

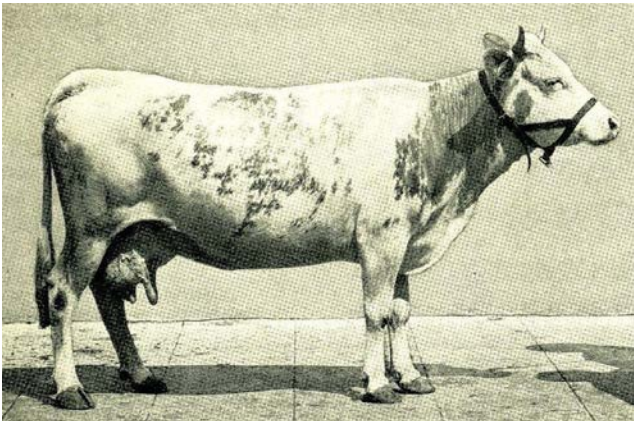
# ***Recovery of native genomes of conserved breeds with optimum contribution selection***

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# Outline

- Objectives of breeding programs
- Methods A-D for OC Selection
- Materials
- Results: Consequences for
  - Migrant contributions
  - Native genome equivalents
  - Gene diversity
  - Native effective size



# ***Motivation***

**Local breeds have been frequently crossed with economically superior breeds.**

- This has increased the economic value of the local breeds.
- It eventually leads to the extinction of the local breeds because their genomes are gradually replaced by the migrant genomes.
- The migrant genomes are not subject to conservation efforts because they usually originate from non-endangered breeds.

# *Objectives of breeding programs*

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The main objectives of a breeding program for a conserved population with historic migration are:

- **Increase the economic value of the breed**
- **Reduce migrant contributions**
- **Drive many different native alleles to high frequencies**
- **Increase or conserve the gene diversity**

Aim of the study: Development of optimum contribution selection methods that take all objectives simultaneously into account.

# *Methods proposed in the literature*

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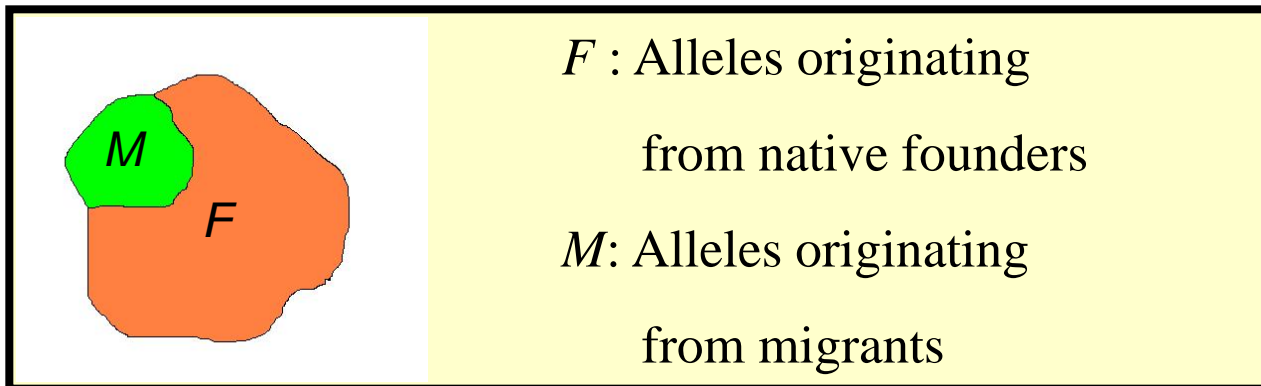
- (A) Maximize the gene diversity of the offspring (Caballero and Toro, 2000).
- Since endangered breeds have a limited effective population size, the individuals are closely related, so maximization of gene diversity would be achieved by maximization of migrant contributions.

