Genebanks in the genomics era

Peer Berg

NordGen

Genomic management of animal genetic diversity
March 23. 2017

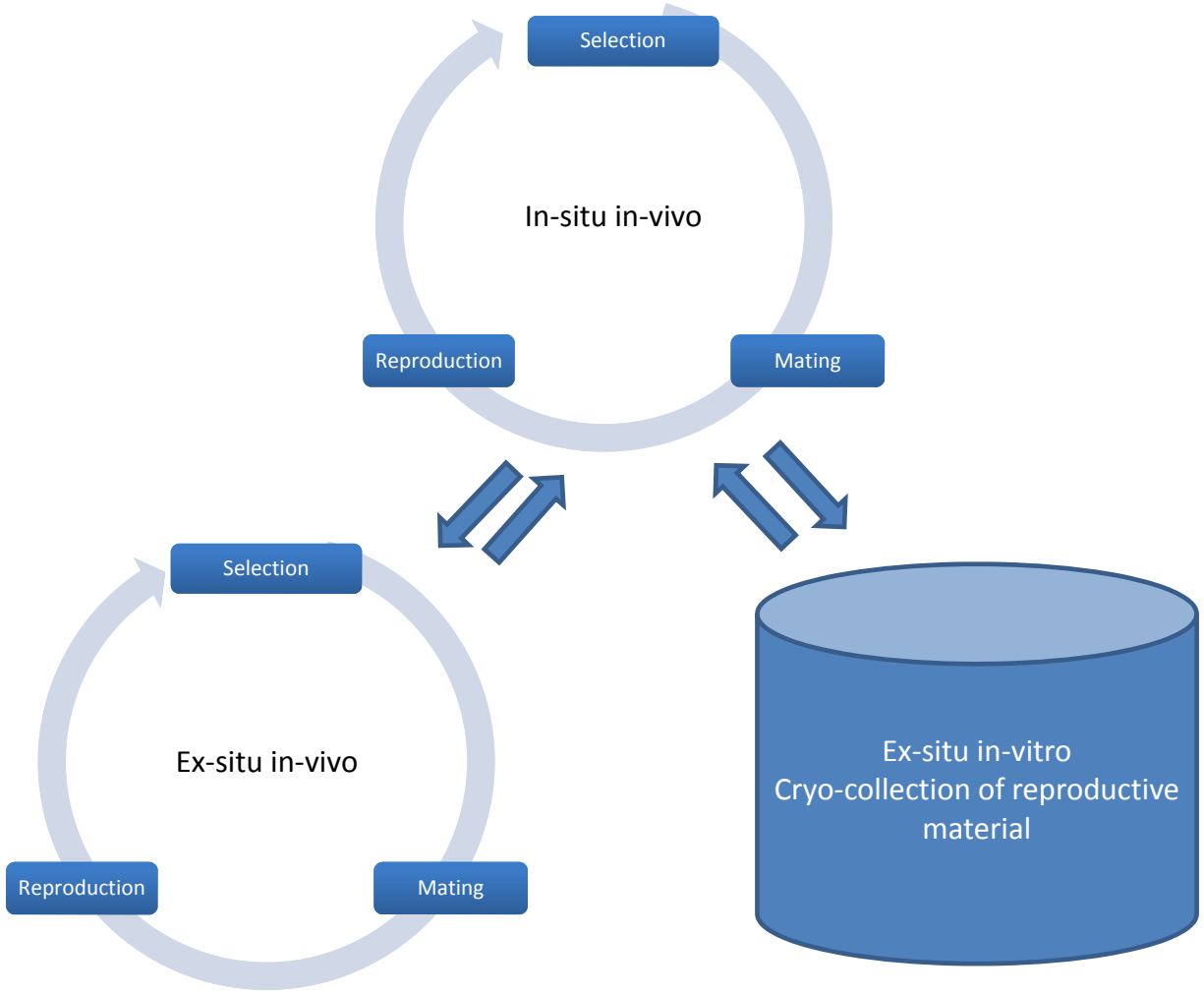
What is a genebank?

