

IMPACT OF THE USE OF CRYOBANK SAMPLES IN A SELECTED CATTLE BREED:

A SIMULATION STUDY

Grégoire Leroy, Coralie Danchin-Burge, Etienne Verrier

*UMR1313 INRA/AgroParisTech Génétique Animale et Biologie Intégrative
IDELE*



Consequences of high selection pressure in domestic cattle

Trait	Impact (/1% F)
Milk litters produced (305d)	-25 L
Functionnal longevity	-14 days
Non return rate (heifer)	-0.14%

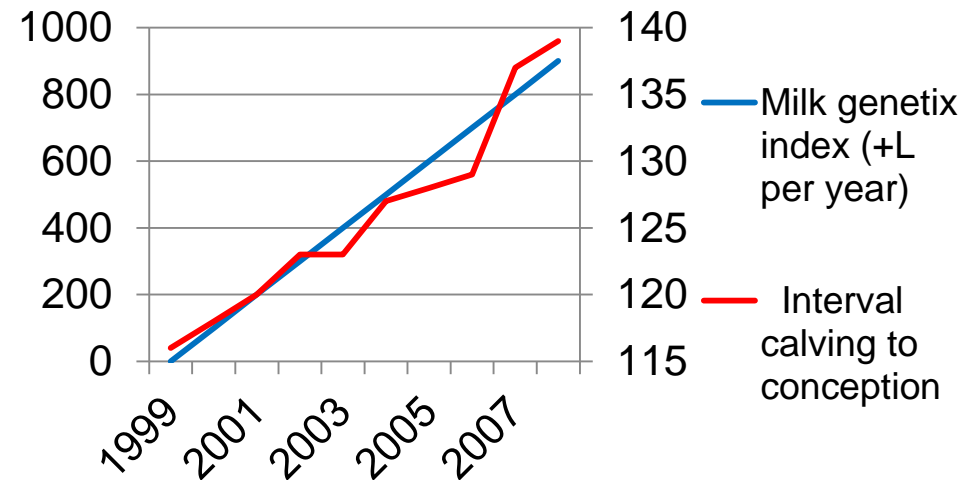
Impact of inbreeding depression on some production traits in Holstein

Deterioration of fonctionnal traits negatively correlated with production traits

Sources: Hudson et al. 1984, Croquet et al. 2007, Miglior et al. 2012, UNCEIA, IDELE

Undesirable increase of inbreeding

- Diffusion of genetic disease (BLAD, bulldog, CVM...)
- Inbreeding depression detected in selected traits

