Utilisation and conservation of genetic diversity in (farm) animals

Guest lecture ABG course 2017

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Centre for Genetic Resources, the Netherlands

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- IVO in Zeist/ASG Lelystad

Population genetics

Breed comparisons

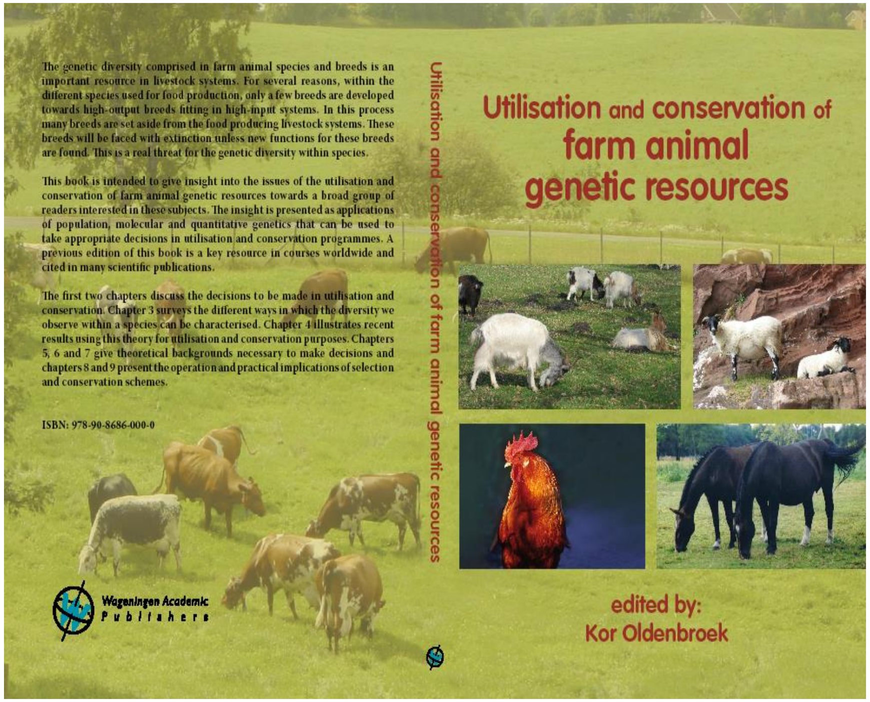
Crossbreeding

- CGN

Teaching material

Breeding in small populations

Further reading



The genetic diversity comprised in farm animal species and breeds is an important resource in livestock systems. For several reasons, within the different species used for food production, only a few breeds are developed towards high-output breeds fitting in high-input systems. In this process many breeds are set aside from the food producing livestock systems. These breeds will be faced with extinction unless new functions for these breeds are found. This is a real threat for the genetic diversity within species.

This book is intended to give insight into the issues of the utilisation and conservation of farm animal genetic resources towards a broad group of readers interested in these subjects. The insight is presented as applications of population, molecular and quantitative genetics that can be used to take appropriate decisions in utilisation and conservation programmes. A previous edition of this book is a key resource in courses worldwide and cited in many scientific publications.

The first two chapters discuss the decisions to be made in utilisation and conservation. Chapter 3 surveys the different ways in which the diversity we observe within a species can be characterised. Chapter 4 illustrates recent results using this theory for utilisation and conservation purposes. Chapters 5, 6 and 7 give theoretical backgrounds necessary to make decisions and chapters 8 and 9 present the operation and practical implications of selection and conservation schemes.