- Cryo-conserved reproductive material
  - Long-term storage
  - Semen and embryoes
    - Technology
    - Species

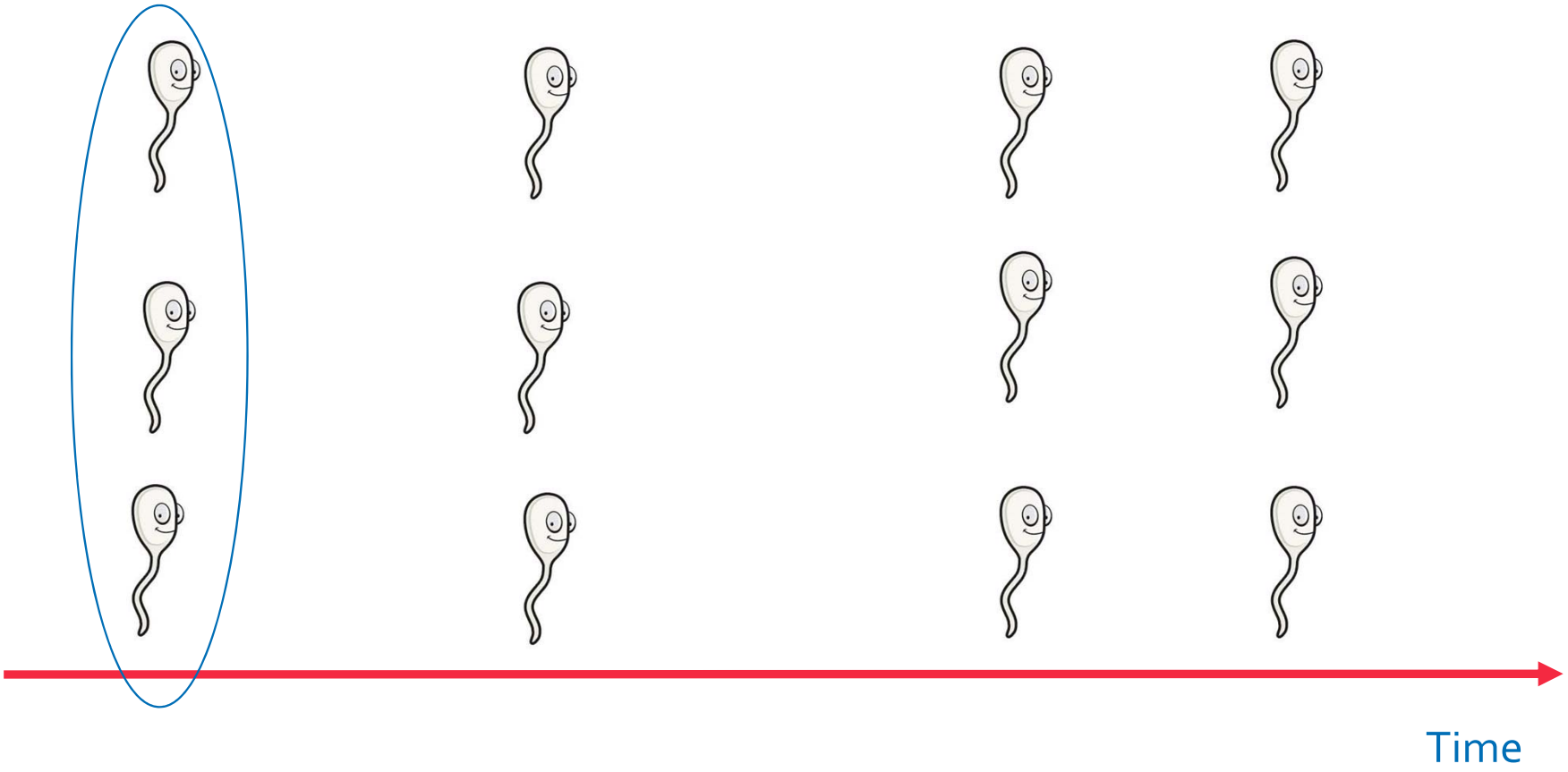
  - Reduced viability after cryo-conservation