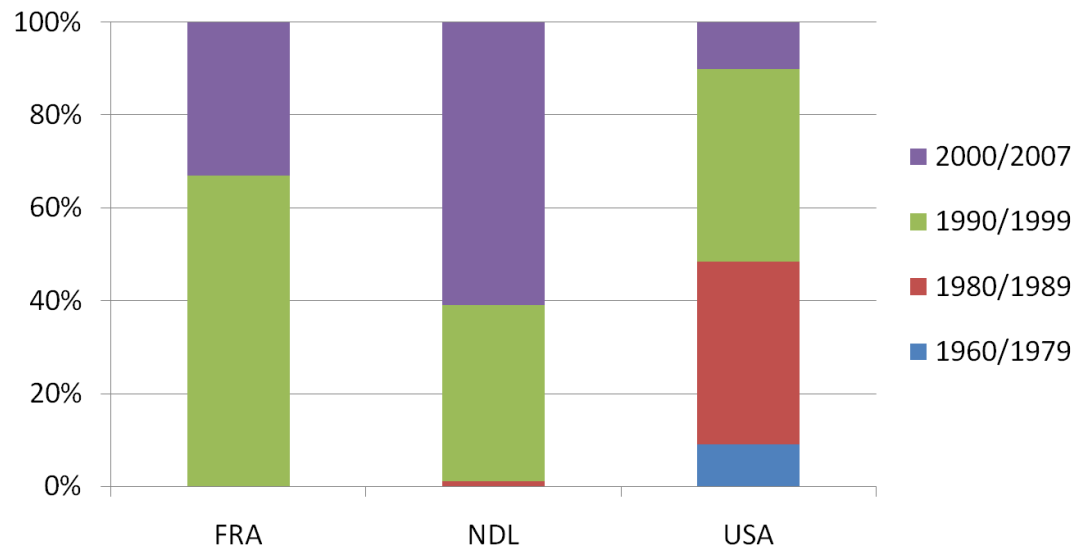


Evolution of production traits in French Holstein



Potentialities of cryopreservation in selected population

- FAO recommended the implementation of *ex situ* programmes to complement *in situ* conservation of animal genetic resources
- Cryopreserved material considered as a backup material to redirect the selection scheme if needed
- Since the 90s several gene banks have been created with different strategies and policies that vary with the breed, species, and country concerned



Decades of birth of the cryobanks bulls according to three countries (Danchin Burge et al. 2010)

Aim of the study

To investigate the benefits of using cryopreserved semen in a selection scheme

- to redirect selection goal
- to limit the loss of genetic diversity in the breed.

Simulation used (1)

Simulated cattle population

- 13 discrete generations with 100 males and 10,000 females
- 10 bulls and 50 cows sampled as parents of male progeny
