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OPTIMISATION OF THE SAMPLING STRATEGY FOR ESTABLISHING A GENE BANK:

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

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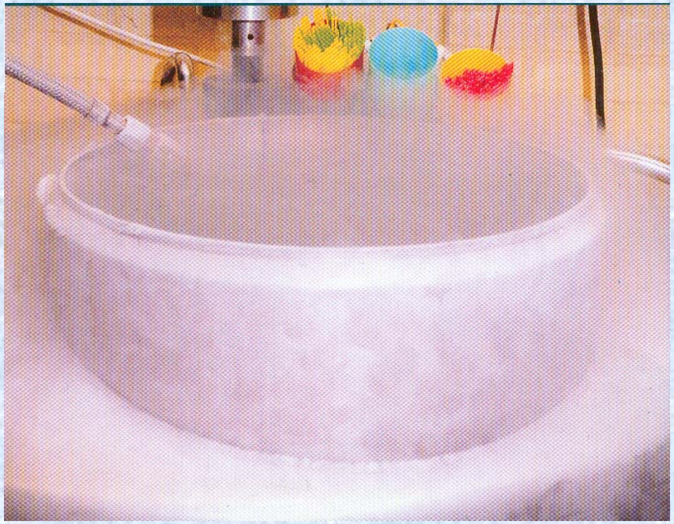
SAC

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** → ***species*** / ***breeds***

➢ **Artificial selection**

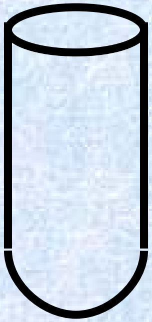
- ✓ **“*classic*” breeding programmes** +
- ✓ **eradication programmes** −

Transmissible Spongiform Encephalopaty

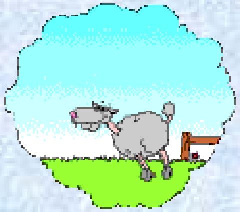
“SCRAPIE”

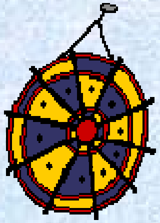

ARR ARQ AHR AHQ VRQ

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 **(target freq. – bank freq.)^2**

s. a. **global bank coancestry**

s. a. **within-allele bank coancestry**

min **distance + λ (coancestry)**

λ: 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_{mean}	*0.52 ARR, 0.33 ARQ, 0.02 ARH, 0.08 AHQ and 0.05 VRQ*
P_{equal}	*0.2 for all alleles*
P_{h_ARR}	*0.80 ARR and 0.05 the rest*
P_{l_ARR}	*0.04 ARR and 0.24 the rest*

➢Population size

S	*100 candidates*
L	*200 candidates*

➢ Genetic diversity

C_{low}	$f = 0.01$
C_{med}	$f = 0.20$
C_{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***

