Measuring between-breed genetic diversity and prioritization of breeds for conservation
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Reasons for conservation of breeds
- Beautiful
- Cultural Heritage
- Have unique genetic characteristics
- Convention Biological Diversity (Rio treaty)
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

Criteria for conservation / prioritization

- Genetic variation
  - Amount
  - Uniqueness relative to other breeds

- Other
  - Extinction risk
  - Special traits
    - Disease resistance
    - Cultural reason
    - ...
Genetic variation

- Set of breeds
  - High variation
  - Lots of overlap
  - But unique
  - Low variation, High inbreeding

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
Additive variance

- Estimation of additive variance
  - Pedigree
  - Estimate relatedness Matrix (A-matrix)
    - Probability inheritance 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

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
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
Contribution of breeds to genetic variation

- Set of breeds

Contribution Vector
0.44 0.05 0.11 0.37 0.03 0.44 0.37 0.11 0.05 0.03

- A-matrix

0.10
0.00 0.90
0.01 0.00 0.10
0.00 0.00 0.08 0.10
0.05 0.00 0.04 0.01 0.50
0.03

Example

- 69 European cattle breeds typed for 30 microsatellite markers

Core set contribution

<table>
<thead>
<tr>
<th>Breed</th>
<th>Contribution</th>
</tr>
</thead>
<tbody>
<tr>
<td>Chianina (I)</td>
<td>22%</td>
</tr>
<tr>
<td>German Shorth. (D/GB)</td>
<td>19%</td>
</tr>
<tr>
<td>Normand (F)</td>
<td>18%</td>
</tr>
<tr>
<td>Red Danish (DK)</td>
<td>15%</td>
</tr>
<tr>
<td>Friesian Holland (NL)</td>
<td>10%</td>
</tr>
<tr>
<td>Guernsey (GB)</td>
<td>8%</td>
</tr>
<tr>
<td>8 other breeds</td>
<td>8%</td>
</tr>
</tbody>
</table>
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

Example

- 69 European cattle breeds typed for 30 microsatellite markers

<table>
<thead>
<tr>
<th>Core set contribution</th>
<th>Safe + 1 set analysis</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Added Diversity</td>
</tr>
<tr>
<td>Chianina (I)</td>
<td>22%</td>
</tr>
<tr>
<td>German Shorth. (D)</td>
<td>19%</td>
</tr>
<tr>
<td>Normand (F)</td>
<td>18%</td>
</tr>
<tr>
<td>Red Danish (DK)</td>
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</tr>
<tr>
<td>Guernsey (GB)</td>
<td>8 %</td>
</tr>
<tr>
<td>8 other breeds</td>
<td>8 %</td>
</tr>
<tr>
<td>Betizu (E)</td>
<td>6.02%</td>
</tr>
<tr>
<td>Mallorquina (E)</td>
<td>4.88%</td>
</tr>
<tr>
<td>German Shorth. (D)</td>
<td>4.71%</td>
</tr>
<tr>
<td>Podolica (I)</td>
<td>4.16%</td>
</tr>
<tr>
<td>Chianina (I)</td>
<td>4.03%</td>
</tr>
<tr>
<td>Retinta (E)</td>
<td>4.02%</td>
</tr>
<tr>
<td>etc.</td>
<td></td>
</tr>
</tbody>
</table>

Safe set: > 1 million
Holstein Friesian, Limousin, Jersey, Mont Beliarde etc.
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 = $\infty$

- **Phylogenetic trees**
  - Generally based on genetic distances
Practical considerations

- At least 20 (microsatellite) 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

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.
### Example: Ethiopian Sheep Breeds (Gizaw submitted)

<table>
<thead>
<tr>
<th>Core Set Contribution</th>
<th>Simien 0.44</th>
<th>Bonga 0.18</th>
<th>Gumz 0.13</th>
<th>Washera 0.07</th>
<th>Menz 0.01</th>
<th>Horro 0.01</th>
<th>etc.</th>
</tr>
</thead>
</table>

#### Ethiopian Sheep Breeds: Extinction Risk

<table>
<thead>
<tr>
<th></th>
<th>Pop. size</th>
<th>Ram/herd</th>
<th>cross breed</th>
<th>Pure Stock</th>
<th>Farmers Appreciation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Simien</td>
<td>0.3</td>
<td>0.3</td>
<td>0.3</td>
<td>0.1</td>
<td>0.1</td>
</tr>
<tr>
<td>Bonga</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Gumz</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Washera</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Menz</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Horro</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
### Ethiopian Sheep Breeds: Utility

<table>
<thead>
<tr>
<th>Breed</th>
<th>Economic Value</th>
<th>Cultural Value</th>
<th>Ecological Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Simien</td>
<td>0.4</td>
<td>0.4</td>
<td>0.4</td>
</tr>
<tr>
<td>Bonga</td>
<td>0.33</td>
<td>0.20</td>
<td>0.20</td>
</tr>
<tr>
<td>Gumz</td>
<td>0.23</td>
<td>0.23</td>
<td>0.23</td>
</tr>
<tr>
<td>Washera</td>
<td>0.40</td>
<td>0.40</td>
<td>0.40</td>
</tr>
<tr>
<td>Menz</td>
<td>0.40</td>
<td>0.40</td>
<td>0.40</td>
</tr>
<tr>
<td>Horro</td>
<td>0.20</td>
<td>0.20</td>
<td>0.20</td>
</tr>
</tbody>
</table>

### Ethiopian Sheep Breeds: Final Priority

<table>
<thead>
<tr>
<th>Breed</th>
<th>Genetic Contribution</th>
<th>Extinction Risk</th>
<th>Utility Value</th>
<th>Priority</th>
</tr>
</thead>
<tbody>
<tr>
<td>Simien</td>
<td>0.44</td>
<td>0.3</td>
<td>0.33</td>
<td>1</td>
</tr>
<tr>
<td>Bonga</td>
<td>0.18</td>
<td>0.4</td>
<td>0.20</td>
<td>4</td>
</tr>
<tr>
<td>Gumz</td>
<td>0.13</td>
<td>0.9</td>
<td>0.23</td>
<td>2</td>
</tr>
<tr>
<td>Washera</td>
<td>0.07</td>
<td>0.1</td>
<td>0.27</td>
<td>5</td>
</tr>
<tr>
<td>Menz</td>
<td>0.01</td>
<td>0.4</td>
<td>0.40</td>
<td>3</td>
</tr>
<tr>
<td>Horro</td>
<td>0.01</td>
<td>0.3</td>
<td>0.20</td>
<td>6</td>
</tr>
</tbody>
</table>

Priority based on $2(C \times E) + U$
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 phenotypically 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)

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
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