

Gene Banking and Cryopreservation Training Workshop

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Sampling strategies

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Gene banks can have a multi-function role:

- To reconstruct breeds / breeding lines;
- To support populations conserved *in vivo*:
 - to increase effective population size of small populations;
 - as a back-up in case genetic problems occur (e.g. loss of allelic diversity, inbreeding, occurrence of deleterious genetic combinations);
- To develop new lines / breeds;
- As a back-up, to quickly modify and/or reorient, the evolution /selection of populations;
- Provide material for research (DNA source; multi-generational samples of genetic variation, etc.).

Operational Steps

Choice of populations

Type of material: evaluate pro and contra

Amount of material: n. of doses
n. of donors

Selection of donors

Frequency of collection

Criteria for selecting donor animals

- **Random: to store a representative sample of the breed genetic variation**
- **Maximise genetic variation**
- **Animals carrying specific genotypes /alleles /haplotypes**

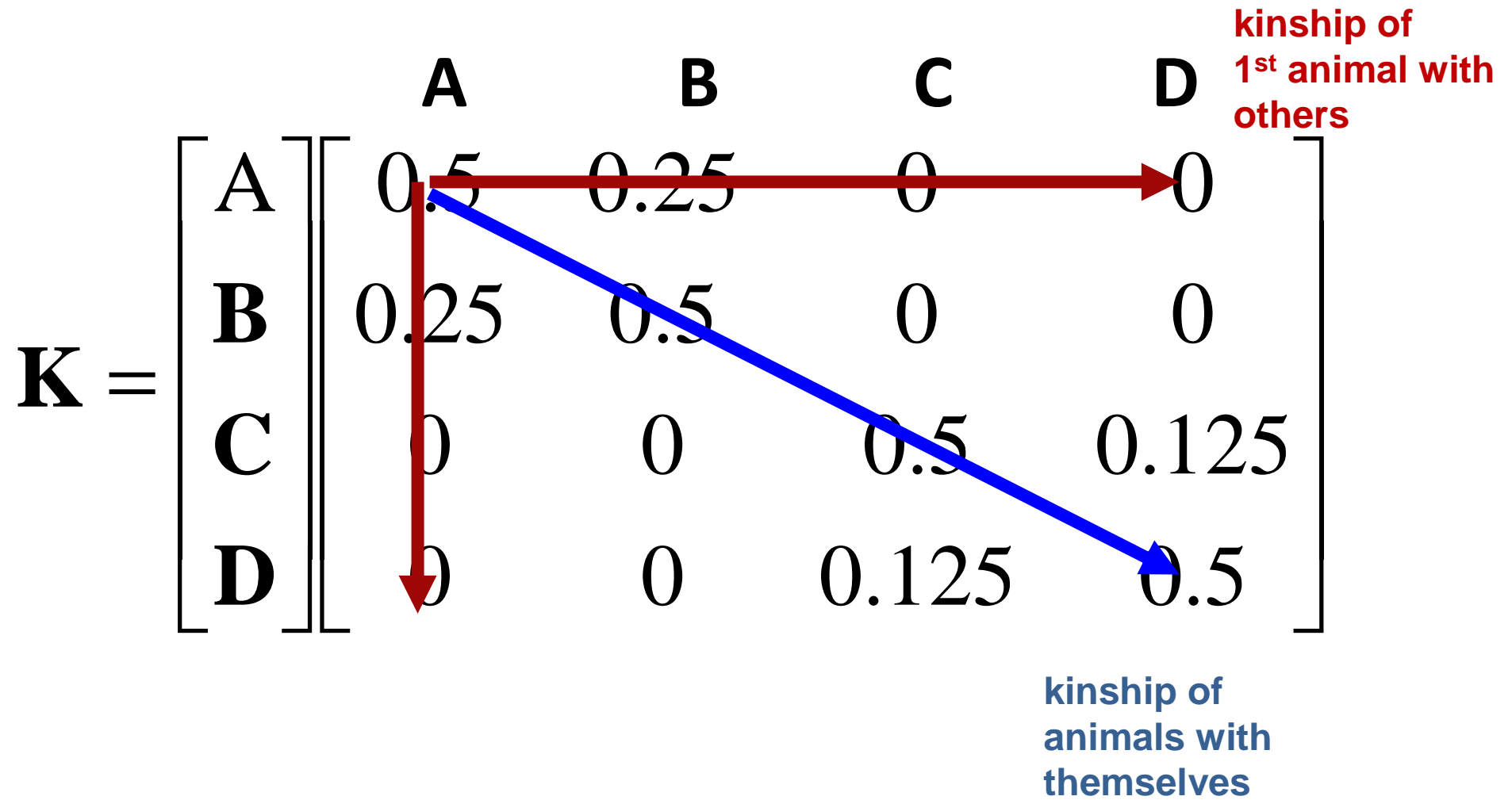
Sampling methodology will depend on sources of information available

