DEVELOPMENT OF A GENETIC INDICATOR OF BIODIVERSITY FOR FARM ANIMALS

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CONVENTION ON BIOLOGICAL DIVERSITY (CBD)

"achieve by 2010 a significant reduction of the current rate of biodiversity loss at the global, regional and national level"

- **Evaluate progress**
- **Communicate effectively**

Need to develop a limited number of indicators of biodiversity

Indicators should ...

- use existing data sources
- be underpinned by sound scientific knowledge
- be easily understood by both technical and non technical audiences

Livestock genetic diversity

- **Important component of biodiversity**
- In contrast to wild species:

  selected by humans for centuries → considerable number of breeds
- **Partition of diversity within and between breeds → unique**
- **Previous indicators ignored diversity within breeds**

Objectives

1. **Identify an indicator of genetic diversity for livestock species**

   accounts for variability within breeds

2. **Evaluate the indicator in UK sheep and cattle**

1. Indicator proposed

Genetic Variation and Ne

- We can not always measure the genetic variation in all traits of interest

- **BUT we can always estimate the average rate of loss in genetic variation**

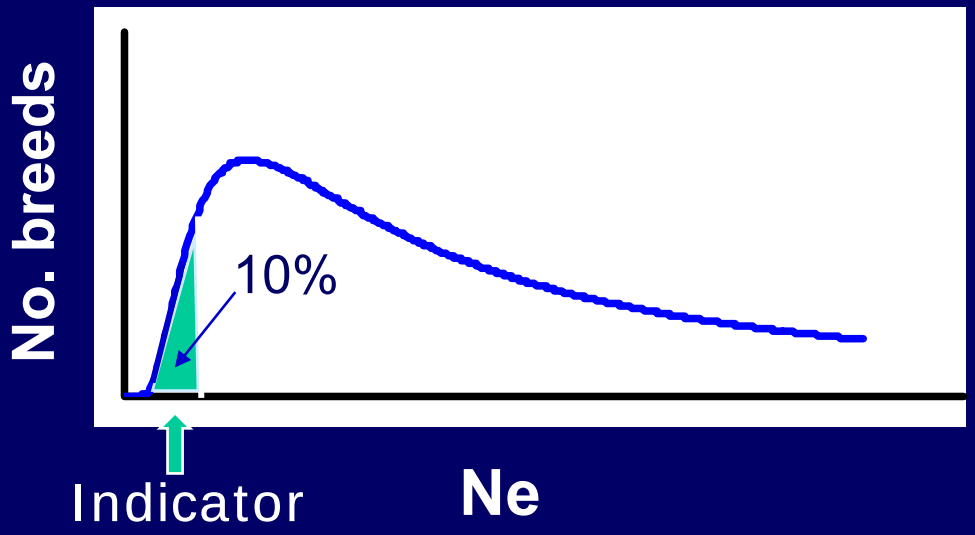
  Related to effective population size (Ne)

$$\Delta V_g = 1/2Ne \times V_g$$

Falconer and Mackay (1996)

One indicator for each livestock species

- Estimate Ne for each native breed
- Calculate the distribution of Ne



- Find the average Ne for the lower 10% tail of the distribution

Choice of 10%

- UK 59 sheep native breeds
  36 cattle native breeds

- 10% provides a good compromise between
  - giving high weight to breeds most at risk
  - without being too sensitive to events surrounding a single breed

Indicator proposed

- Sensitive to genetic variation within breeds (based on Ne)
- Responds negatively (↓) when
  - breeds become extinct (Ne = 0)
  - when management within breeds deteriorates
- Simply obtained

2. Evaluation of the indicator

a. Sheep

b. Cattle

Information needed

- **Requested to breed societies**
  - Breeds with pedigree available
    → electronic copy
  - Breeds without pedigree available
    → estimates of numbers of parents and proportions selected

Guarantee that breed names will be kept confidential

Responses

NATIVE BREEDS

59 sheep

36 cattle

Responding...

31 sheep (53%)

20 cattle (58%)

With pedigree

21 sheep

18 cattle

Use the lower 20%

Sheep

31 breeds

Boreray
(93)

Swaledale
(750,000)

Cattle

20 breeds

Chillingham
(17)

South Devon
(11,500)

Estimation of Ne with pedigree

- **Equivalent to estimate ΔF (ΔF = 1/2 Ne)**
- **Method very well established for long and complex pedigrees**
  - Compute
    - F for each animal *RelaX2*
    - ΔF per year (ΔF_y)
    - generation interval (L)
    - ΔF per generation ($\Delta F = L\ \Delta F_y$) and $Ne = 1/2\Delta F$

To show temporal trends

Indicator computed in 2 years:
2001, 2007

How many generations to use to estimate Ne in both years?

Regressions using 1, 2, 3 o 4 generations back for a particular year

4 generations

Estimation of Ne without pedigree

- **From predictive equations**
- **Breeds not artificially selected** (e.g. Chillingham)

  $Ne = 4N_mN_f/(N_m+N_f)$

  Falconer and Mackay (1996)
- **Other breeds**
  - **Selection**
    - **Based only on phenotypes of candidates**
    - **$h^2 = 0.4$ → conservative**

  Daetwyler et al. (2007)

Estimation of Ne without pedigree

- **Prediction of ΔF (y Ne) for populations with overlapping generations under mass selection**

Bijma, van Arendonk, Woolliams (2000)