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Utilisation and conservation of farm animal genetic resources

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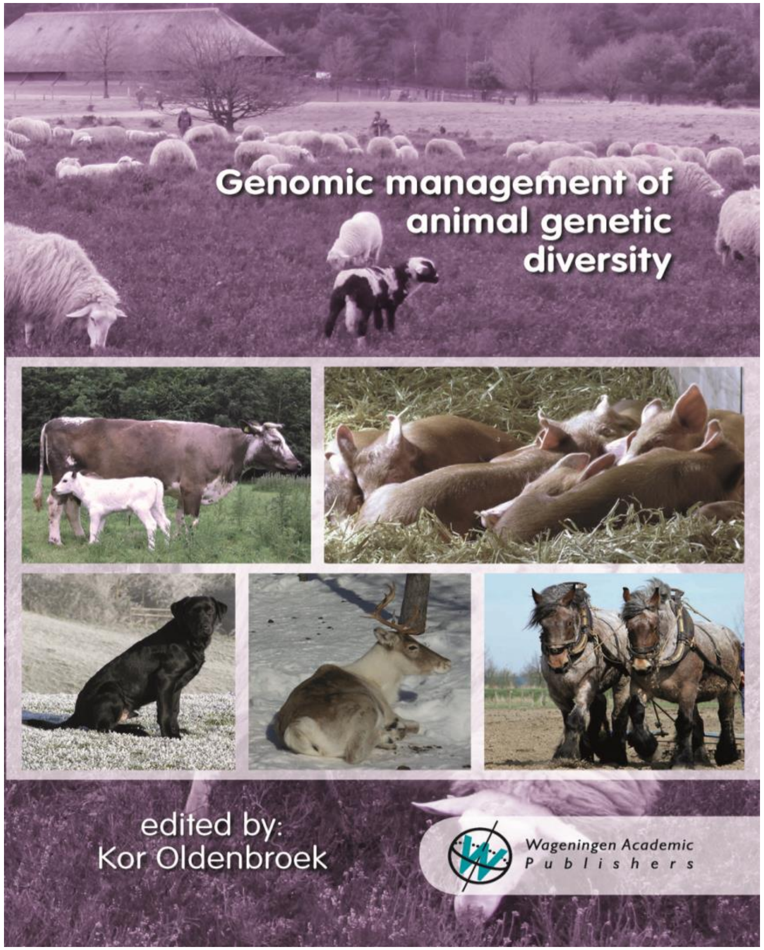

Genomic management of animal genetic diversity

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Further reading in Dutch

Raad van Beheer
Voor alle (ras)honden!

Het fokken
van rashonden

Omgaan met verwantschap en inteelt

Kor Oldenbroek
Jack Windig

Programme

- What is genetic diversity, what is a breed?
- Why and how to conserve genetic diversity?
- Opportunities of genomics for the conservation and use of genetic diversity
- Examples of the exploitation of rare breeds and of DNA-research with rare breeds

What is genetic diversity?

It is the set of differences

- between species,
- breeds within species, and
- individuals within breeds

These differences are expressed as a consequence of the differences in their DNA

On average, the genetic variance within a species =

0.5*variance between breeds + 0.5*variance within breeds

What is a breed?

- "Animals that, through selection and breeding, have come to resemble one another and pass those traits uniformly to their offspring."

And when we hear violent discussions among breeders:

- "A breed is a breed if enough people say it is"

- "A breed is a breed when the owners of the animals are willing to collaborate and maintain the breed"

All dog breeds are descendend from the wolf

Large variation: Danish dog 107 cm high; Chihuahua: 19 cm

Dog species > 400 breeds; but only 20 % of DNA variation in the wolf

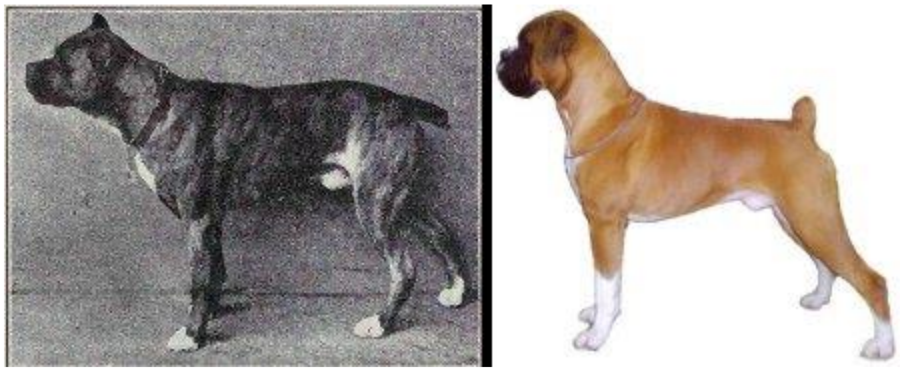
Domestication is accompanied with a restriction of the genetic diversity