Role of genebanks

- ❑ Long-term storage
- ❑ Back-up
- ❑ Supplementary to in-situ
- ❑ Population management
- ❑ Document genetic progress
- ❑ Research



Role of genebanks



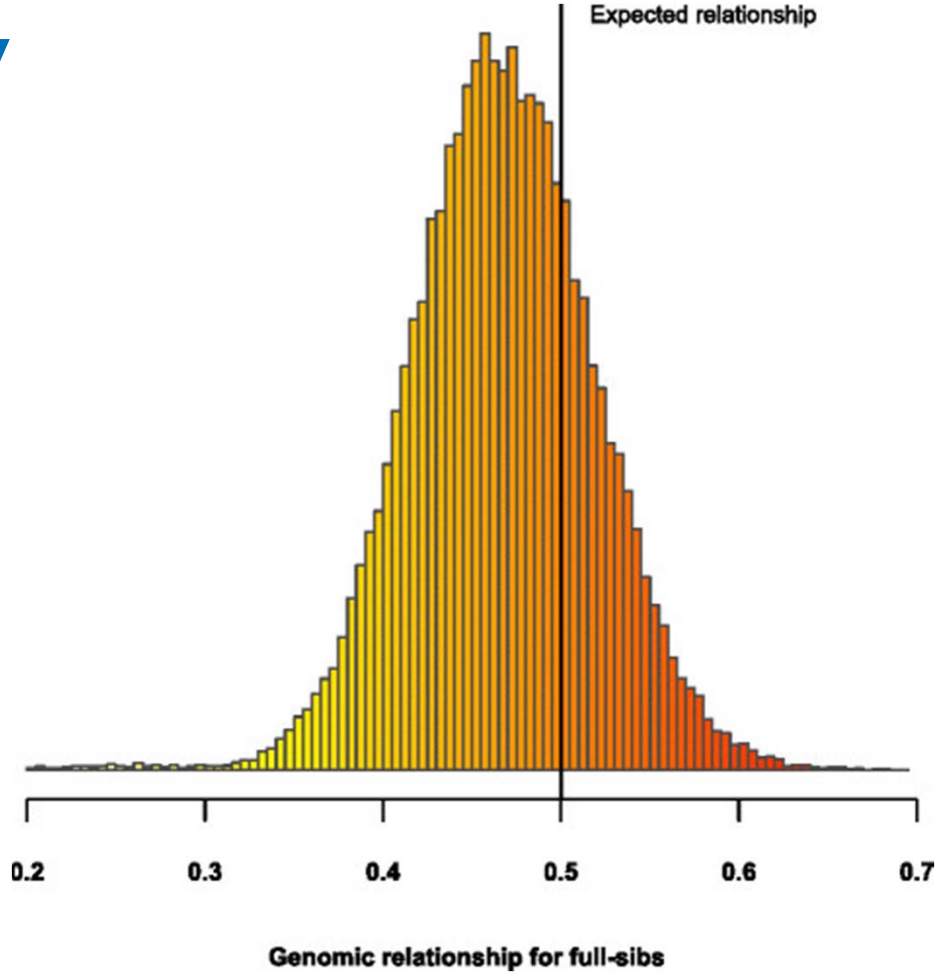
Added value of genomic information

- Inventory
- Maintaining specific alleles/haplotypes
- Sampling animals for cryo-conservation
- Use of genebank samples
- Research
- More efficient introgression

