OPTIMISATION OF THE SAMPLING STRATEGY FOR ESTABLISHING A GENE BANK:

STORING PrP ALLELES FOLLOWING A SCRAPIE ERADICATION PLAN AS A CASE STUDY

J. Fernández, T. Roughsedge, J. A. Woolliams and B. Villanueva
GERMOPLASM BANKS

✓ Reservoirs of genetic information

✓ Complementation of management strategies on “living populations”
When is a germplasm bank worthy?

✓ Loss of genetic variability

Genetic drift

Selection

Natural

Artificial
- Reduced census sizes
  - endangered populations

- Artificial selection
  - “classic” breeding programmes
  - eradication programmes
Transmissible Spongiform Encephalopathy

“SCRAPIE”

ARR  ARQ  AHR  AHQ  VRQ

Future reintroduction

- disease is not a concern
  ⇒ reintroduce all removed alleles

- effect of allele on other trait
  ⇒ replace ARR by a single allele

- associated variability
  ⇒ reintroduce all removed alleles
More complex OBJECTIVE

- optimal contributions per candidate donor

  ✓ Locus of interest

    ⇒ collecting predetermined frequencies

  ✓ Non-linked loci

    ⇒ keeping genetic variability
Minimum Quadratic Distance

\[ \min (\text{target freq.} - \text{bank freq.})^2 \]

\( s. \ a. \) global bank coancestry

\( s. \ a. \) within-allele bank coancestry

\[ \min \text{ distance} + \lambda (\text{coancestry}) \]

\( \lambda \): importance of genetic variability

\( \lambda\uparrow\uparrow \): target frequencies may be unfeasible

\( \lambda\downarrow\downarrow \): variability only accounted for after frequency term
MATERIAL AND METHODS

- Allelic frequencies
  - \( P_{\text{mean}} \): 0.52 ARR, 0.33 ARQ, 0.02 ARH, 0.08 AHQ and 0.05 VRQ
  - \( P_{\text{equal}} \): 0.2 for all alleles
  - \( P_{h_{\text{ARR}}} \): 0.80 ARR and 0.05 the rest
  - \( P_{l_{\text{ARR}}} \): 0.04 ARR and 0.24 the rest

- Population size
  - \( S \): 100 candidates
  - \( L \): 200 candidates

- Genetic diversity
  - \( C_{\text{low}} \): \( f = 0.01 \)
  - \( C_{\text{med}} \): \( f = 0.20 \)
  - \( C_{\text{high}} \): \( f = 0.40 \)

- Cost function
  - £120 per ram / £ 2.5 per collected dose
Computer simulations

✓ All combination of factors
  ⇒ mimic different breed types

✓ 20 replicates per scenario

✓ Controlled parameters
  ⇒ alleles frequencies
  ⇒ global coancestry
  ⇒ coancestry within alleles
  ⇒ distribution of contributions
  ⇒ cost of the program

BANK

no. donors
doses per donor
type of donor
### Degree of coancestry in the breed

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### Allelic

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SUMMARISING …

✓ Effective in balancing frequencies/diversity

✓ Main factors
  ⇒ allelic frequencies
  ⇒ diversity in target population

✓ Heterozygotes favoured
  \[\text{two alleles at a time (cheap)}\]
  \[\text{speed of reintroduction}\]

✓ Costs
  ⇒ careful design before starting the program
✓ Other diseases with genetic determination

✓ Marker assisted fixation of QTLs

✓ Conservation programmes
  ⇒ maintenance of frequencies in adaptative locus
  ⇒ use of molecular markers