Dogs: a few genes (loci) responsible for large variation

- One gene for coat structure: curled, long and sleek
- A few genes for skeleton: lenght of bones and nose, shape of the head, skull shape and dwarfism: one gene for a protein hormone with large effect on weight
- Creation of a dog breed: Crossing of a few breeds with required traits and selective breeding to create uniformity in offspring

>> In dogs it is easy to create extreme phenotypes

From landraces > standardized breeds



- **Landraces:** a lot of variation in phenotype and created by isolation and adaptation (e.g. to high altitude)
- **Standardized breeds:** less variation, breed standard, registration of pedigree, classification and registration of performance (breeding programme); start in the 18th century (Bakewell, Scotland)

Some factors affecting genetic diversity

Variance between breeds:

- Number of breeds
- Number of generations they exist
- Population sizes
- Differences between breeding goals

Variance within a breed:

- Population size
- Number of founders
- Selection intensity

Reasons for maintaining genetic diversity (1)

- In farm animal production intensification still takes place, started after World War II

- Role of species may change: e.g. sheep from wool > meat and horses from draught > sport

- Breeding programmes are expensive > mergers of breeding companies with loss of breeds or selection lines e.g. in pigs in 2000 25 Dutch lines; 2015 discussion about 5 or 3 lines for the future

> Many (standardized) breeds are set aside

Reasons for maintaining genetic diversity (2)

Within a population to:

- Prevent inbreeding depression (decreased fitness)
- Maintain adaptability (large genetic variance needed)
- Preserve alleles that may be useful in the future
- Limit occurrence of recessive genetic defects

Objectives conservation genetic diversity

Sustainable use in the rural area:

Economic potential

Social cultural role

Environmental services

Conservation of the flexibility of the genetic system: food security

Risk of change environment

Risk of change in demand

Disasters (diseases)

Research and training

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Comparison of conservation methods (complementary)

- ***In situ* conservation**

  Active breeding

  Used (short term)

  Adaptation possible

- ***Ex situ* conservation**

  <u>in vitro</u>

  Cryoconservation in liquid nitrogen

Purposes of Animal Gene Banks (*in vitro*)

- Preserve the present wealth of genetic diversity →Secure it for future generations
- To be able to recreate extinct breeds or breeding lines
- As a back-up in case genetic problems would occur
- To allow development of new lines or breeds
- To support *in situ* conservation
- For research and genetic characterisation purposes

Characteristics of the CGN semen collection

- Stored at two places: Wageningen – Utrecht (50 kms)

- Cattle: > 1960; >1990 unproven bulls; selected bulls from native breeds sampled at the farm (strict conditions)
- Pigs: 2001 16 different lines from industry; 5 > 3 in use now!
- Horses: stallions from native breeds (>1960)
- Poultry: semen from 20 native breeds collected at CGN
- Sheep and goat: collected at farms or at slaughter

Semen collection CGN 2016

Species	# Breeds	# Males per breed	# Doses
Cattle	18	1 – 5,223	239,793
Sheep	10	8 – 71	31,154
Goat	5	5 – 33	6,590
Horse	9	1 – 41	3,307
Pig	28	1 – 56	20,464
Chicken	31	1 – 20	18,828
Duck	3	14 – 34	1,588
Dog	5	1 – 8	410
Rabbit	8	3-12	1,957

Aim of Dutch AnGR Gene Bank

Long term

- To safeguard all rare/native/endangered breeds of farm animals in the gene bank
- To promote and facilitate conservation of back-up samples of all (commercial) breeds in the gene bank

Short term

- To support breeding programs of endangered breeds - by distribution of gene bank semen

What to conserve in a genebank?

