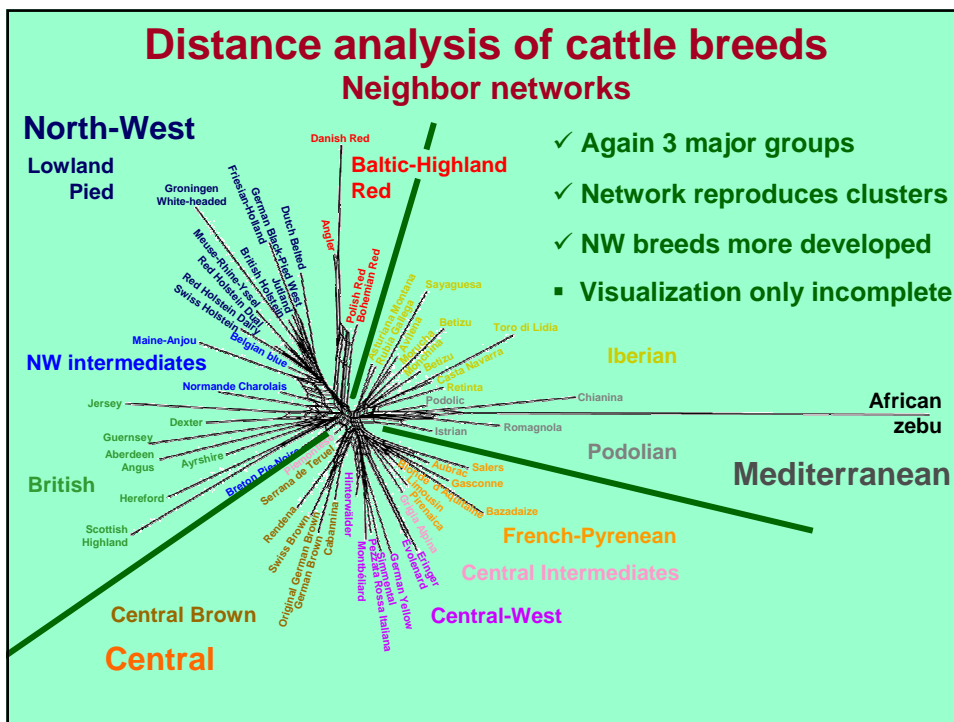
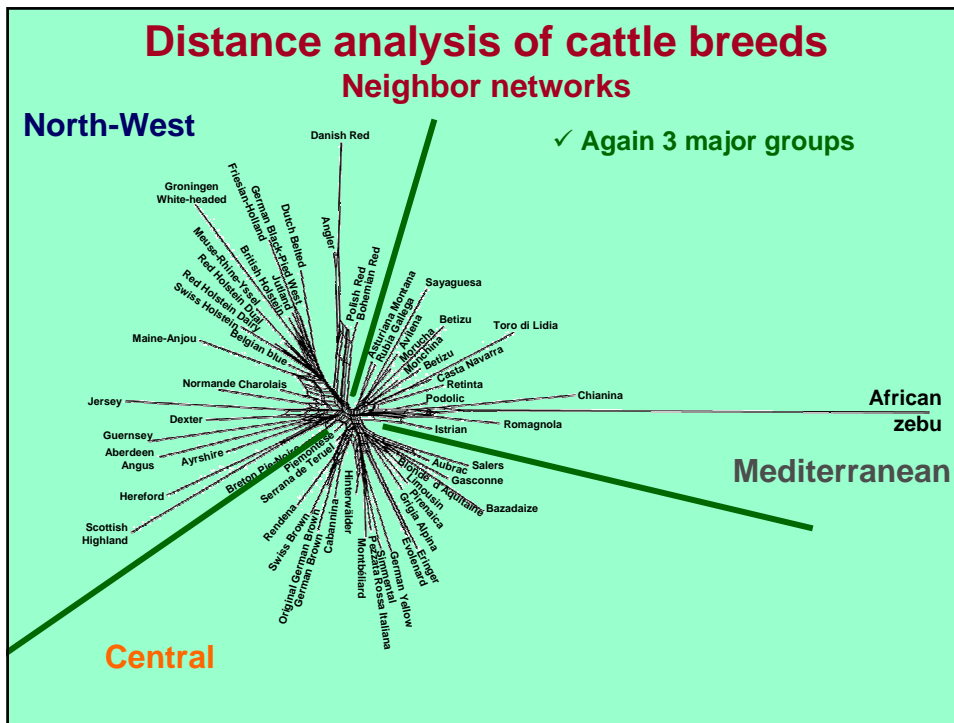
- **Trees** (hierarchical clustering)
  - confounded by reticulation
  - (e.g., relationships of breeds from different clusters)
- **Coordinate plots** > geospatial gradients
  - display part of the information
  - confounded by inbred breeds
- **Networks** for more complex situations