# Methods considered by us

(B) Maximize the probability

$$P(X_J \neq Y_J \text{ and } X_J \in F \text{ and } Y_J \in F)$$

that two randomly chosen alleles  $X_J, Y_J$  from the offspring  $J$  are different (not IBD) and are from native founders.



# *Methods considered by us*

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(C) Maximize the probability

$$P(X_J \neq Y_J \text{ and } (X_J \in F \text{ or } Y_J \in F))$$

that two randomly chosen alleles  $X_J$ ,  $Y_J$  from the offspring  $J$  are different (not IBD) and at least one of them descends from a native founder.

# *Methods considered by us*

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## (D) Maximize the **conditional gene diversity**

$$P(X_J \neq Y_J | X_J \in F, Y_J \in F),$$

i.e. the conditional probability that two alleles  $X_J$ ,  $Y_J$  randomly chosen from the offspring  $J$  are different (not IBD), given that both descend from native founders.

- This approach requires constraining the maximum permissible value for the migrant contributions.
- For all methods (A) – (D) the minimum acceptable mean breeding value of the offspring could be constrained.



# Materials



- Pedigrees and additional information on  
185 315 Vorderwald cattle,  
25 412 Hinterwald cattle,  
4 150 Limpurg cattle.



Results are shown only for the **Vorderwald cattle**. For this breed

- pedigrees trace back to 1948,
- cattle from other breeds were considered migrants,
- cattle with unknown pedigree born after 1970 were also considered migrants.

# *Migrant contributions*

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The **migrant contribution** of population  $J$  is the probability