Genetic diversity:

1. Breeds

2. Animals

3. Alleles

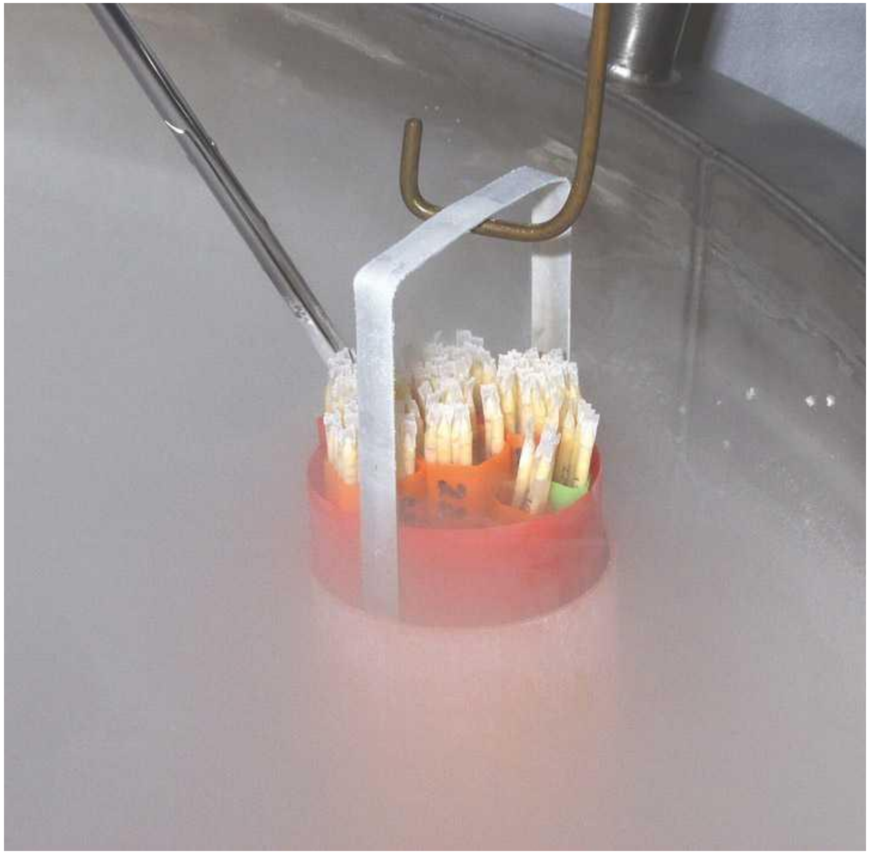
Conservation of breeds within species

Core collection per breed:

Genebank:

- 50 sires per breed

- Doses of semen: species dependent (Breeding success; litter size) varies per breed from 600 (pigs and poultry) up to 5000 (sheep and goats)



Examples of use of rare breeds

High quality products for niche markets:

- Breed specific products based on unique characteristics
- Produced with traditional techniques for regional markets with premium
- Collaboration between producers

Exploit ecological functions: nature management

- Herbivore species differ in grazing behaviour
- Breeds also and differ in robustness
- Large numbers required > great opportunity

Exploiting potential societal/cultural functions

- Attractive elements rural area (tourists)
- Cultural services (ceremonies, games)
- Sport or hobby function