## Distance analysis example of reticulation



## Distance analysis networks for reticulated data set NeighborNet: networks via Neighbor-Joining

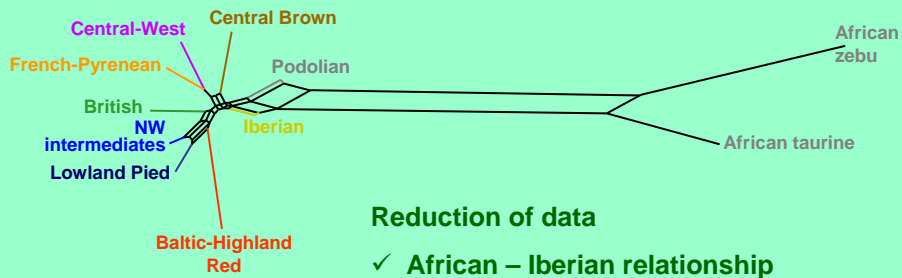






## Distance analysis of cattle breeds

### Neighbor networks of clusters



Reduction of data

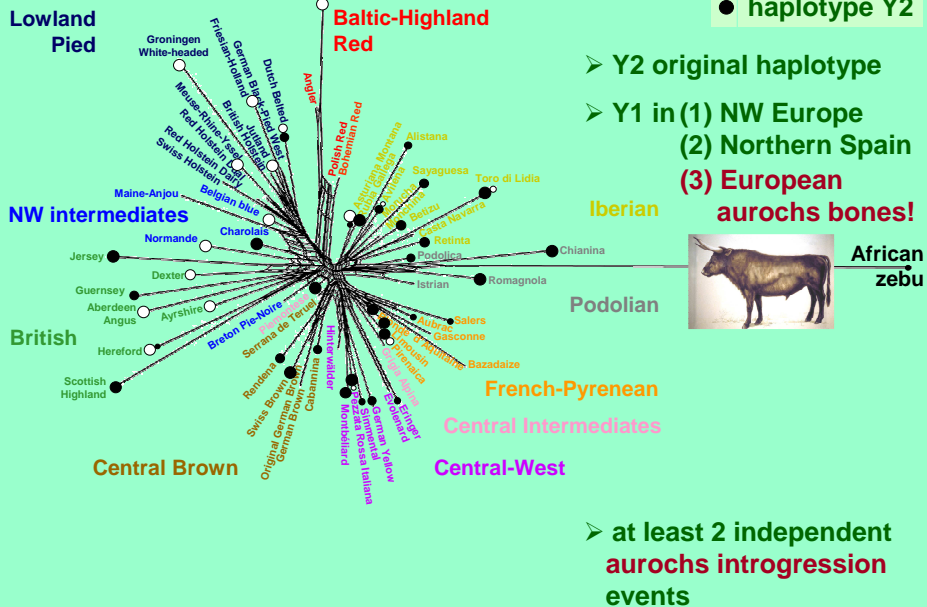
- ✓ African – Iberian relationship
- ✓ dairy NW clusters most distal

What about the **Y-chromosomes**?

