Measuring between-breed genetic diversity and prioritization of breeds for conservation

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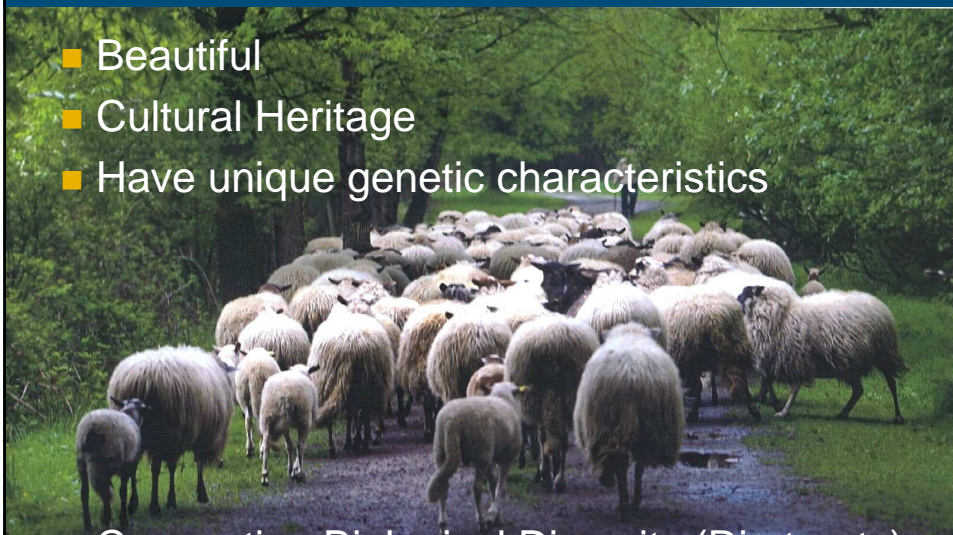
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Reasons for conservation of breeds

- Beautiful
- Cultural Heritage
- Have unique genetic characteristics
- Convention Biological Diversity (Rio treaty)

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Population genetics of breeds

- **Breed = Population**
  - Limited exchange of genetic material between populations/breeds
  - Populations diverge
    - Selection
    - Genetic drift
  - Small populations loose diversity
    - Low genetic variation
    - Inbreeding

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Criteria for conservation / prioritization

- **Genetic variation**
  - Amount
  - Uniqueness relative to other breeds
- **Other**
  - Extinction risk
  - Special traits
    - Disease resistance
    - Cultural reason
    - ...

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Genetic variation

- Set of breeds

High variation

Lots of overlap

Low variation,
High inbreeding

But unique

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Measuring genetic variation

- Animal Breeders
  - Additive genetic variance
    - Variation in breeding values
    - Different for different traits
- Population Geneticists
  - Allelic variation
    - Heterozygosity (Expected / Observed)
    - No. of (unique) alleles
    - Fst
    - Genetic distance
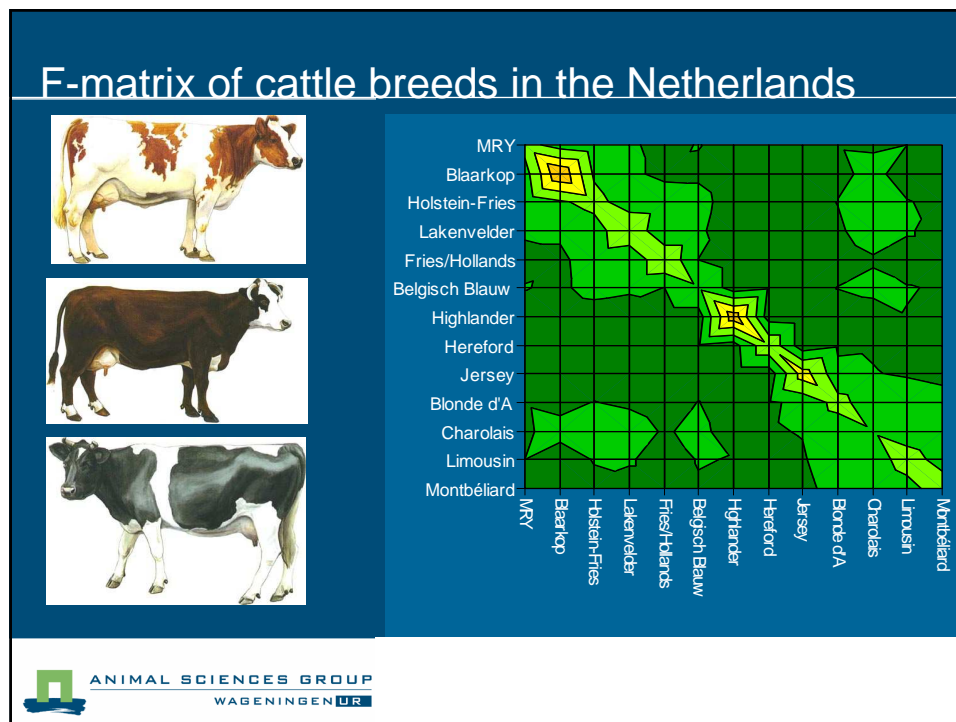
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Additive variance