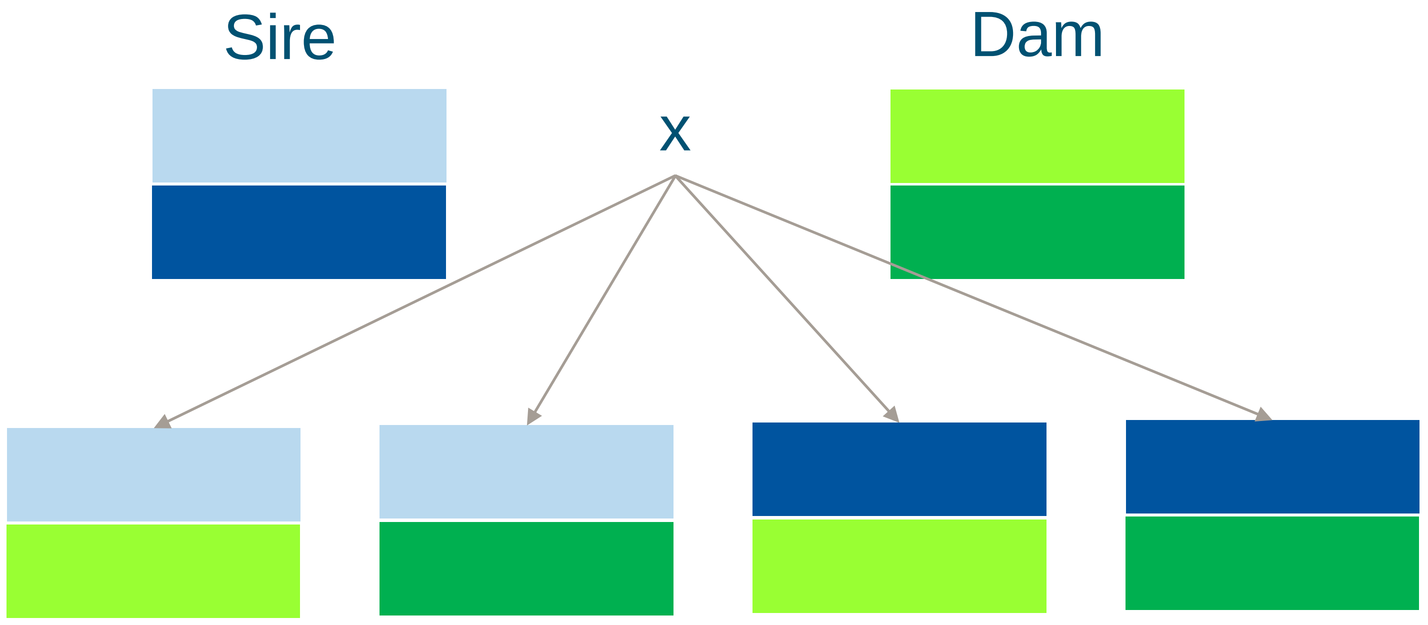
Genomic management of genetic diversity

- **Genomics** is the detailed analysis of the DNA of an animal with high-troughput techniques (DNA-chips) from 10.000 SNPs (10k) > Whole Genome Scan (WGS)
- **Management** (in animal breeding) is: 1) the choice of the animals as parents for the next generation, 2) the choice of the sires and of dams for the individual matings and 3) the number of offspring each parent may produce
- **Genetic diversity** is the set of differences between species, breeds within species, and individuals within breeds expressed as a consequence of differences in their DNA

Genomics: determination and tracing of alleles by DNA analysis

DNA

- Present in two copies (pairs of chromosomes)
- Always 50% submitted by the dam and 50% by the sire
- A random process determines which part from the sire and from the dam



Genomics determines which part from the sire and which part from the dam!

Conservation of genetic diversity: past and future

- Past: Decisions based on pedigree and phenotypic information

Genebank collections optimised based on pedigrees

- Genomics era: Decisions based on DNA information (SNPs en WGS) and phenotypic information

Genebank collections optimised based on DNA-relationships

Detection of interesting QTL’s (link with QTL databases)

>> Compose core collection more efficient and is better characterised

Utilisation of genetic diversity: past and future

- Past: BV estimated based on pedigree and phenotypic information

  Selection based on estimated breeding values (EBV)

- Genomics era: BV estimated based on DNA information (SNPs)

  Phenotypic information still required!