More detailed inventory

- Genomic vs. pedigree relationships
  - Within breeds
  - Between breeds

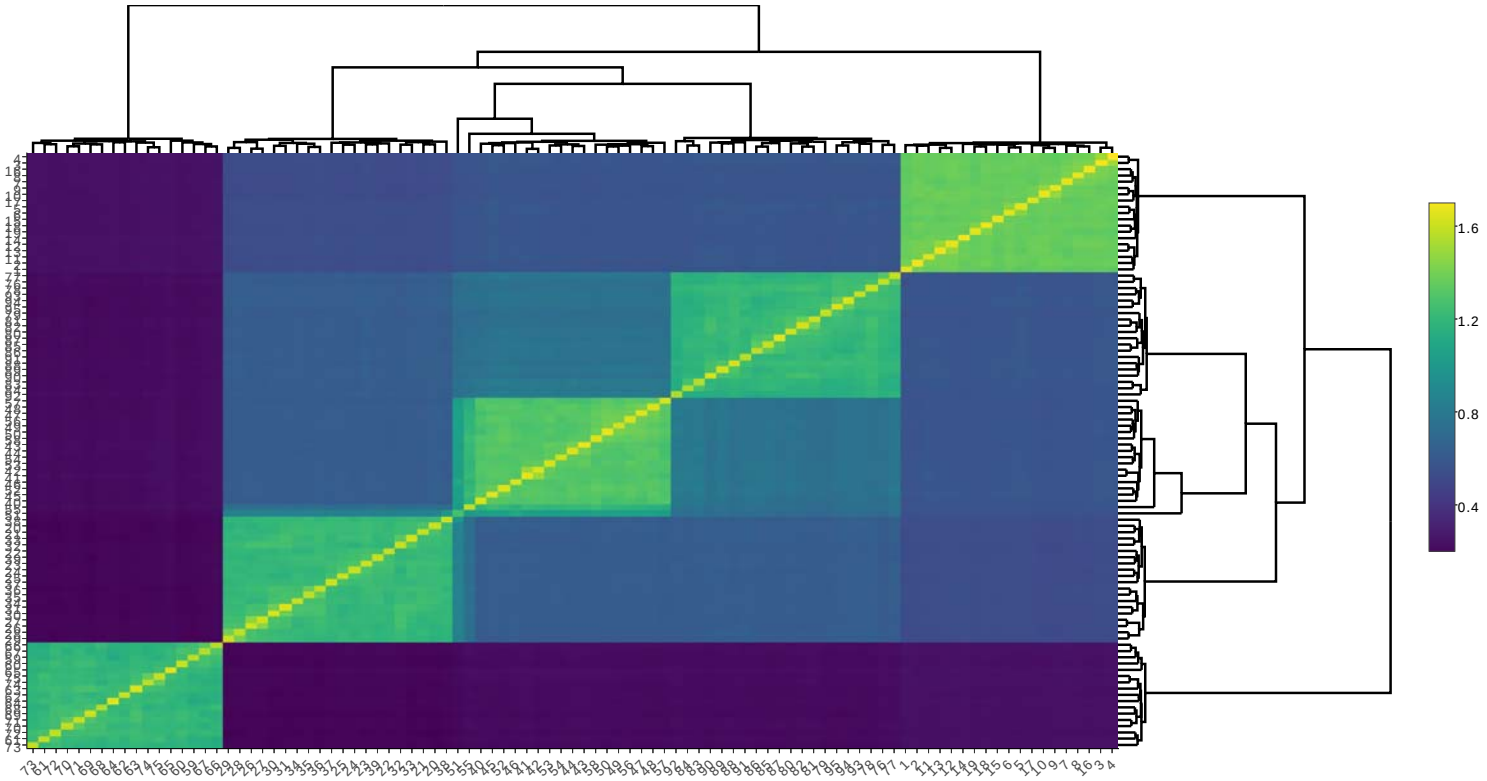
- Specific alleles or haplotypes
  - E.g. Halothane sensitivity allele
  - E.g. PrnP haplotypes