- Estimation of additive variance
  - Pedigree
  - Estimate relatedness Matrix (A-matrix)
    - Probability inheritence of same allele of ancestor
  - Relate A-matrix to phenotype
- A-matrix common to all traits
- Average of A-matrix related to average genetic variation
  - High r, same genes, low genetic variation
- Pedigree across breeds generally not known

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Relatedness from alleles

- Relationship coefficient
  - Probability that two alleles taken at random from two individuals (populations) are Identical By Descent (IBD)
- Expected heterozygosity (Similarity)
  - Probability that two alleles taken at random from two individuals (populations) are (not) Alike In State (AIS)
  - IBD: always AIS
  - Not AIS: never IBD
  - AIS: IBD or not IBD
- Eding/Meuwissen (2002): method for estimating kinships with correction for alleles AIS but not IBD

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F-matrix of cattle breeds in the Netherlands

Eding/Meuwissen – (Caballero/Toro) method

- Minimise average relatedness to maximise diversity
- Estimate relatedness
- Genetic variation = 1 - average kinship = 1 - c'Ac
  - C = Contribution vector
  - Calculate c so that genetic variation is maximised = core set

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Contribution of breeds to genetic variation

■ Set of breeds
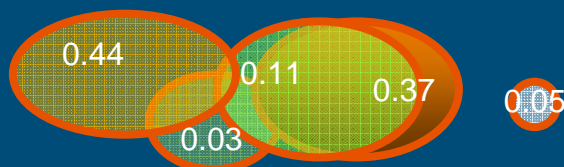
					Contribution Vector
0.10					0.44
0.00	0.90				0.05
0.01	0.00	0.10			0.11
0.00	0.00	0.08	0.10		0.37
0.05	0.00	0.04	0.01	0.50	0.03

■ A-matrix

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Example

■ 69 European cattle breeds typed for 30 microsatellite markers

Core set contribution

Chianina (I)	22%
German Shorth. (D/GB)	19%
Normand (F)	18%
Red Danish (DK)	15%
Friesian Holland (NL)	10%
Guernsey (GB)	8 %
8 other breeds	8 %

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Prioritisation of breeds

- Some breeds can be considered safe
  - High input/high output breeds that dominate the world
    - Holstein Friesian in dairy cattle
    - Texelaar in sheep
    - Hy-line in chicken
    - Etc.
- Eding method:
  - Determine safe set
  - Calculate genetic diversity
  - Add rare breed
  - Recalculate genetic diversity
  - Repeat for all breeds
  - Prioritise rare breeds according to added genetic diversity

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Example

- 69 European cattle breeds typed for 30 microsatellite markers

Core set contribution		Safe + 1 set analysis Added Diversity	
Chianina (I)	22%	Betizu (E)	6.02%
German Shorth. (D)	19%	Mallorquina (E)	4.88%
Normand (F)	18%	German Shorth. (D)	4.71%
Red Danish (DK)	15%	Podolica (I)	4.16%
Friesian Holland (NL)	10%	Chianina (I)	4.03%
Guernsey (GB)	8 %	Retinta (E)	4.02%
8 other breeds	8 %	etc.	