  Selection based on prediction formula with SNP-input

  <u>Detection of heterozygous carriers of recessive lethal alleles</u>

>> Genomic selection possible at a young age of the animals

Opportunities of genomics

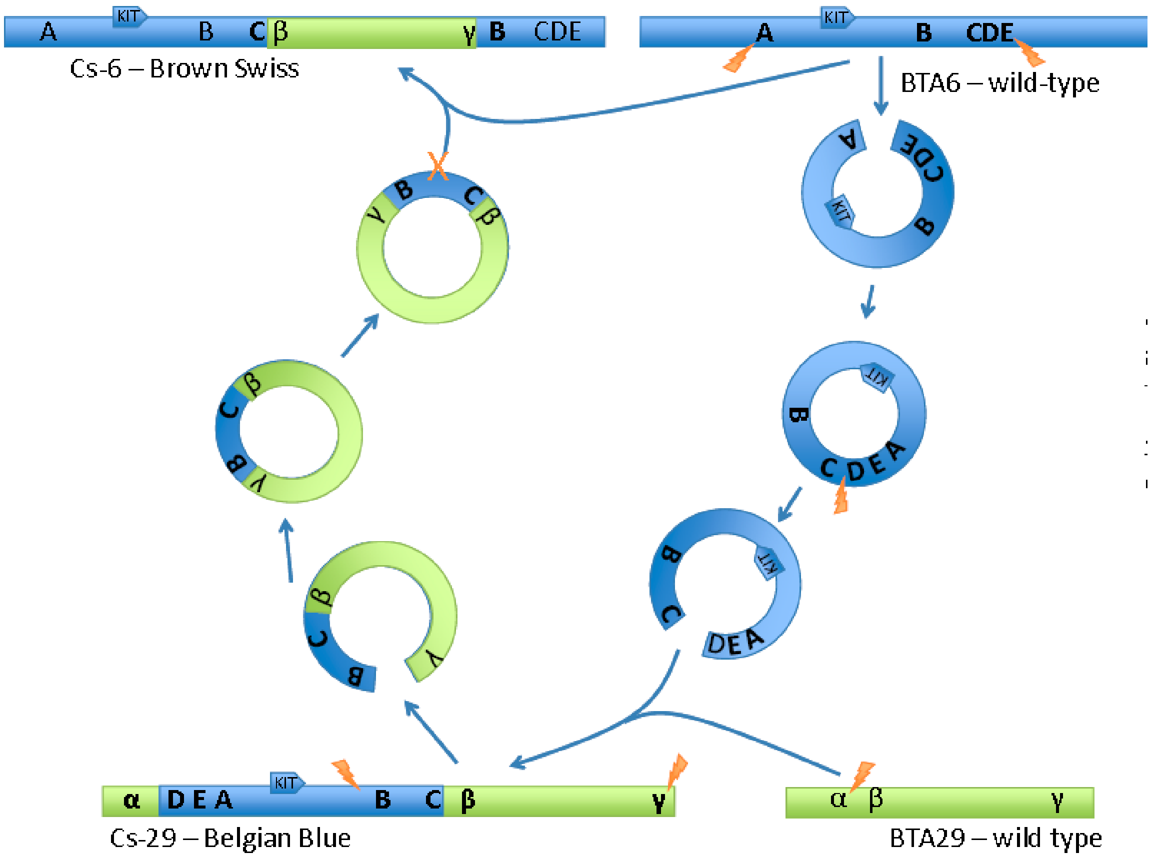
- Improving pedigree quality (verifying pedigrees)
- More effective use of genetic variation to obtain genetic gain
- Better optimisation of genetic gain and inbreeding
- Identifying carriers of deleterious alleles
- Identifying carriers of interesting alleles or QTLs

Genomics example (1): history of a unique trait

Color sided cattle

- Locus for spotted is located on chromosome 6
- Long ago: during meiosis part of chromosome 6 created a circle and was incorporated (other sequence) in chromosome 29
- Color sided locus is on chromosome 29
- Epistasis with spotted
- WW = nearly white
- W/- = color sided
- -/- = spotted

Recombination of circles between different chromosomes, Nature (2010)



Example (2) of application of genomics on genebank material: SNP-analysis solves questions on the genetic background of the rare Dutch breed of Red Friesian cattle

Kor Oldenbroek, Ina Hulsegge, Jack Windig and Mario Calus

JAM 2015, Orlando, Florida

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History of the Dutch Red Friesian Cattle breed

- Herdbook established 1879
- Bottleneck in 1990 (n < 20)
- Genebank sires 1960-1970
- Regenerated in 25 years
- > 600 females; > 50 sires