## Cattle Y-chromosomes

results also from Götherström *et al.*, 2005

○ haplotype Y1  
● haplotype Y2





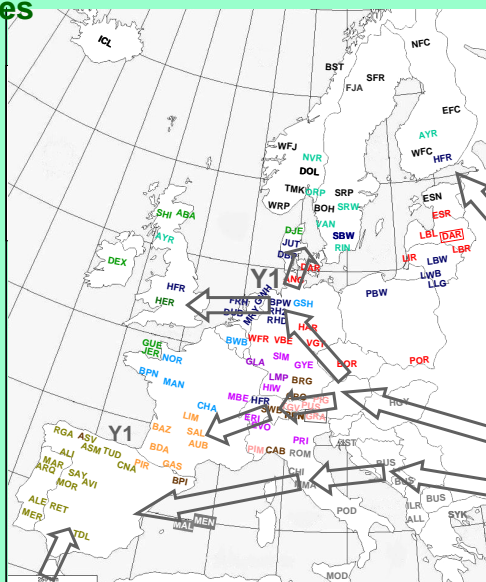
# Genetic history of European cattle

## 1. Neolithic migration routes

- Mediterranean coast
- Africa > Iberia
- Danube > France, NW
- Russia > Scandinavia

## 2. Differentiation by adaptation, breeding

- divergence of old British breeds
- divergence of dairy NW clusters (Lowland Pied, Baltic-Highland Red, NW intermed.) with Y1 haplotype and wild introgression?



# Genetic history of European cattle

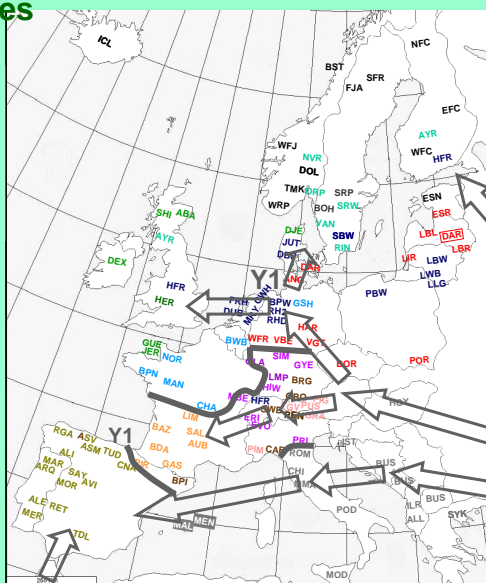
## 1. Neolithic migration routes

- Mediterranean coast
- Africa to Iberia
- Danube > central, >NW
- Russia > Scandinavia

## 2. Differentiation by adaptation, breeding, wild introgression

## 3. Historic North-South contrasts maintained

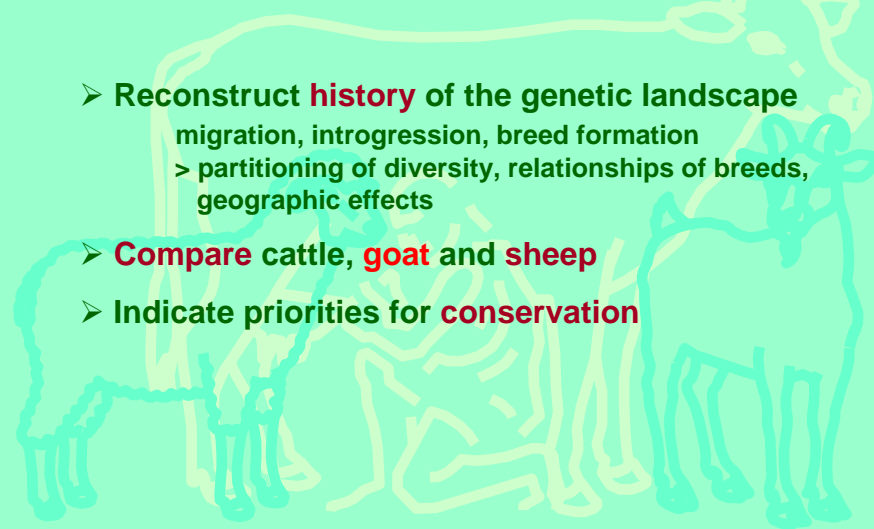
- Langue d'oc - d'oïl
- Hoch - Niederdeutsch
- Catholic - Protestant
- Landscape effect?



