

Effective population size

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2023 Joint WG




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European Regional Focal Point
for Animal Genetic Resources



INSTITUT DE
L'ELEVAGE **idele**

1

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Based on a FAO document drafted by:


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<https://www.fao.org/3/cc3758en/cc3758en.pdf>

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2







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Genetic variability vs demography

French example

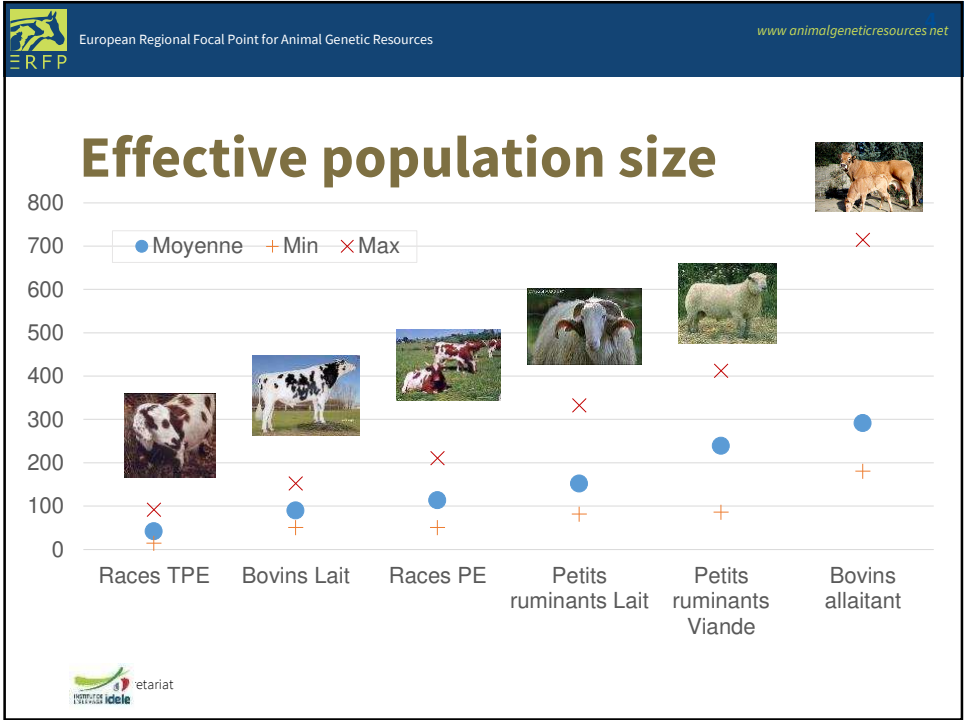


+ two groups of breeds


- Local breeds (between 1,000 and 5,000 females registered on a 4 years period)
- Rare breeds (less than 1,000 females registered on a 4 years period)

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3



4



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What is the effective population size - Ne?

- Effective population size (Ne): the size of a hypothetical idealized population (population with equal numbers of males and females, contributing uniform numbers of progeny, and not subject to other forces that change genetic diversity, such as mutation, migration and selection) that would generate the same amount of genetic drift or change of inbreeding as the population under study
- Many calculation methods... and very different results!

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5



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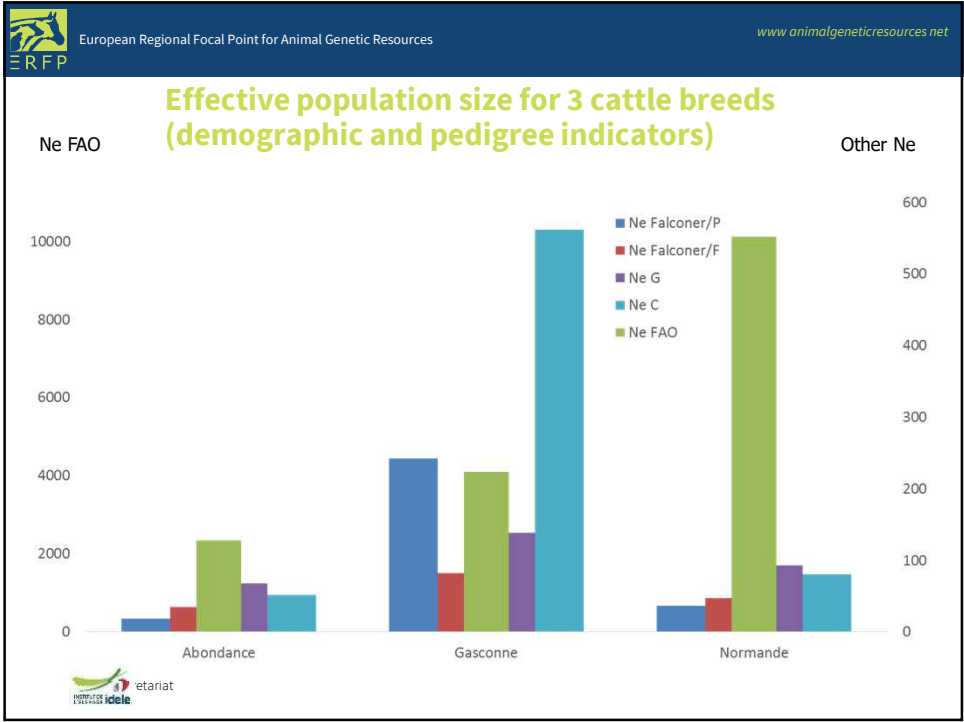
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Various estimation methods


- Simplest = demographic parameters (« Ne FAO »)
 Example: $N_e = 4 (N_m \times N_f) / (N_m + N_f)$
 $N_m N_f$ = number of sires and dams
- Use of pedigree information
 Example: $N_e = 1 / 2 \Delta F$
 ΔF : inbreeding rate between two generations
- Use of genomic information

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6



7



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Opportunities and challenges

Demographic information

Main properties	Data collection	Applicability of results
Provides insight on demographic stochasticity and underlying causes behind the changes in genetic variation	Censuses, surveys or animal identification systems	Basic interpolations which often underestimate loss of genetic variation

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8



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Opportunities and challenges

Pedigree information

Main properties	Data collection	Applicability of results
Provides inferences on the genetic variation of selectively neutral loci and assuming no mutation, based on knowledge of parent-offspring relationships	Registration of pedigree information as complete as possible	Results do not consider mutation, Mendelian sampling and selection, prone to bias related to incomplete or incorrect pedigree

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9



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Opportunities and challenges

Genomic information

Main properties	Data collection	Applicability of results
Yields information directly on genomic variation, but provide no direct information on demographic stochasticity	Accurate sampling in terms of individuals and markers	Choice of appropriate parameters used for analyses requires skill, and may yield inaccurate results with incorrect parameters

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10


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Recommendations

- Genetic variation within livestock populations should be measured, using at least one indicator of Ne.
- Livestock populations shall be monitored on a regular basis => generation interval.
- An estimate of Ne should be included in the data fields of (DAD-IS).
- Molecular tools = opportunity to obtain more accurate estimates of Ne compared to demographic indicators and pedigree based measures, especially if pedigree information is of low quality.
- Whenever possible, samples of DNA for genetic diversity analysis of a population, should be collected from at least 100 animals, to be genotyped with a 50K. The animals should be selected include both sexes, old and young individuals representing multiple generations.
- For the assignment of breeds to risk-status categories based on demographic information, the thresholds presented in the FAO guidelines on In vivo conservation of animal genetic resources should be used

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11





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12