- 20 bulls and 10,000 cows (no selection) sampled as parents of the female progeny
- Random mating

Reproducers selection

- Simulation of breeding values for two traits A (production trait) and B (functional trait) negatively correlated ($r=-0.3$)
- Total Merit Index (TMI) computed as a weighted sum of EBV_A and EBV_B ($w_B=1-w_A$)
- Reproducers selected as the best on EBV_A from generation 0 to 8.

Simulation used (2)

Each generation, bulls semen sampled according to the current rules of French National Cryobank for original bulls (type II)

- EBV_A 3 s.d. above or below the mean of the generation
- EBV_B 2 s.d. above the mean of the generation
- Bull is a sire of sires with no male offspring selected after the evaluation process

Simulation outputs

- Average breeding values for trait A and B
- Average coancestry
- Origin of genes within population (genedropping)

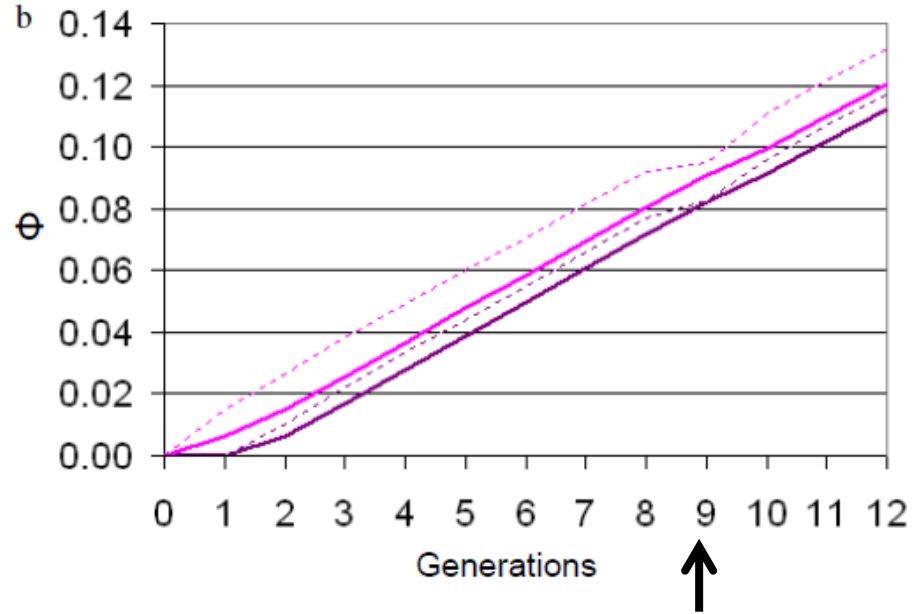
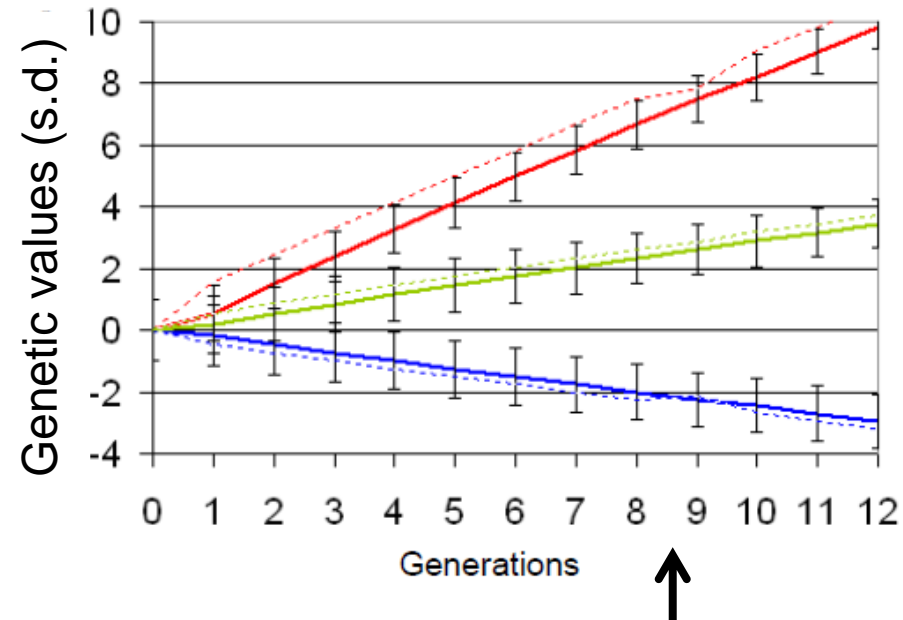
Simulation used (3)