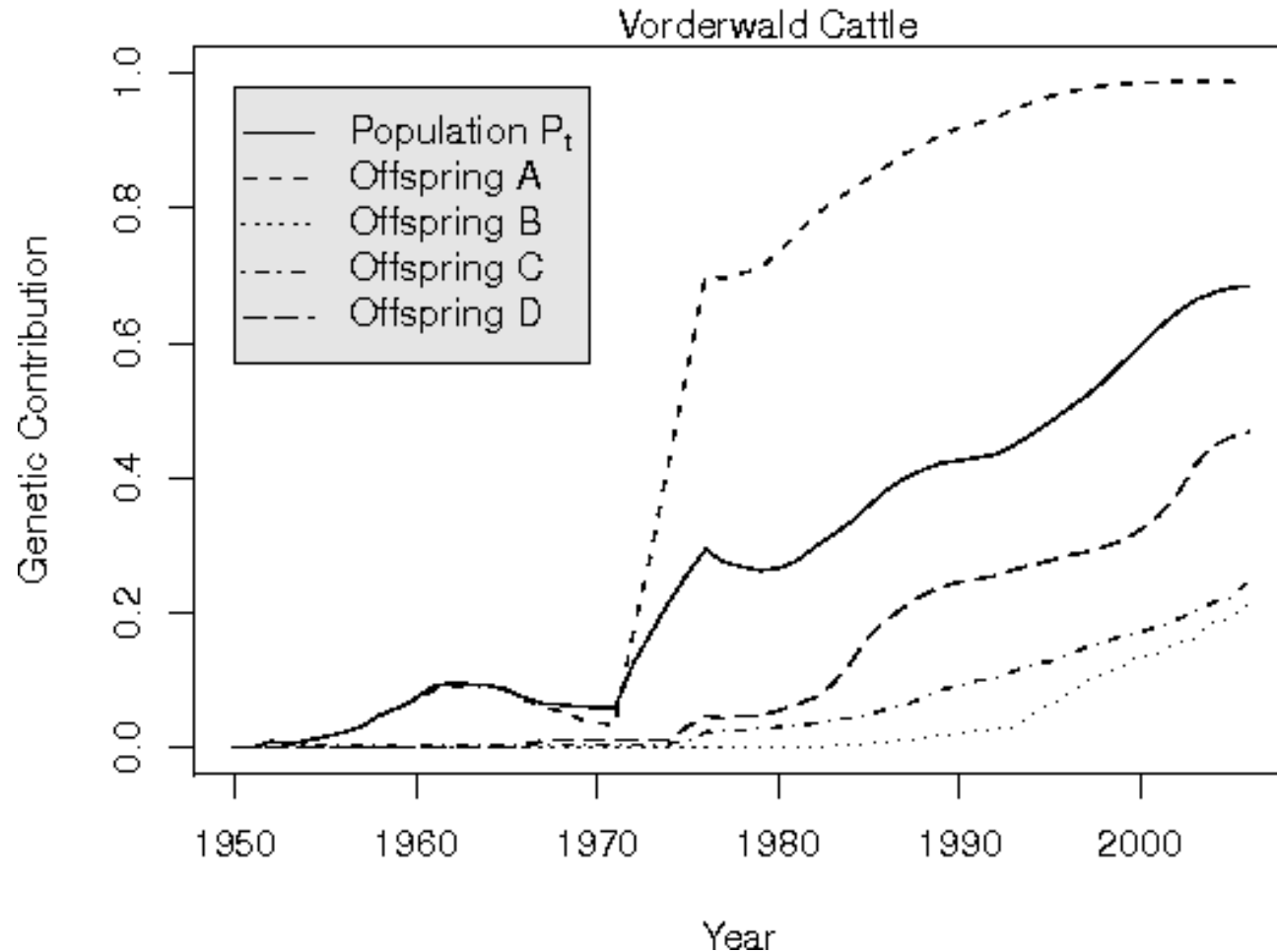
$$P(X_J \in M)$$

that an allele  $X_J$ , randomly chosen from population  $J$ , belongs to the migrant alleles  $M$ .

→ The migrant contribution should be small.

# Results: Migrant Contributions

## Genetic Contributions from Migrants



- Maximization of gene diversity (Method A) would lead to the extinction of the breeds.

# *Native Genome Equivalents*



The **native genome equivalents**  $NGE_{t_0}(J)$  of population  $J$  are the number of unrelated founders that would be needed to establish a population whose gene diversity is equal to the conditional gene diversity of population  $J$ .

Individuals are assumed unrelated in base year 1800. For the time between 1800 and 1970 an effective size of 150 was assumed.