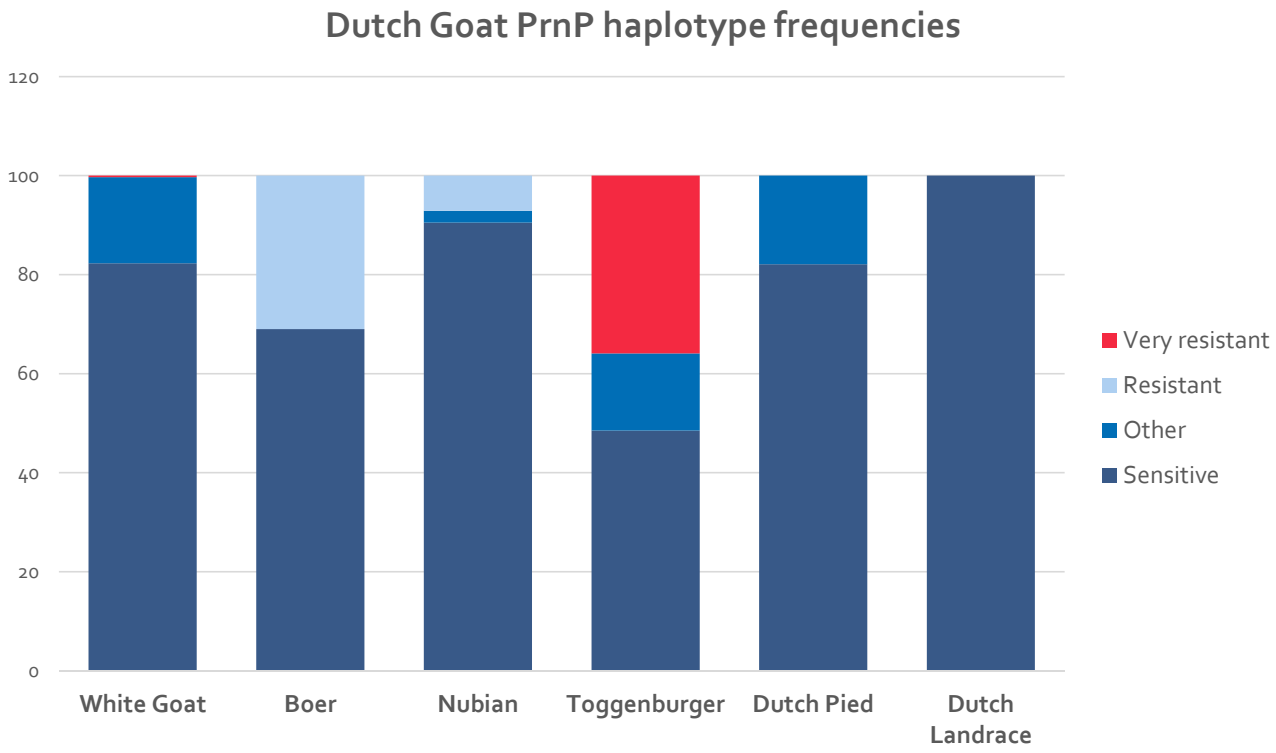
Lourenco et al. 2015

Genomic relationships

5 Norwegian poultry breeds



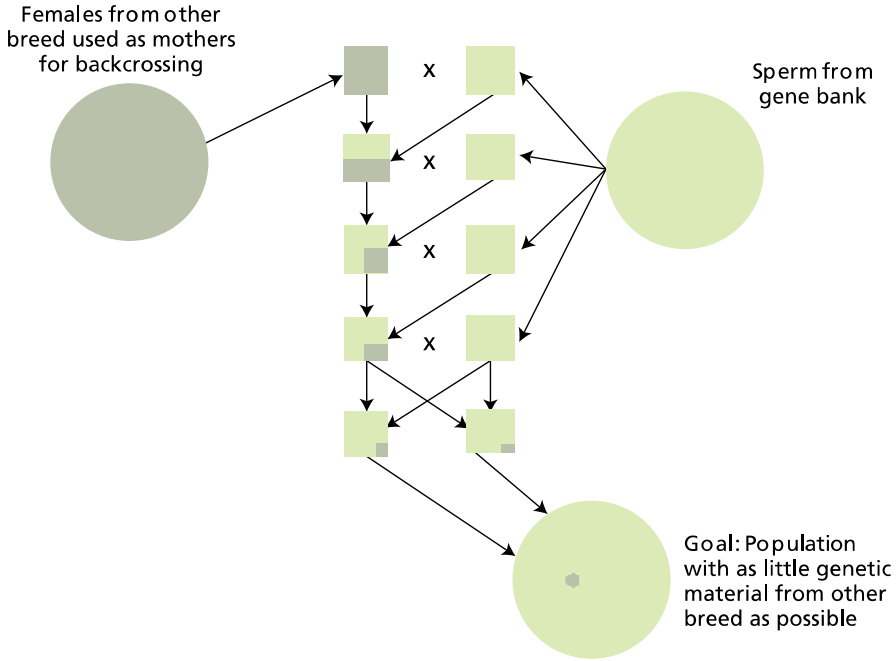
PrnP haplotypes in Dutch goats



Modified from Windig et al. 2016

FAO recommendations

FIGURE 3
Population reconstitution with cryoconserved semen



FAO 2012

TABLE 7
Number of semen doses required to reconstitute a breed of cattle, small ruminant or horse

Founder females (N)	Pregnancy rate			
	0.4	0.5	0.6	0.7
75	...*	...	449 (26)	460 (37)
100	...	564 (22)	599 (35)	615 (49)
150	771 (17)	846 (33)	897 (53)	...
200	1 029 (23)	1 128 (44)	...	...
250	1 287 (29)	1 410 (55)	...	...
300	1 544 (34)	...	...	...
350	1 800 (40)	...	...	...
400	2 058 (46)	...	...	...

Note: The figures in parenthesis show the effective population size of the reconstituted population.
The quantity of semen is calculated at the 150 percent level (see main text for explanation).
* Missing values indicate that results are not practical, resulting in either too few (upper-left corner) or too many (lower-right corner) animals or requiring large quantities of semen.

TABLE 8
Number of doses per male required to reconstitute a breed of cattle, small ruminant or horse

Founder females (N)	Pregnancy rate											
	0.4 Males (N)			0.5 Males (N)			0.6 Males (N)			0.7 Males (N)		
	25	50	100	25	50	100	25	50	100	25	50	100
75	...	...	...	...	...	...	18	9	5	19	10	5
100	...	...	...	23	12	6	24	12	6	25	13	7
150	31	16	8	34	17	9	36	18	9	...	...	...
200	42	21	11	46	23	12	...	...	...	...	...	...
250	52	26	13	57	29	15	...	...	...	...	...	...
300	62	31	16	...	...	...	...	...	...	...	...	...
350	72	36	18	...	...	...	...	...	...	...	...	...
400	83	42	21	...	...	...	...	...	...	...	...	...