- **Pedigree (depth and completeness)**
- **Markers**
- **Information on distribution / exchange of animal across herds**
- **Phenotypes**
- **None**

1. Selection based on kinship (computed on pedigrees or molecular markers)

Aim: To maximise variance among donors by minimising kinship among them (e.g. Caballero and Toro 2000; 2002)

Kinship matrix among candidate donors



Genetic variability among the donors is maximized by minimizing the following:

$$k_a = \sum_i \sum_j c_i c_j k_{ij}$$

Where

k_a is the average kinship among selected donors

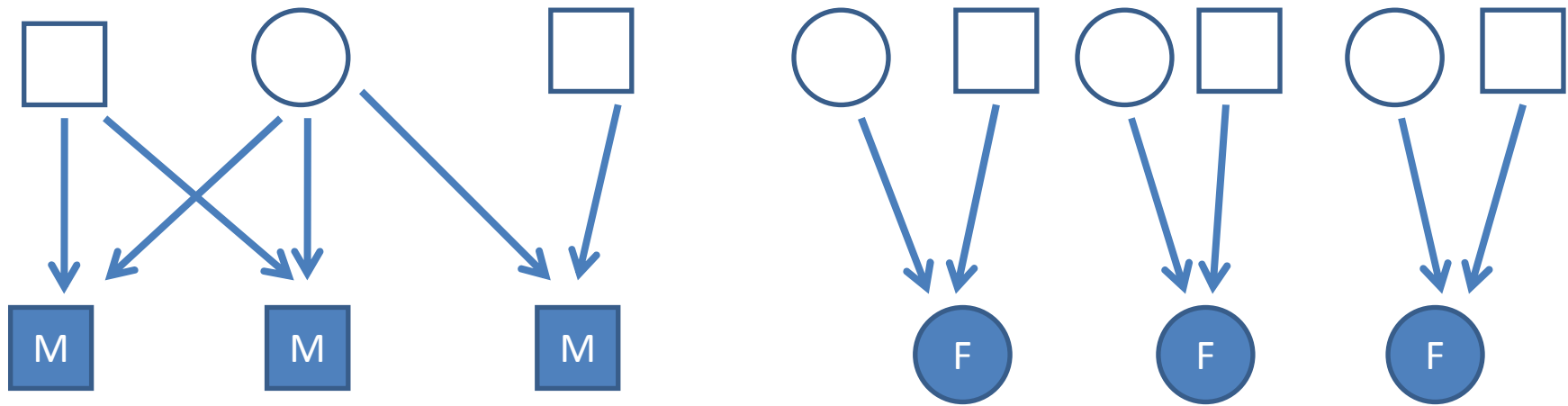
k_{ij} is the kinship between candidates animals i and j