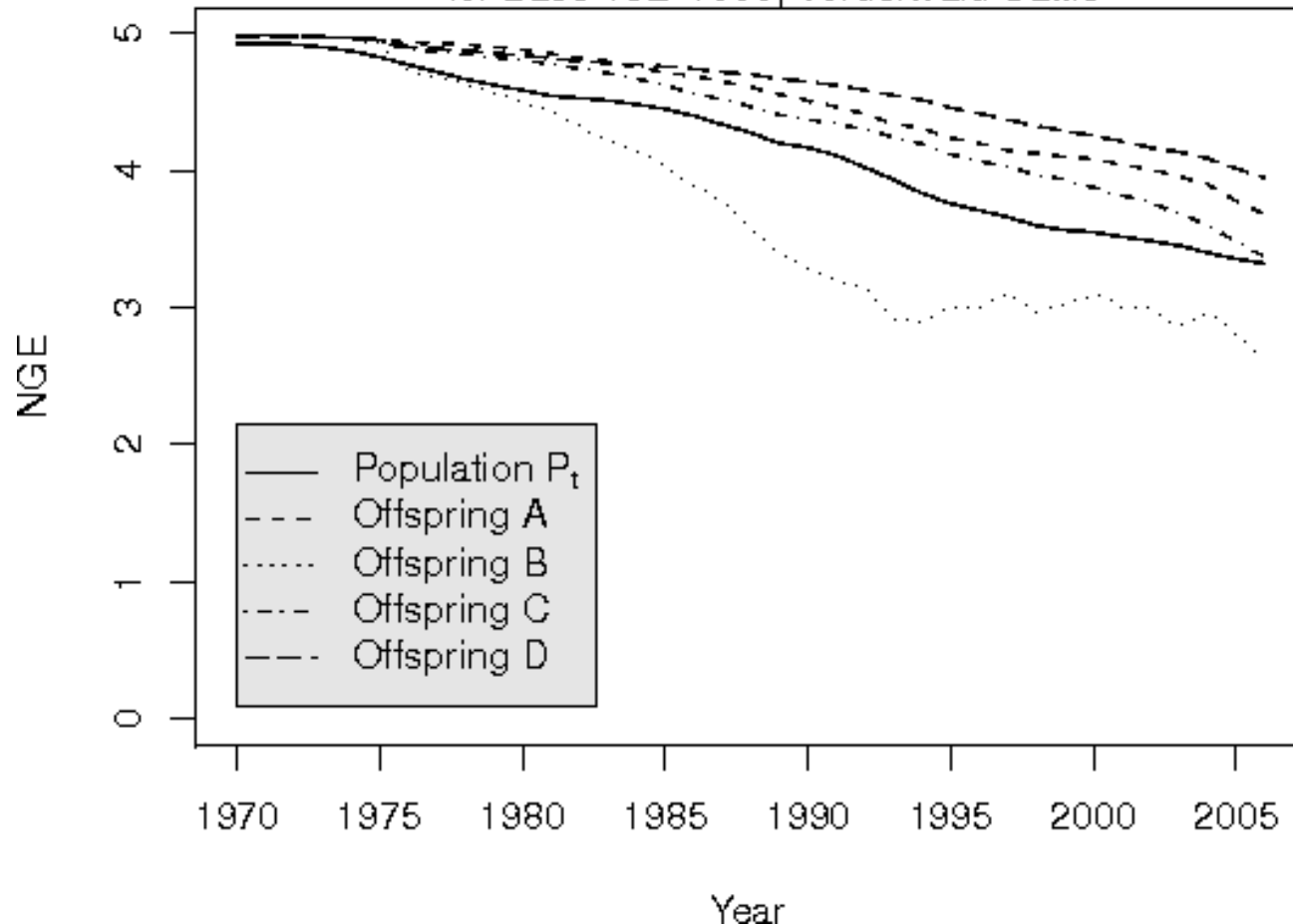
→ The native genome equivalents should be large.

# Results: Native Genome Equivalents



## Native Genome Equivalents

for Base Year 1800, Vorderwald Cattle



- Method B does not put enough weight on the conservation of the native genomes.