BANK

   ⇒ ***distribution of contributions***

      no. donors

      doses per donor

      type of donor

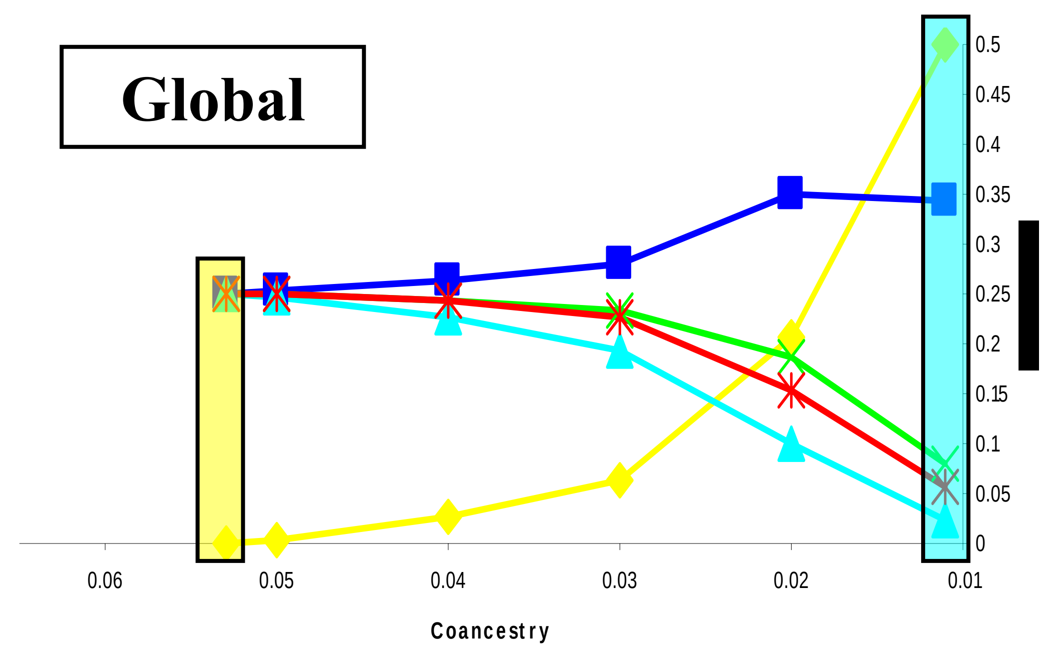
   ⇒ ***cost of the program***

Frequencies

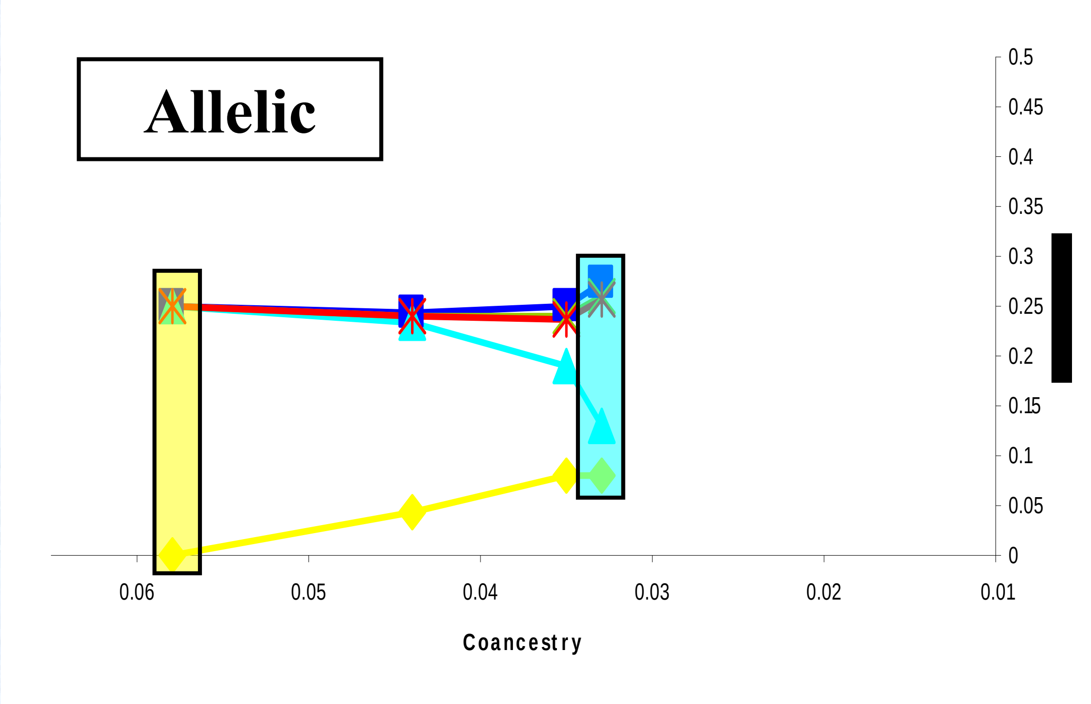
L

C_{low}

P_{mean}



ARR ◆
ARQ ■
ARH ▲
AHQ ✕
VRQ ✳



Global

Diversity

L

		Degree of coancestry in the breed								
		Low			*Medium*			*High*		
		R	*G*	*A*	*R*	*G*	*A*	*R*	*G*	*A*
P_{mean}		WR	*.058*	.162	WR	*.239*	.321	WR	*.428*	.489
		<.005	*.009*	.079	<.19	*.200*	.254	<.37	*.399*	.439
P_{hARR}		WR	*.065*	.175	WR	*.246*	.333	WR	*.433*	.499
		<.005	*.009*	.044	<.19	*.200*	.229	<.35	*.399*	.421
P_{lARR}		WR	*.010*	.016	WR	*.200*	.205	WR	*.399*	.403
		<.005	*.009*	.015	<.19	*.200*	.205	<.35	*.399*	.403
P_{equa}		WR	*.011*	.020	WR	*.202*	.209	WR	*.400*	.406
		<.005	*.009*	.017	<.19	*.200*	.206	<.35	*.399*	.404