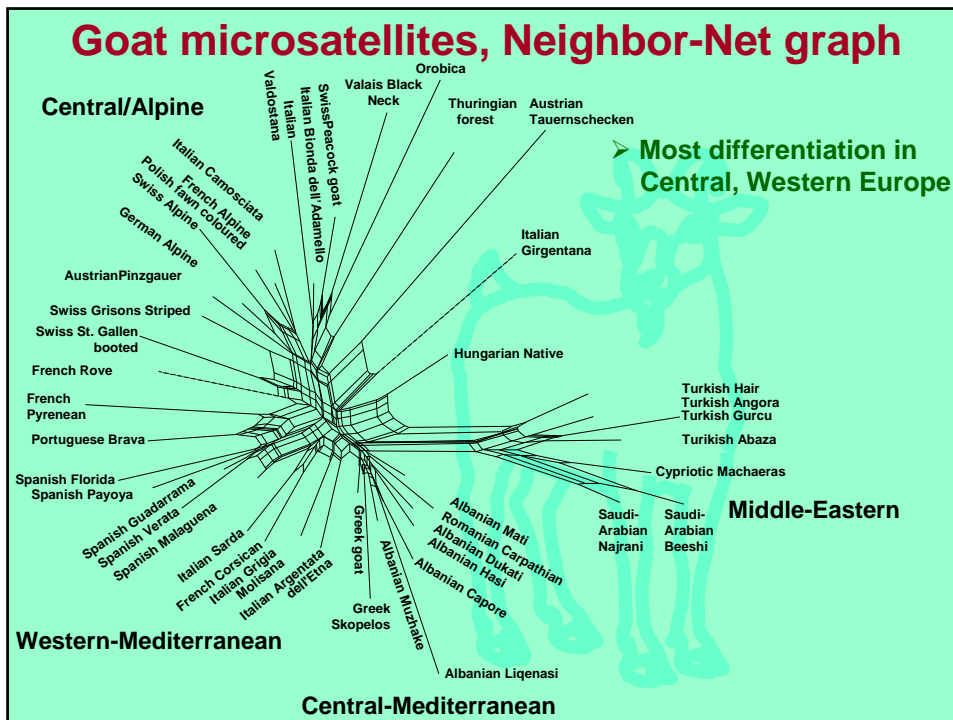
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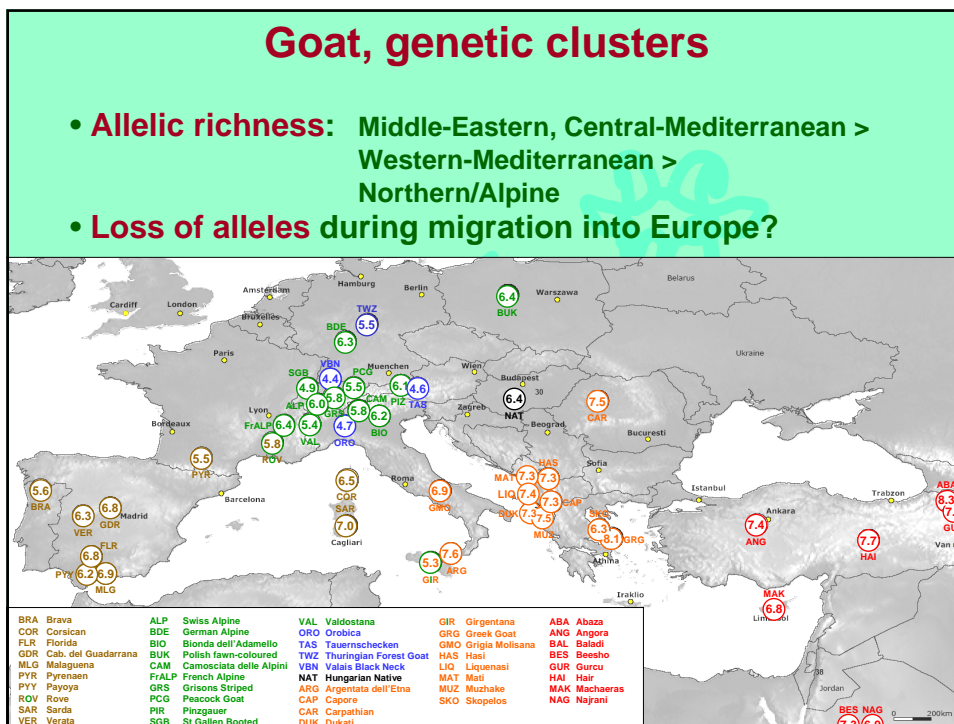
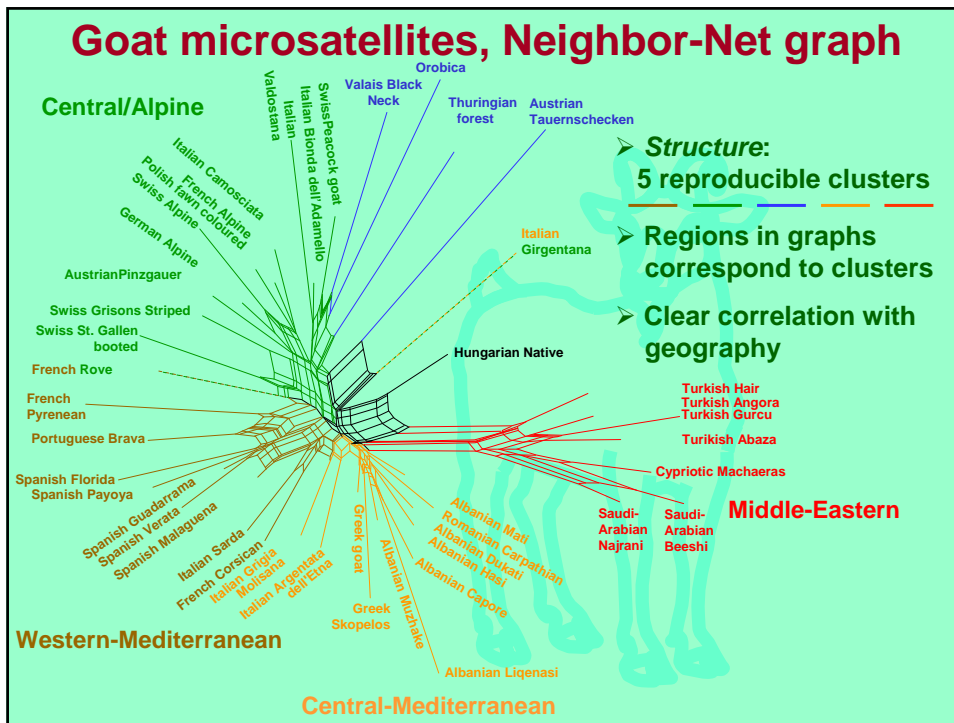