c_i is the relative proportion of genetic material of animal i in the genebank

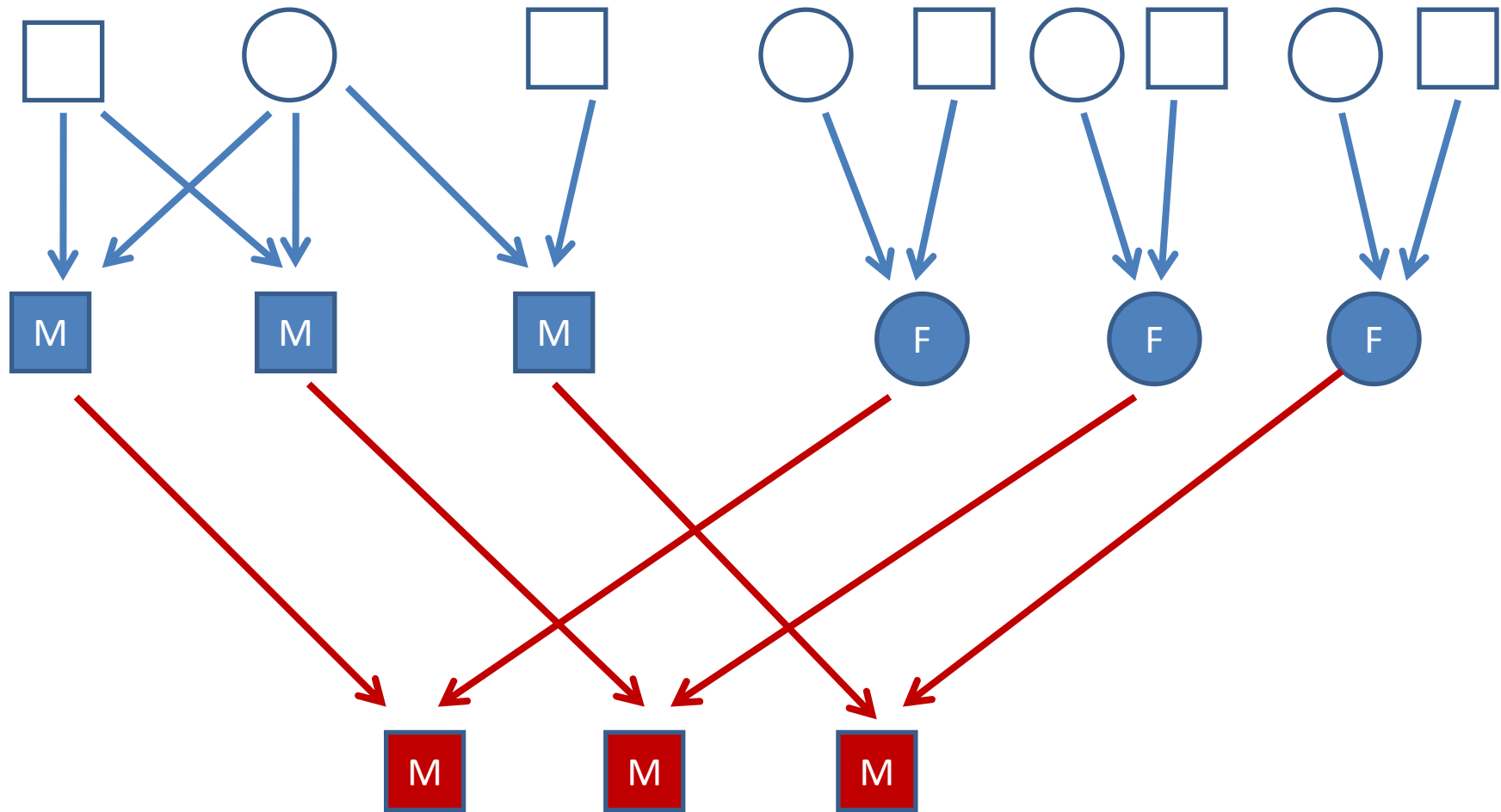
Minimising average kinship among a subset of three donors. Select **A C D = 0.19**; **Select BCD = 0.19**; Select ABC = 0.22; Select ABD = 0.22

$$\mathbf{K} = \begin{matrix} & \begin{matrix} \mathbf{A} & \mathbf{B} & \mathbf{C} & \mathbf{D} \end{matrix} \\ \begin{matrix} \mathbf{A} \\ \mathbf{B} \\ \mathbf{C} \\ \mathbf{D} \end{matrix} & \begin{bmatrix} 0.5 & 0.25 & 0 & 0 \\ 0.25 & 0.5 & 0 & 0 \\ 0 & 0 & 0.5 & 0.125 \\ 0 & 0 & 0.125 & 0.5 \end{bmatrix} \end{matrix}$$

In some cases it might be necessary to create through appropriate mating new bulls to be used as donors, in order to retrieve genetic variation present only among females



The three males do not carry the genetic variation of the three females !