# *Gene Diversity*

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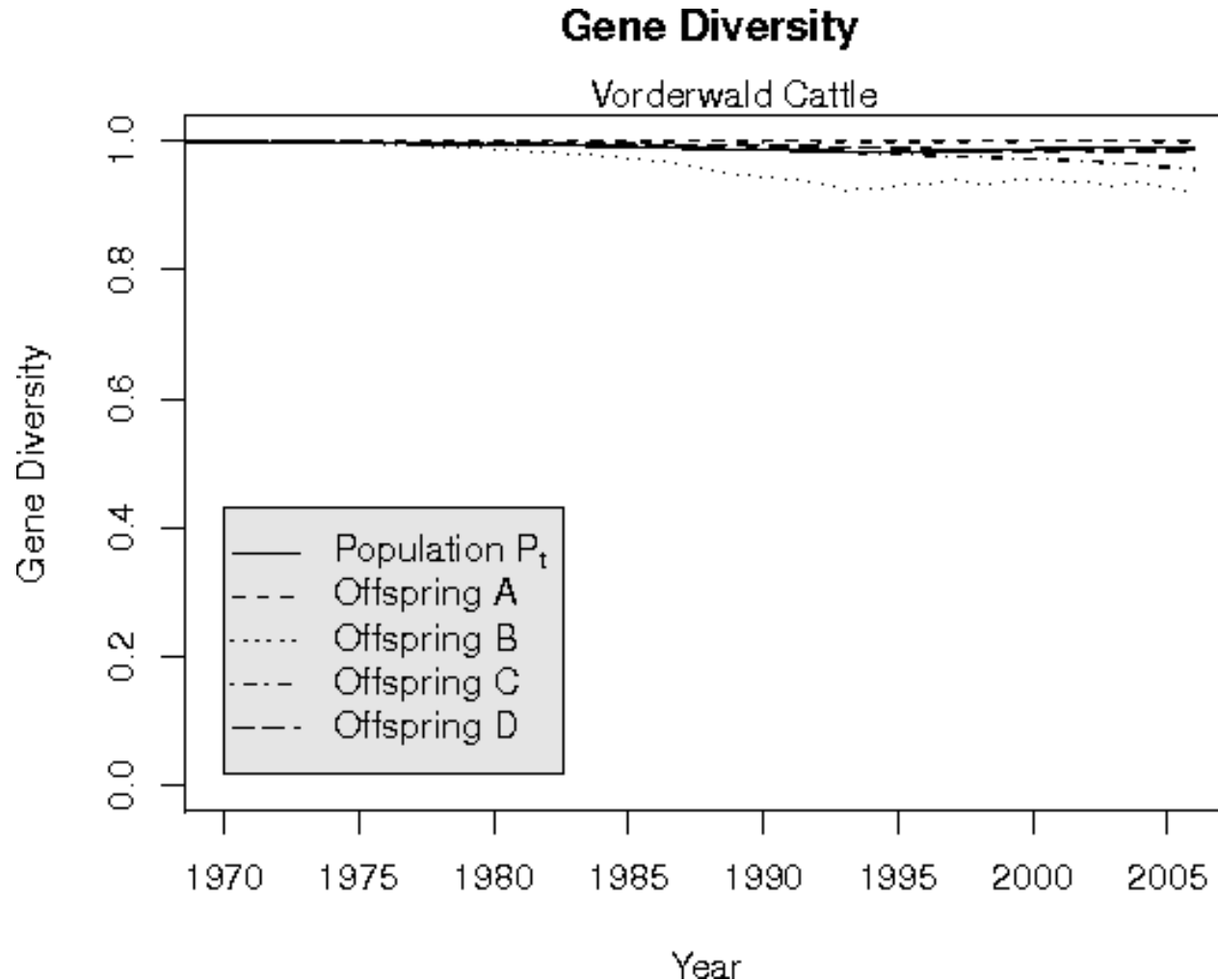
The **gene diversity** of population J is the probability

$$P(X_J \neq Y_J)$$

that two alleles  $X_J, Y_J$ , randomly chosen from population J, are different (not IBD).

➔ The gene diversity should be large.

# Results: Gene Diversity



- Because of the high gene diversity, migration is not required for the avoidance of inbreeding depression.



# *Native Effective Size*

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The **native effective size**  $N_{eN}(t)$  is the size of an idealized population whose gene diversity decreases as fast as the conditional gene diversity of the true population.