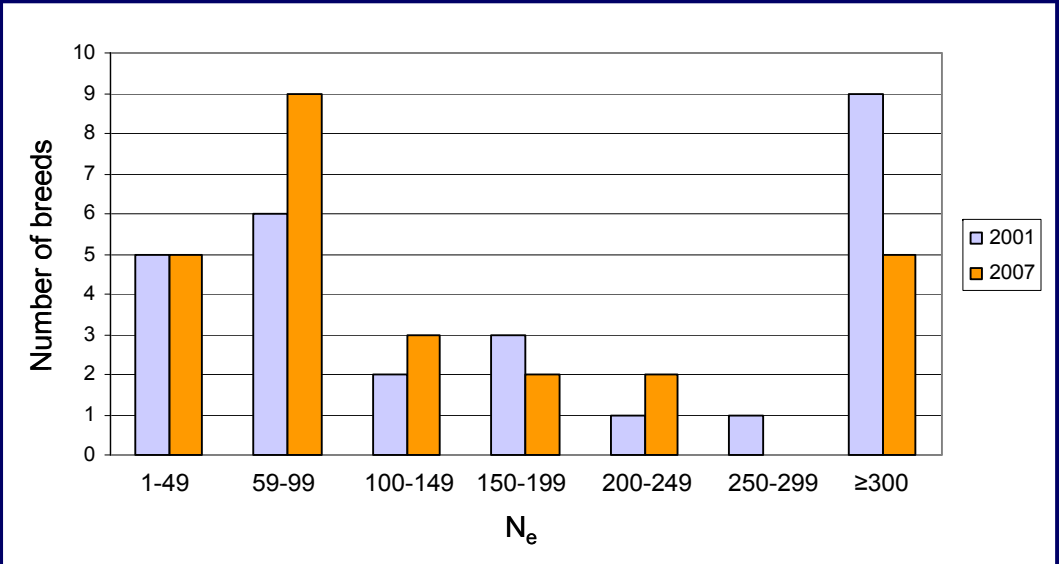
  - h^2 (h^2 = 0.4)
  - Number of breeding animals per year
  - Minimum and maximum breeding ages
  - Proportion of breeding animals that remain in the flock/herd next year
  - Average total number of offspring per dam surviving at breeding age

Estimation of Ne without pedigree

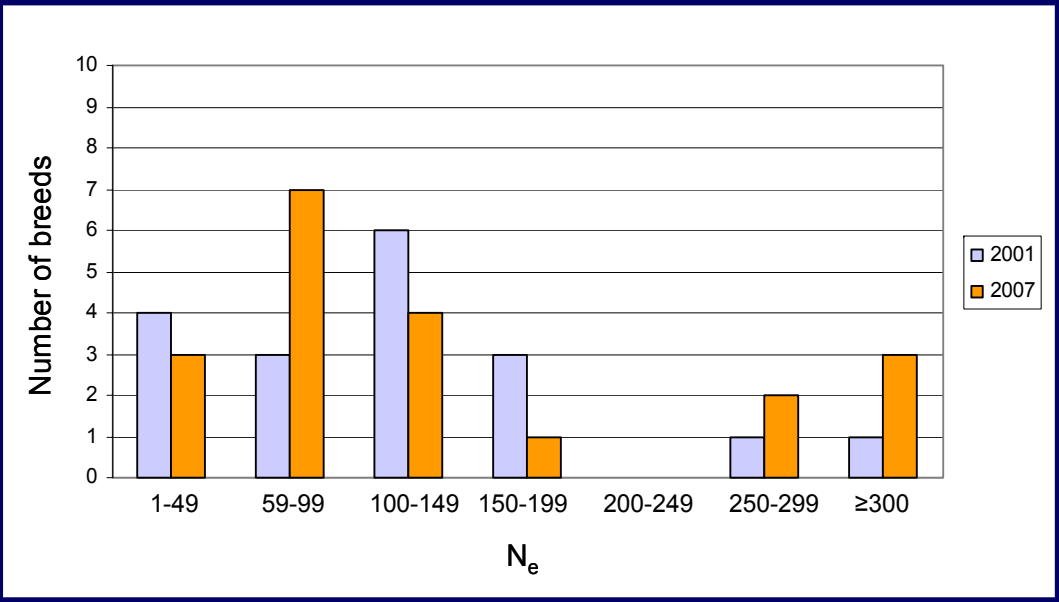
- **Information for 2007**
  - **Responses from societies**
  - **Expert opinion**

- **Information for 2001**
  - ***Number of breeding females***
    - **UK Country Report (Defra 2002)**
    - **Responses from societies**
  - ***Mating ratio and other parameters: assumed same as in 2007***

Distributions of Ne



sheep



cattle

Sheep breed	Ne 2001	Ne 2007
1	14	25
2	29	38
3	35	47
4	36	30
5	48	61
6	56	122
7	63	98
8	79	61
9	86	93
10	91	44
11	96	96
12	112	83
.	.	.
.	.	.
.	.	.

2001: **36.3**

2007: **40.8**

Not significant

Cattle breed	Ne	
	2001	2007
1	10	10
2	16	24
3	34	36
4	42	65
5	71	97
6	73	82
7	78	112
8	107	82
9	110	118
10	113	97
.	.	.
.	.	.
.	.	.

2001:
25.5

2007:
33.8

Significant
($P < 0.05$)

Conclusions

- **Indicator developed**
  - Measures status and trends of genetic diversity in farm animals
  - Presents change in genetic diversity in native breeds, as measured by their Ne
  - Sensitive to events in breeds most at risk of disappearing
  - Insensitive to events in breeds where Ne remains high

Conclusions

- Increase observed from 2001 to 2007 in sheep and cattle but only significant in cattle

Thanks to

- Defra (Department for Environment Food and Rural Affairs)
- Breed societies, Rare Breeds Survival Trust
- Grassroots Systems
- Mark Stevenson, Mike Roper, James Williams, Bill Hill, Miguel Toro