Allelic

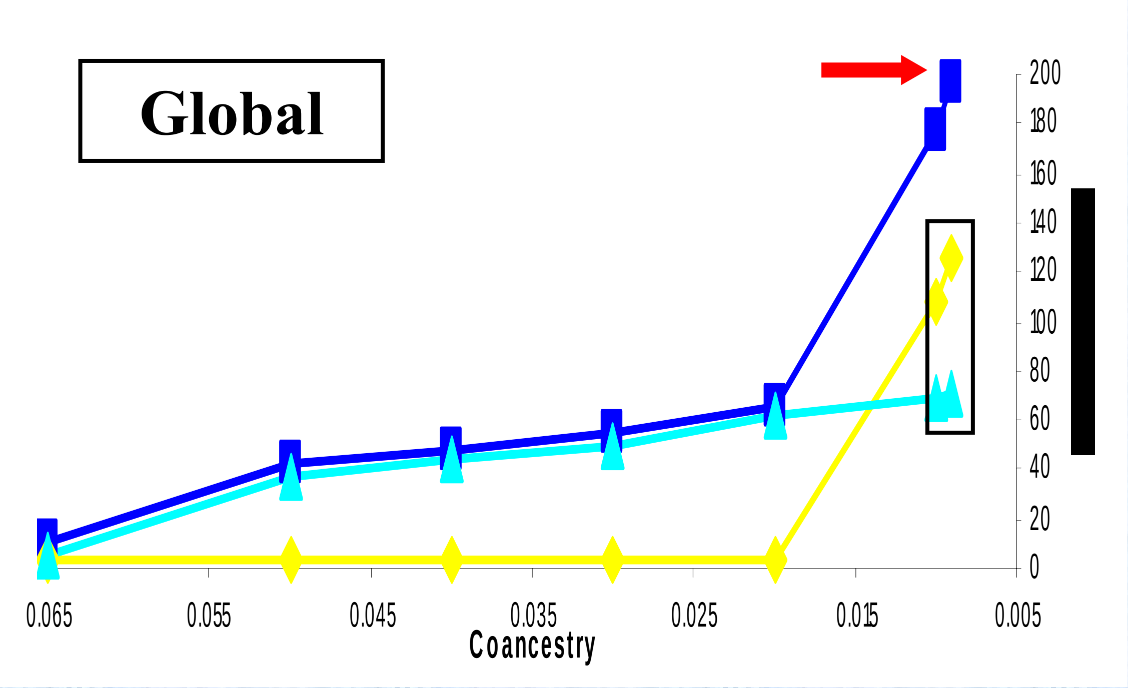
P_{mean}	0,02	WR	.059	*.162*	WR	.241	*.321*	WR	.430	*.489*
		<.050	.033	*.070*	<.20	.218	*.248*	<.40	.411	*.434*
P_{hARR}	0,05	WR	.065	*.168*	WR	.246	*.331*	WR	.433	*.491*
		<.010	.016	*.040*	<.20	.206	*.226*	<.40	.403	*.418*
P_{lARR}	0,24	WR	.010	*.015*	WR	.201	*.205*	WR	.399	*.403*
		<.010	.010	*.014*	<.20	.200	*.204*	<.40	.399	*.402*
P_{equa}	0,20	WR	.012	*.020*	WR	.202	*.209*	WR	.401	*.405*
		<.010	.010	*.015*	<.15	.201	*.205*	<.40	.399	*.403*