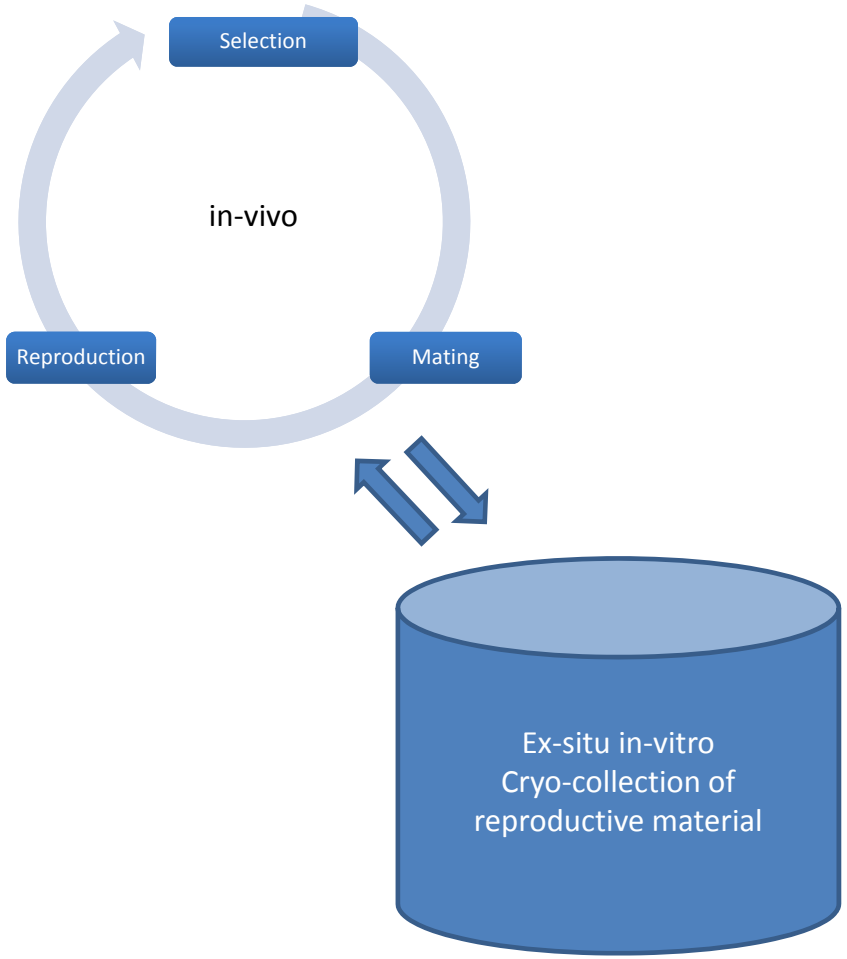
Note: Quantity of semen is calculated at the 150 percent level (see main text for explanation).

Selecting animals for cryo-conservation

- **Maximise diversity in cryo-collection**
- **Minimise relationships between donors**

$$\bar{r} = c' H c$$

- **Subject to constraints**
  - Non-negative contributions
  - Maximum contributions
  - Sum of contributions