The three new males carry the genetic variation of the three females !

1.2 Aim: To maintain allelic frequencies

- Molecular data can be used if the goal is to maintain population genetic frequencies, minimize (Saura et al., 2008)

$$KL = \sum_m^M \sum_k^{K_m} p'_{km} \log \left(\frac{p'_{km}}{p_{km}} \right)$$

where

- KL = difference between population frequencies and frequency of a subset
- p_{km} is the population frequency of allele k at locus m
- p'_{km} is the frequency of allele k at locus m in the optimized set

$$p'_{km} = \sum_{i=1}^N c_i g_{mki}$$

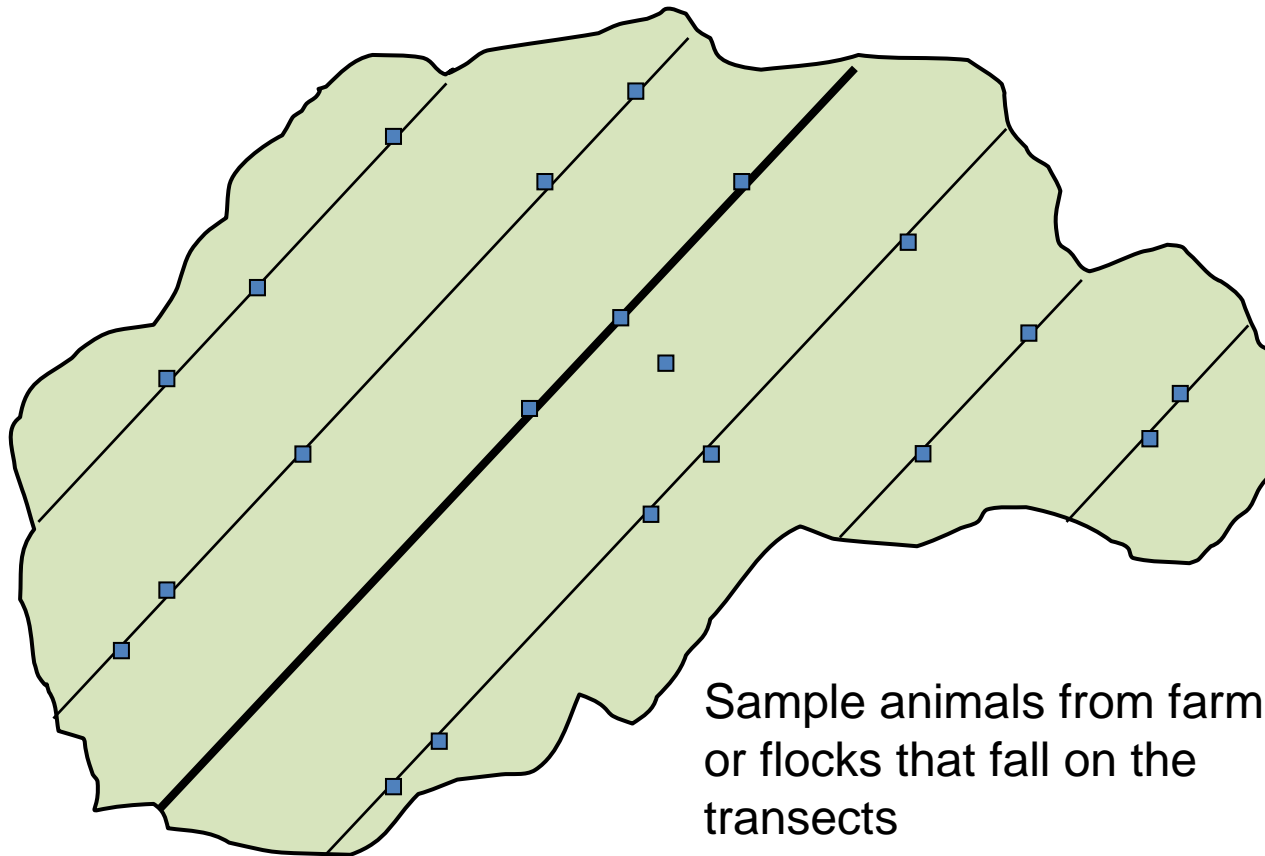
where,

- c_i is the proportional contribution of animal i
- g_{mki} is the gametic contribution of animal i to allele k of locus m
 - 1.0 for homozygote
 - 0.5 for heterozygote
 - 0.0 for other

2. Selection based on geographical distribution (no pedigrees available)

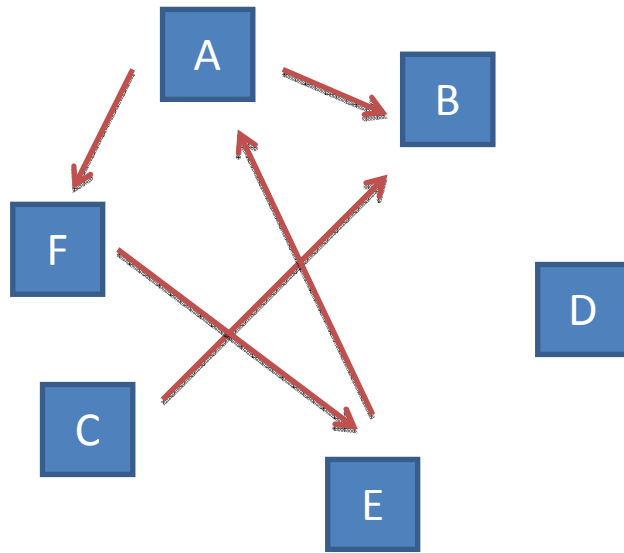
- Animals may not be organized into “breeds”, but simply a population dispersed across a given area, no herds registration
- Commonly-faced situation in developing countries, sometime small ruminants in Western-Southern Europe, wildlife populations
- We can assume that geographical variability is associated with genetic variability
 - separation by distance
 - separation by geographical features

Line Transects



Sample animals from farms or flocks that fall on the transects

3. Selection based on information on exchange of animal among herds (no pedigrees available)



Information: exchange of animals among flocks during the period $t - t+1$