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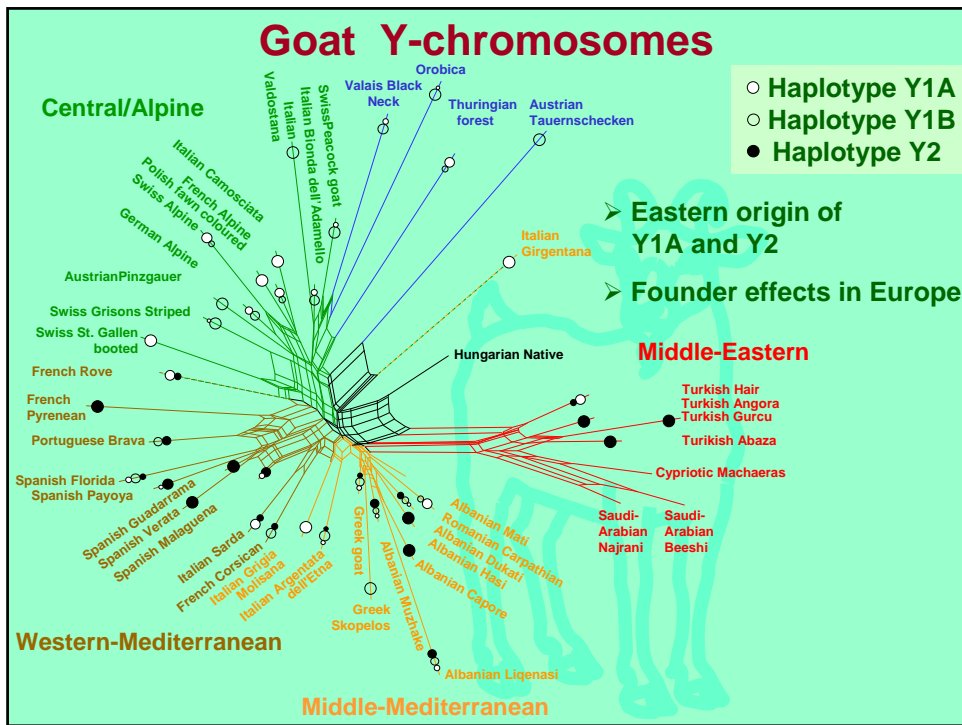
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## Goat microsatellites, Neighbor-Net graph