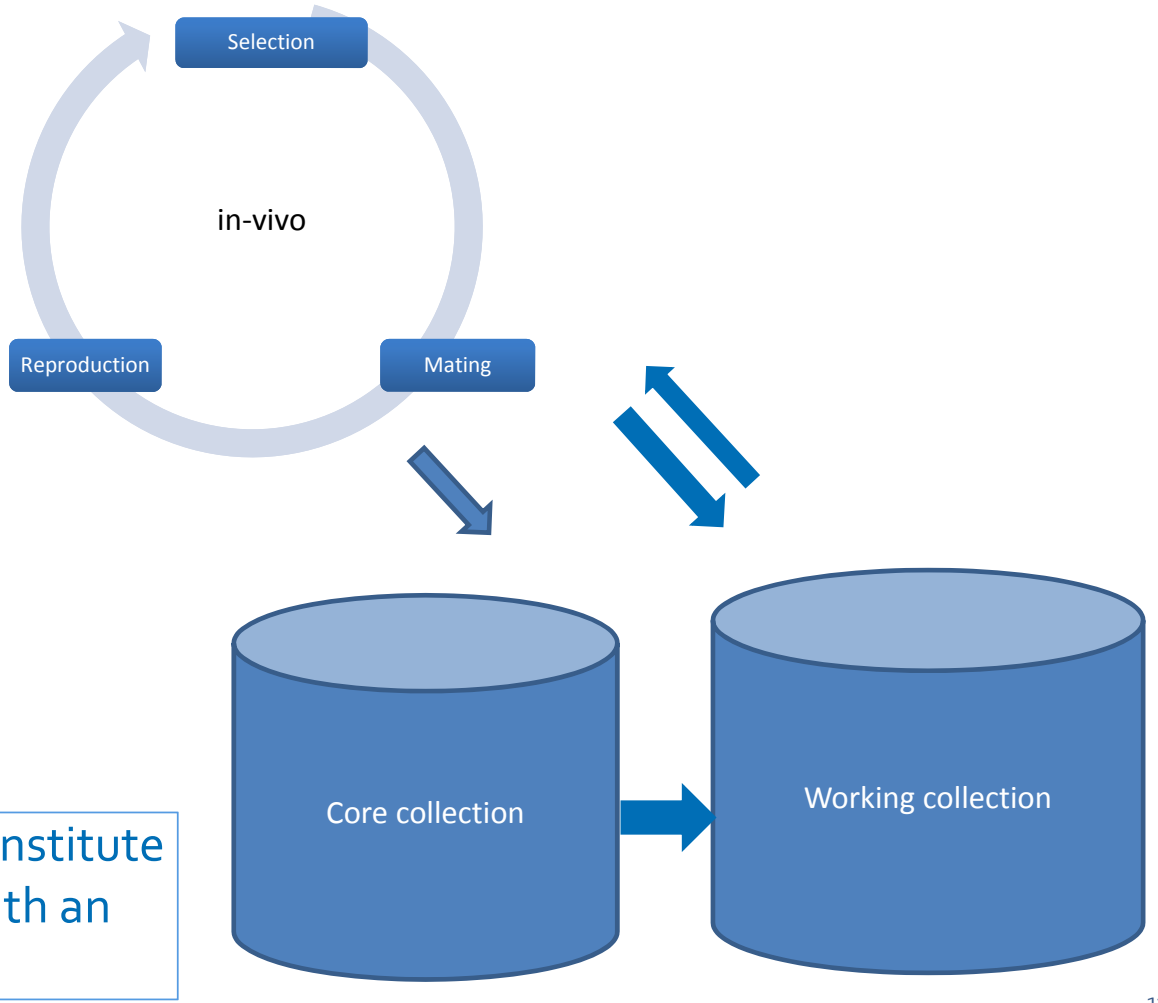
Using samples from cryo-collections

- **Maximise diversity in cryo-collection**
- **Minimise relationships between donors**

$$\bar{r} = c' H c$$

- **Subject to constraints**
  - Non-negative contributions
  - Maximum contributions
  - Sum of contributions

Collection to reconstitute a population with an Ne of 50



International conservation value

Norwegian poultry breeds

Set	Genetic Diversity	% lost	Priority
Synbreed + NO breeds	0.5299	-	
Jærhøns lost	0.5287	0.22	4
Rokohøns lost	0.5287	0.23	3
NorBrid 1 lost	0.5249	0.94	2
NorBrid 4 lost	0.5290	0.17	5
Norbrid 8 lost	0.5149	2.84	1

Cathrine Brekke

Research

- Genomic selection
- Deleterious alleles with pleiotropic effects
  - E.g. Halothane sensitive alleles
- Historical information
  - Effects of selection
  - Extreme genotypes
  - Links to phenotypic information

Documentation
Link cryo-conserved samples to
- Phenotypic records (EBV)
- Genomic data
- Socio-cultural descriptors

1000 Bulls Genome Project

- IMAGE project (Horizon2020)
- Genotype bulls in genebanks least related to genotyped bulls
- More complete inventory of genomic variation

Gene-editing

- "Correct" deleterious alleles
  - Several candidate loci
- Introduce variation at specific loci
  - Few candidate loci
  - Identification of candidates
    - Historical diversity
    - Comparative diversity across breeds and species

Acknowledgement

Jack Windig

Kor Oldenbroek