Based on the historical information about exchange of animals among flocks, we could construct an index of similarity among flocks.

This index could be used to select donors, minimising similarity among them.

SAUVAGE Software (Raoul et al., 2004) computes for populations without (poor) pedigrees, and index of similarity between each male of the population and the females of each flocks. The similarity index is constructed from the information on migration of animals between flocks.

SAUVAGE could be implemented to select donors of material for cryo-banking ?

4. Selection based on phenotypic data (no pedigrees available)

- Selection for specific phenotypes
- Selection for maximum diversity
 - select animals with a wide range of phenotypic values for a given trait
 - select animals with unique phenotypes for a battery of traits
 - quantitative, qualitative
 - calculate EBV and select animals to ensure a large amount of variation (implies pedigree information available)

Selection for animals carrying specific genotypes /alleles /haplotypes

Example: UK semen banking - Scrapie (Fernandez et al, 2006)

EU breeding plans: increase freq. (fixation) of ARR haplotype

Risks associated to eradication of susceptible haplotypes

- New TSE appearing
- Loss of favourable genotypes associated to the eradicated haplotypes
- Loss of genetic variation

Solution: creation of a semen banks with donors carrying haplotypes expected to disappear with the selection for ARR haplotype.

Age-group	m 1	m 2	m3	f1	f2
Herd							
A	1			1	0.9		
B		0.5			0.1		
C		0.5					
D			0.8				
E			0.2				
F							