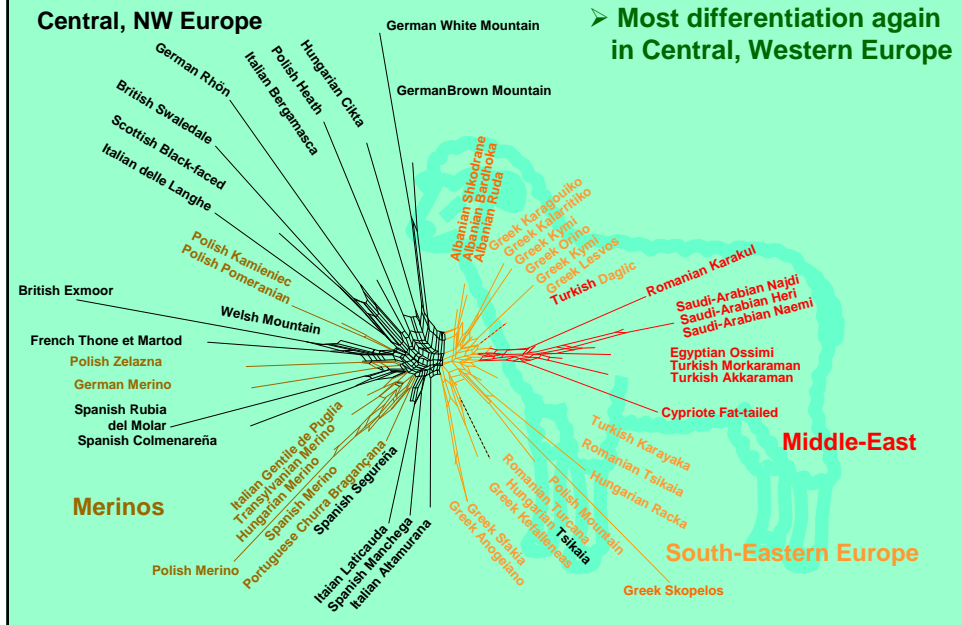


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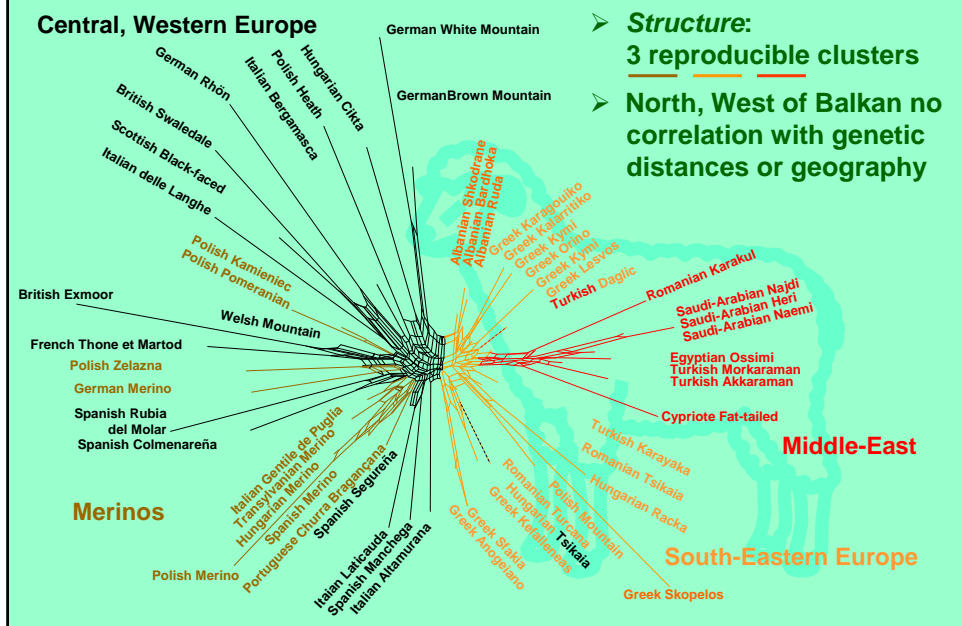
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## Sheep microsatellites, Neighbor-Net graph