Distribution of contributions

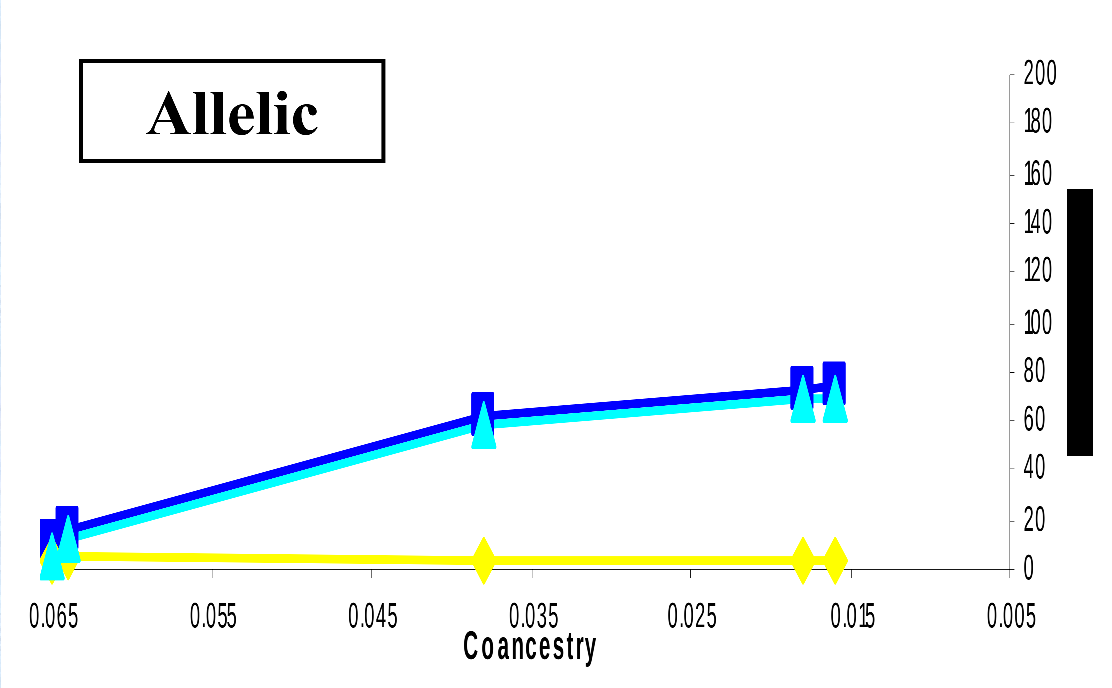
L

C_{low}

P_{h_ARR}



Hom ◆ **Het** ▲ **Total** ■

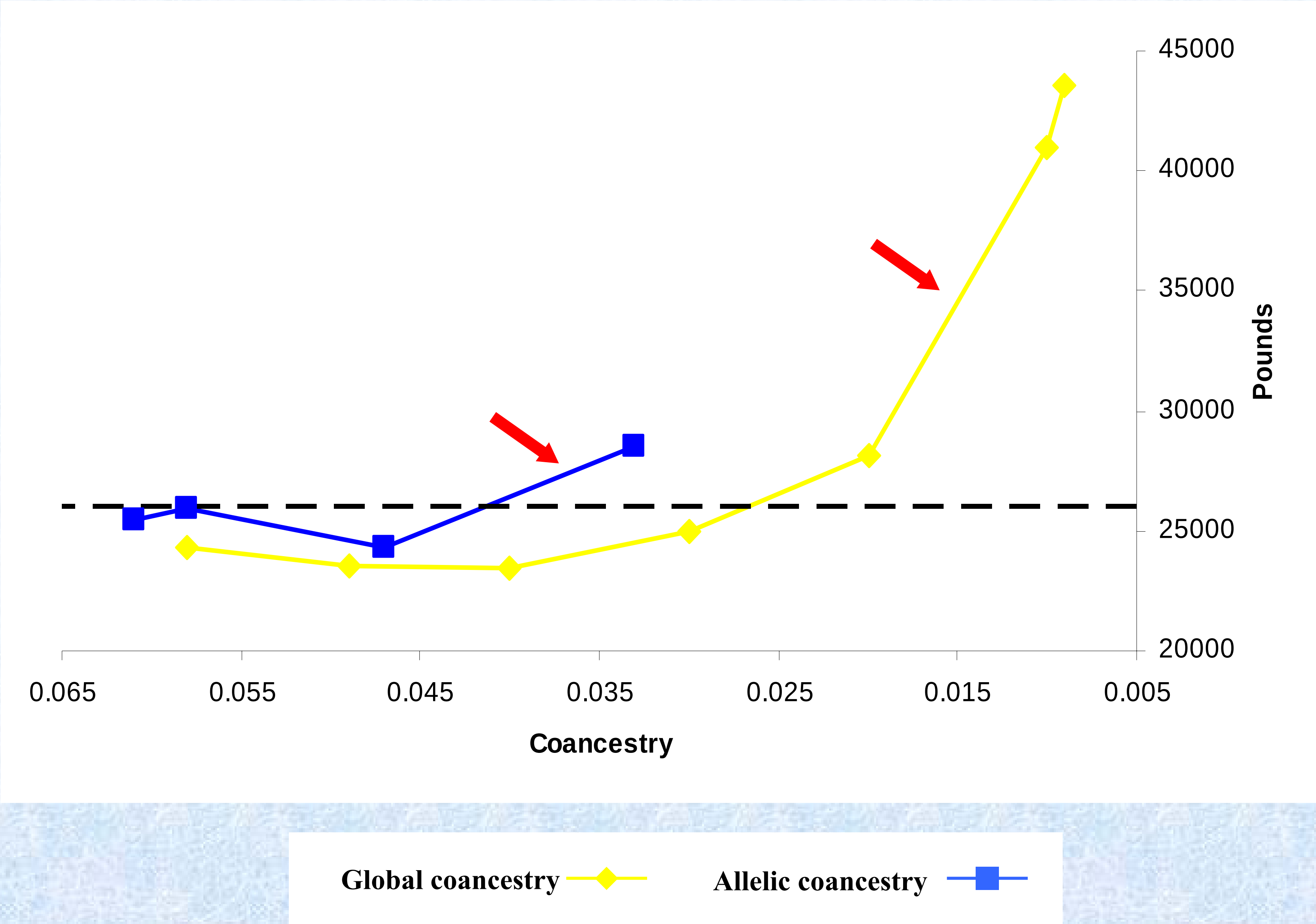


Cost

L

C_{low}

P_{mean}



SUMMARISING …

- ✓ **Efective in balancing frequencies/diversity**
- ✓ **Main factors**
  - ⇒ **allelic frequencies**
  - ⇒ **diversity in target population**
- ✓ **Heterozigotes favoured** {
  - **two alleles at a time (cheap)**
  - **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**