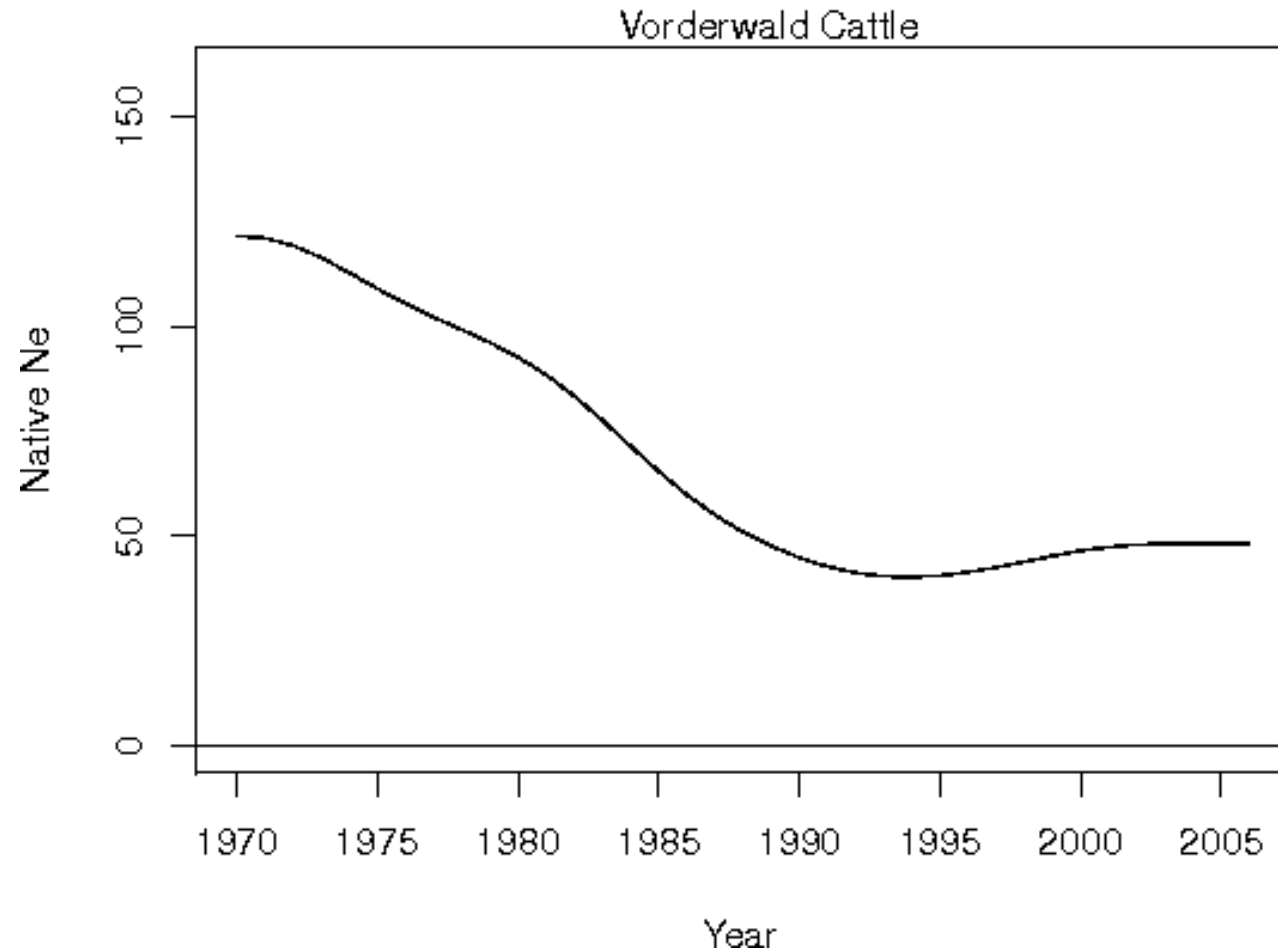
- ➔ The native effective size quantifies how fast the native genome equivalents are decreasing.
- ➔ The native effective size should be large, i.e. the native genome equivalents should decrease slowly.



# Results: Native Effective Size



## Effective Population Size



- The decrease of the native effective size between 1970 and 1990 is probably due to introduction of artificial insemination.

# Conclusion

- All three breeds have retained only few native genome equivalents.
- All three breeds have a high gene diversity because of migration.
- The use of individuals from other breeds was much more intense than required for avoidance of inbreeding depression.
- Methods C and D can be recommended.

Method C: Choose individuals for breeding such that for the offspring the probability is maximized that two randomly chosen alleles are different and that at least one of them descends from a native founder.