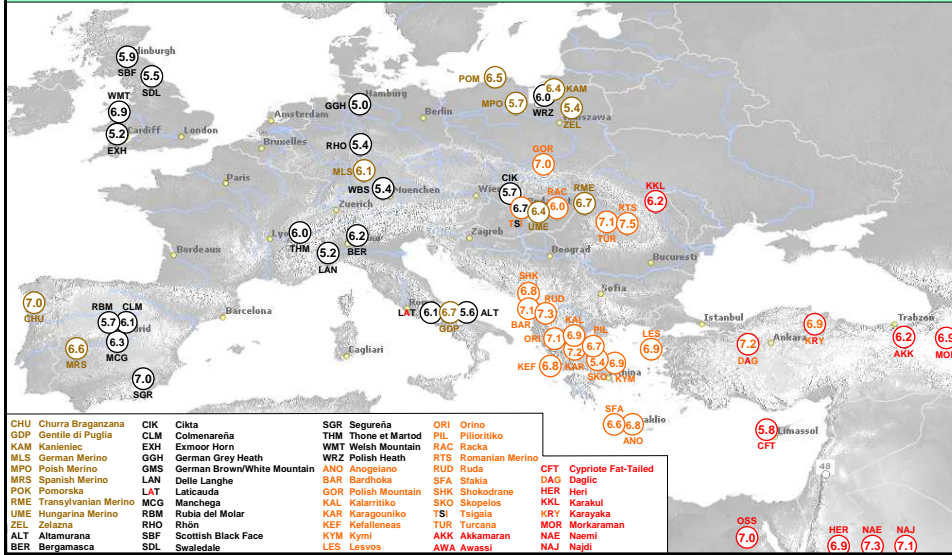


## Sheep microsatellites, Neighbor-Net graph



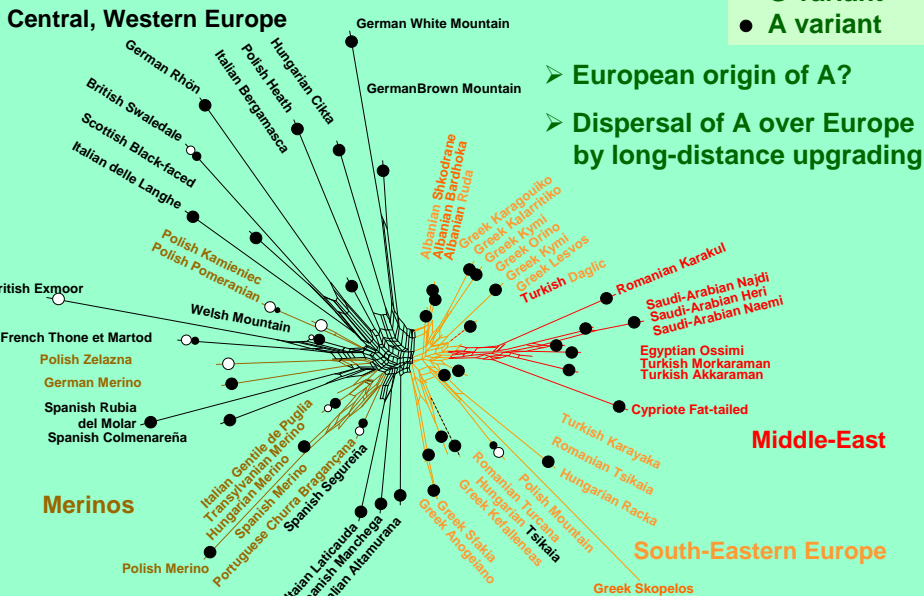
# Sheep genetic clusters

- 2 clusters in the East, dispersal in the North and West
- Allelic richness: again decrease SE > NW



# Sheep Y-chromosomes

- G variant
- A variant



## Comparison of cattle, sheep and goat

### Expected effects of migration and breeding

- correlation geography and genetic distance
- decrease of allelic richness SE > NW
- phenotypes of NW breeds more developed

**Goat** - **prototype** species

**Sheep** - more panmictic in NW Europe **by upgrading with rams from other regions**

**Cattle** - less effect on allelic richness within continent  
- outstanding position of NW dairy breeds explained by **introgression of aurochs bulls**



## Geographical patterns of cattle, sheep and goat diversity

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## Criteria for conservation

1. Genetic distances  
mainly determined by genetic drift of allele frequencies

$F_{ST}$  distances,  
via Weitzman algorithm

> priority of **inbred** breeds

2. Low kinships

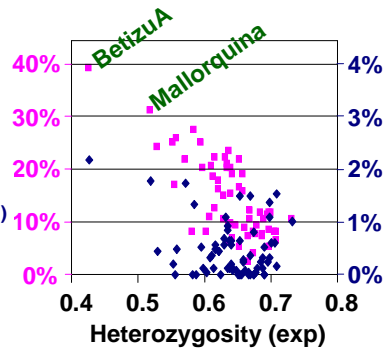
Marker-Estimated Kinships  
(J. Windig, K. Engelsma, H. Eding, Lelystad)

> priority of **Eastern** breeds

3. Molecular diversity  
number of alleles

To be tested with realistic datasets. Correlation with kinship?

Contributions of cattle breeds to diversity of *safe set* of non-endangered breeds



4. Diverse phenotypes

## Criteria for conservation

1. Genetic distances by random drift