Three questions of the breeding organization

1. Is the Dutch Red Friesian Cattle breed a unique breed or a strongly related to the Dutch Black and White breed?

2. Is it relevant to distinguish five different sire lines within the breed?

3. Are two herds of non-registered Dutch Red Friesian Cattle related to the registered population?

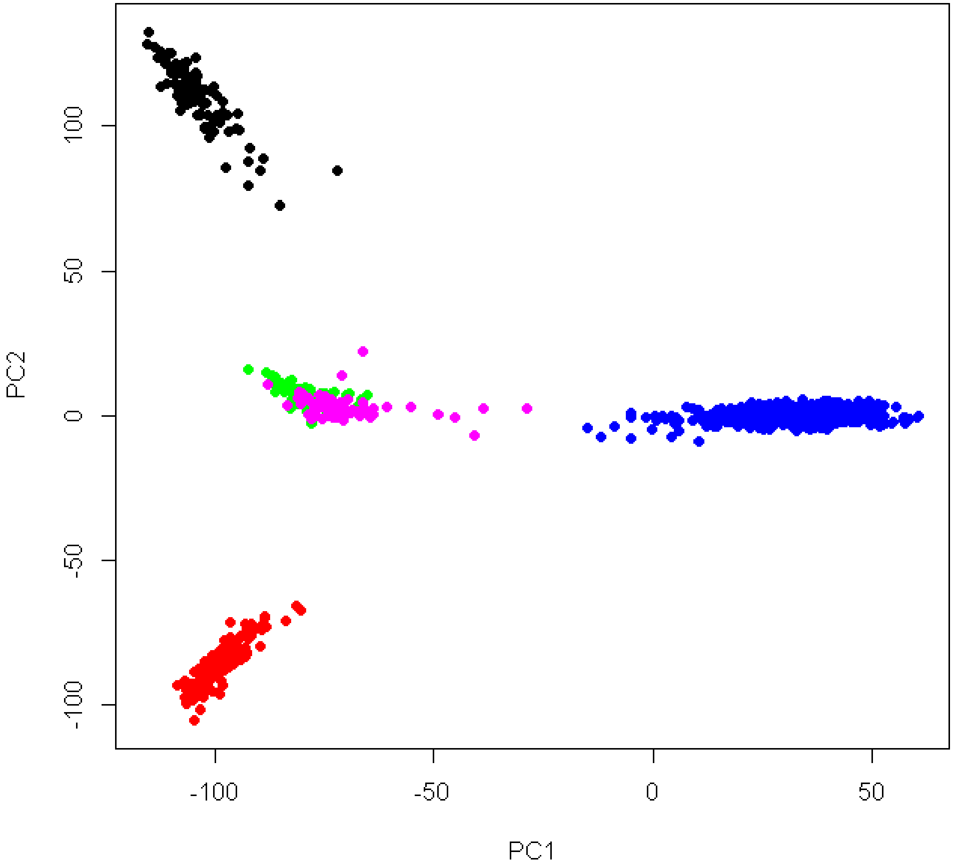
Five lines and two candidate populations

- Jet (n=9)
- Marco/Kei (n=8)
- Koos (n=10)
- Reitsma (n=11)
- Black and White Friesian sires Rf (n=10)
- Not registered F (n=11)
- Not registered T (n=9)

- 43 living animals (females; hair roots)
- 25 sires out of the genebank (semen)