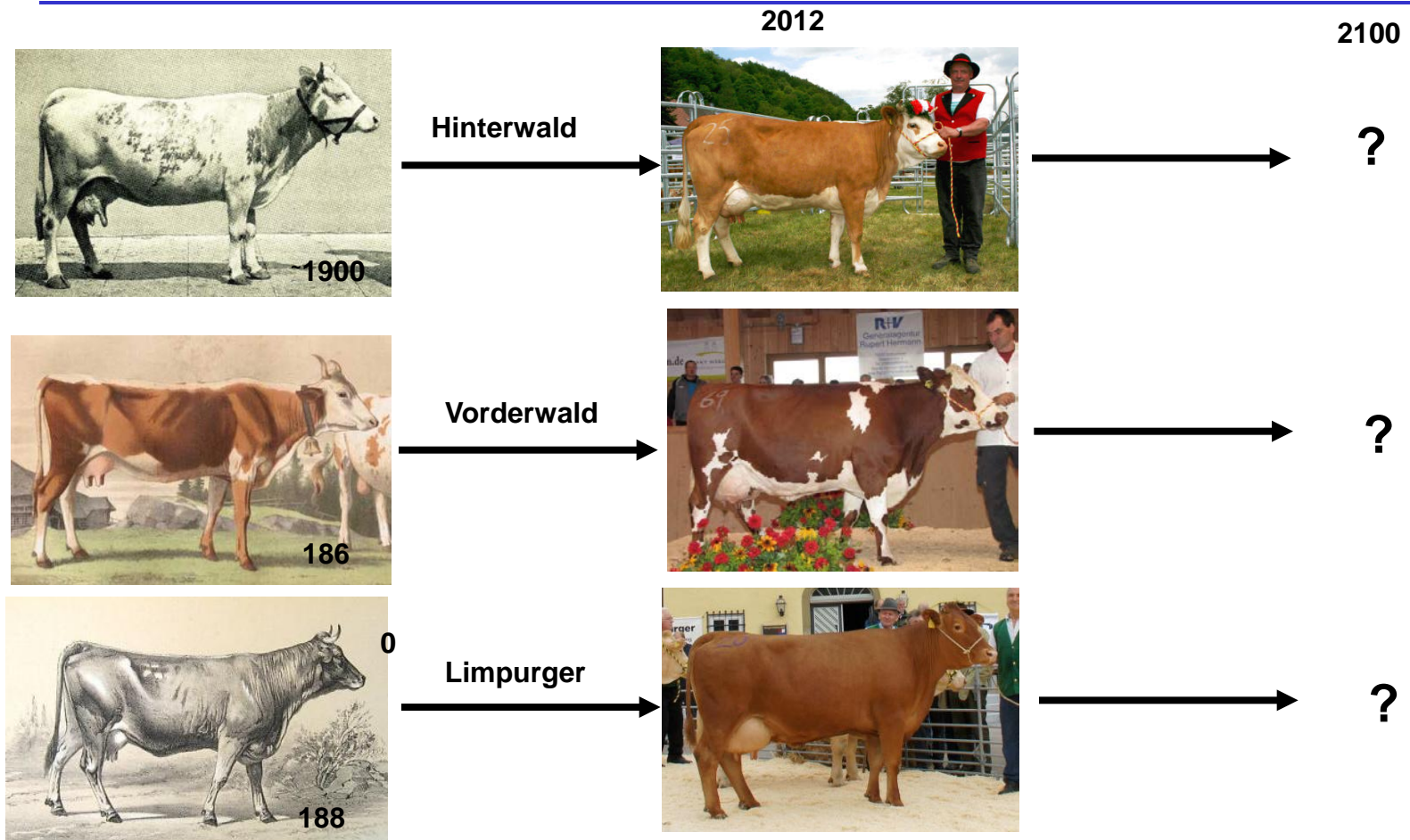
This can be done by constraining the minimum acceptable average breeding value of the offspring.



# Literature

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Wellmann, R., Hartwig, S., Bennewitz, J. (2012). Optimum contribution selection for conserved populations with historic migration. *Genet Sel Evol.* **44**:34



**Thank you for your Attention!**