2. Low kinship,
3. Molecular diversity

```
GCAACAAACTACTCTCGGCTTTTAGGAAAGACTCTTGTGCACAGACAGT
..G.....T.....
..G.....G.....T.....
..G.....A.....C.....T.....
```

> priority to **Middle-Eastern** breeds

4. Diverse phenotypes



> priority to **Northern/Western/Central** breeds

## Dilemma for conservation

1. Genetic distances by random drift
2. Low kinship,
3. Molecular diversity

```
GCAACAAACTACTCTCGGCTTTTAGGAAAGACTCTTGTGCACAGACAGT
..G.....T.....
..G.....G.....T.....T.....
..G.....A.....C.....T.....
```

> priority to **Middle-Eastern** breeds

4. Diverse phenotypes



> priority to **Northern/Western/Central** breeds

**Two obvious criteria lead to different choices**

## Recommendations for conservation

1. Forget genetic distances on the basis of genetic drift
2. Conserve molecular diversity  
**primitive** breeds, **hybrid species** origin

```
GCAACAAACTACTCTCGGCTTTTAGGAAAGACTCTTGTGCACAGACAGT
..G.....T.....
..G.....G.....T.....T.....
..G.....A.....C.....T.....
```

3. Specify valuable phenotypes to be conserved



4. Breed management

select on desired **phenotype**  
but also protect the **heterozygosity**: consider **outcrossing**

**Genetic purity**: > considerable sentimental appeal  
> direct threat of animal health  
> yet difficult to define on the DNA level

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- **History** of the genetic landscape
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- **Differences** between cattle, sheep and goat
- **Conservation:** dilemma, considerations