Clusteranalysis of the Dutch cattle breeds

- Black = GWH
- Red = MRIJ
- Green = DBWF
- Blue = HF
- Magenta = DRF



Conclusions positions of Dutch cattle breeds

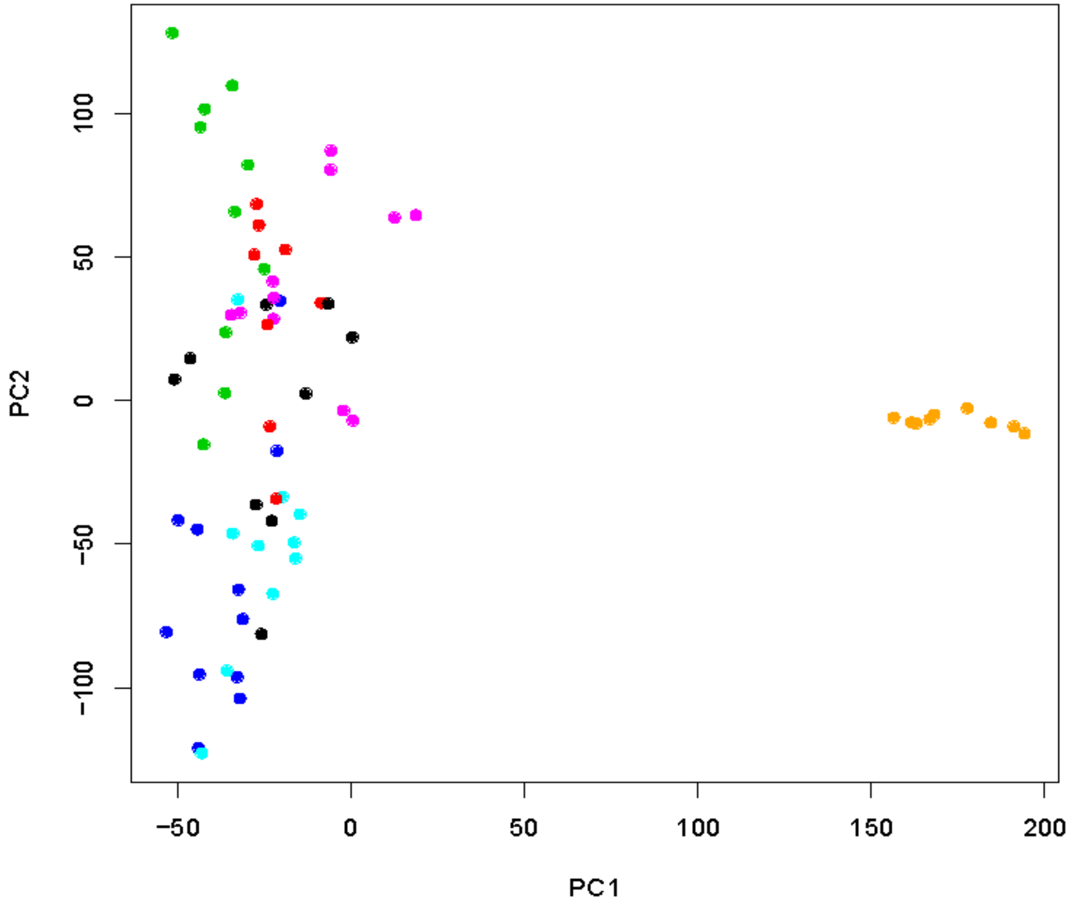
- Clear differences

GWH <> DBWF/DRF <> MRIJ

- DBWF and DRF closely related

- Each breed contained 1 % unique DNA and has its own genetic identity

Clusteranalysis of the 7 lines of DRF-cattle



- PCA evidently distinguished DFR line 7 (orange) from the other lines

Conclusions for the 7 lines

- Line 6 and 7 related to DRF
- Line 6 and 7 some unique diversity
- Line 6 small HF influence
- Line 7 unique DRF diversity
- Much overlap among the lines

Conclusions Red and White Friesian cattle

1. The Dutch Red Friesian Cattle breed is a unique breed strongly related to the Dutch Black and White breed.
2. It is not relevant to distinguish five different sire lines within the breed, but it can be used in an effective conservation programme.
3. Two herds of non-registered Dutch Red Friesian Cattle can be added to the registered population.

Conclusion: conservation and use of genetic diversity is important

- Within a species and within a breed for **natural selection** that leads to adaptation to climate change, higher disease resistance and results in robust and fertile animals

- Between breeds it facilitates the choice of the right breed in the right livestock system and of efficient crossbreeding

- Within breeds it determines the efficiency of **artificial selection** and will diminish the occurrence of inbreeding effects: the expression of genetic defects and a decrease in health and fertility traits