Safe set: > 1 million
Holstein Friesian, Limousin, Jersey, Mont Beliarde etc.

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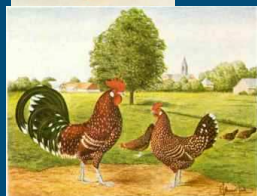
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Other methods

- **FST**
  - Heterozygosity relative to total set of breeds
  - Measure for divergence (amongst others)
- **No. of (private) alleles**
  - Focus on uniqueness of breeds
- **Genetic distances**
  - Based on mutation model
  - - ln (Similarity weighted by maximum similarity possible given population frequencies)
    - Equal frequencies: distance = 0
    - no alleles in common: distance = ∞
- **Phylogenetic trees**
  - Generally based on genetic distances

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Poultry

Safe set

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Practical considerations

- At least 20 (microsattelite) loci across the genome needed
- If no molecular data available
  - Use other indicators
  - Historical evidence of breed histories
  - Larger breeds -> more genetic variation
  - (Geographically) Isolated breeds less related

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Other considerations

- Special breeds
  - Special traits
  - Culturally or otherwise important
  - Almost extinct
- Designate as to be conserved or already conserved
  - Treat as safe
  - Prioritize other breeds accordingly
- Weighing several aspects (Simianer, Reist-Marti)
  - Genetics * Extinction
  - Economics
  - Ecological
  - Etc.

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Example: Ethiopian Sheep Breeds (Gizaw submitted)

	Core Set Contribution
Simien	0.44
Bonga	0.18
Gumz	0.13
Washera	0.07
Menz	0.01
Horro	0.01
etc.	

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Ethiopian Sheep Breeds: Extinction Risk

	Pop. size	Ram/ herd	cross breed	Pure Stock	Farmers Appreciation	
	0.3	0.3	0.3	0.1	0.1	
Simien						0.3
Bonga						0.4
Gumz						0.9
Washera						0.1
Menz						0.4
Horro						0.3

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Ethiopian Sheep Breeds: Utility

	Economic value	Cultural value	Ecological value	
	0.4	0.4	0.4	
Simien	🟨	🟨	🟩	0.33
Bonga	🟨	🟥	🟥	0.20
Gumz	🟥	🟧	🟩	0.23
Washera	🟩	🟨	🟥	0.27
Menz	🟩	🟩	🟩	0.40
Horro	🟩	🟨	🟥	0.20

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Ethiopian Sheep Breeds: Final Priority

	Genetic Contribution	Extinction Risk	Utility Value	Priority
Simien	0.44	0.3	0.33	1
Bonga	0.18	0.4	0.20	4
Gumz	0.13	0.9	0.23	2
Washera	0.07	0.1	0.27	5
Menz	0.01	0.4	0.40	3
Horro	0.01	0.3	0.20	6

Priority based on 2(C * E) + U

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What is a breed?

- "Either a sub-specific group of domestic livestock with definable characteristics that enable it to be separated by visual appraisal from similarly defined groups within the same species, or a group for which geographical and/or cultural separation from phenoypically separate groups has led to acceptance of its separate identity" (FAO definition)
  - No fixed entity
  - Partly arbitrary
  - There are different kind of breeds
- A breed is a breed if enough people say it is (Hammond)

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Breed definition and conservation

- Number of conserved breeds does not tell you how much genetic variation is conserved
  - Take into account genetic overlap
  - And within breed diversity
- Too narrow a definition:
  - Risk of spending resources on conservation of unimportant traits – small differences between breeds
  - Risk of high inbreeding within breeds
- Too broad a definition
  - Risk of loosing special traits of distinctive groups
  - Risk of loss of variation through cross-breeding and selection

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Transboundary breeds (Population genetic viewpoint)

- Can be seen as consisting of sub-populations
  - Highly related
  - The smaller the subpopulations the more divergence
  - Genetic variation within countries is lost at a higher rate if no or limited exchange between countries
  - Diversity lost in one country may be conserved in another

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