At generation 9, use of cryobank bulls as sires of 40 % of newborn bull calves, according to 6 scenarios

Scenarios		Use of cryobank bulls in generation 9		Selection scheme during stage 2 (generations 9-12)	
Objective	Code	Selection of cryobank bulls	% of male offspring	Selection criterion	Use of sire of bulls
Improving trait B	b1	Higher TMI value	40	EBV _A	No change
	b2	Not used	0	TMI	No change
	b3	Higher TMI value	40	TMI	No change
Maintaining genetic diversity	d1	Minimizing kinship with current population	40	EBV _A	No change
	d2	Not used	0	EBV _A	Conservation of male lines
	d3	Minimizing kinship with current population	40	EBV _A	Conservation of male lines

Scenario b1

Evolution of genetic values (a) and average kinship (b) when cryobank bulls are used as bull sires without change in selection scheme



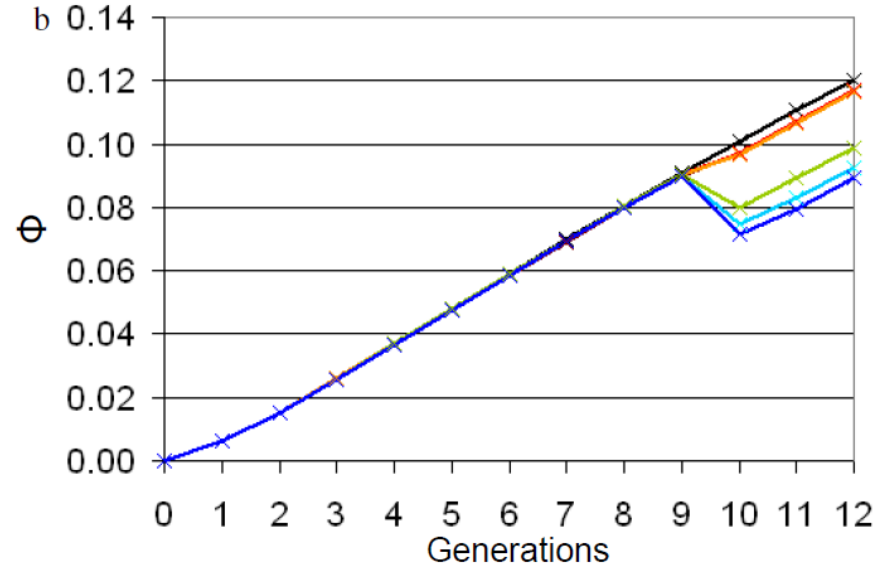
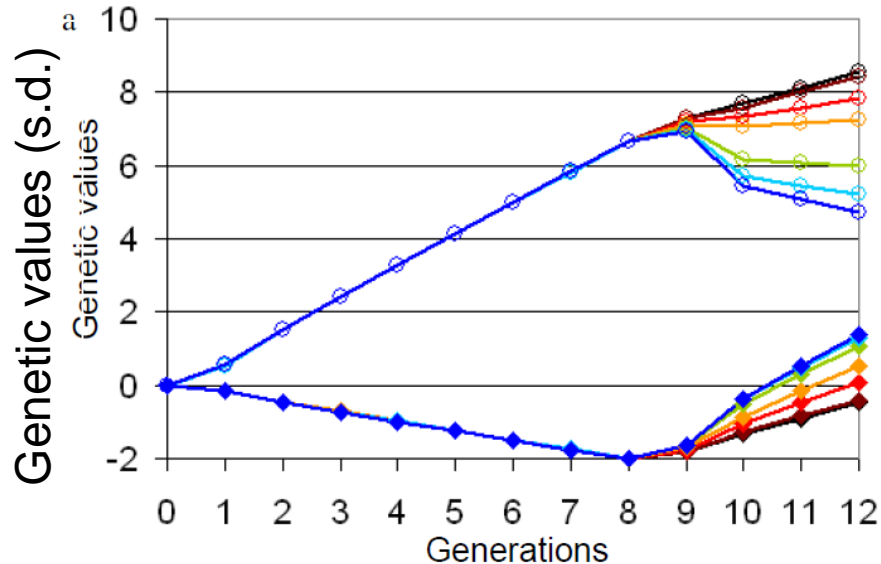
Trait A, *Trait B*, *TMI*, *Inbreeding*, *Kinship*,

Dotted lines: young bulls; solid lines: whole population

As expected, without change in selection scheme, cryobank bulls sons are removed for breeding schemes

Scenario b3

Evolution of genetic values (a) and average kinship (b), when trait B is included within TMI, in parallel to the use of cryobank bulls



Evolutions considered according to weight given to B (w_B) in Total Merit Index TMI

$w_B = 0.5$; $w_B = 0.6$; $w_B = 0.7$; $w_B = 0.8$; $w_B = 0.9$; $w_B = 1$;

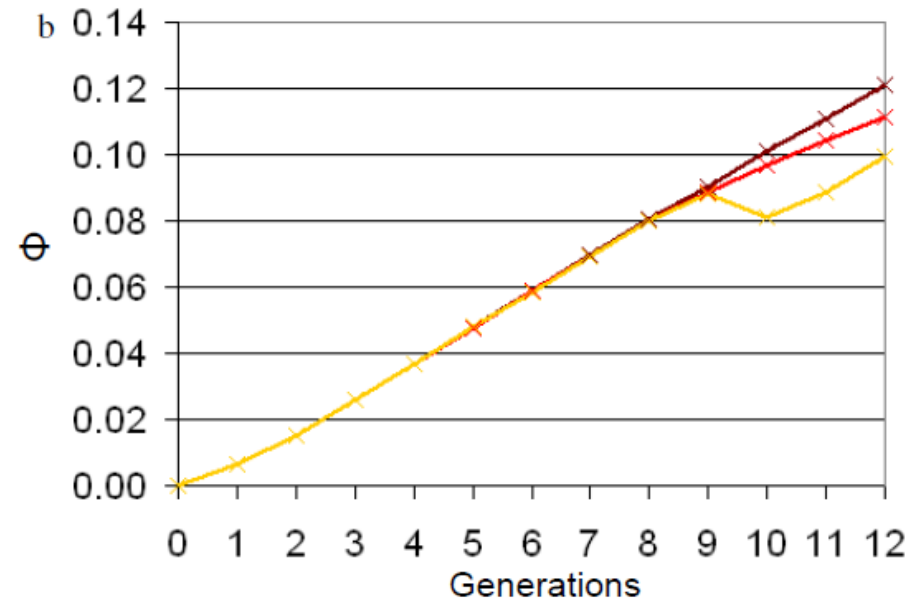
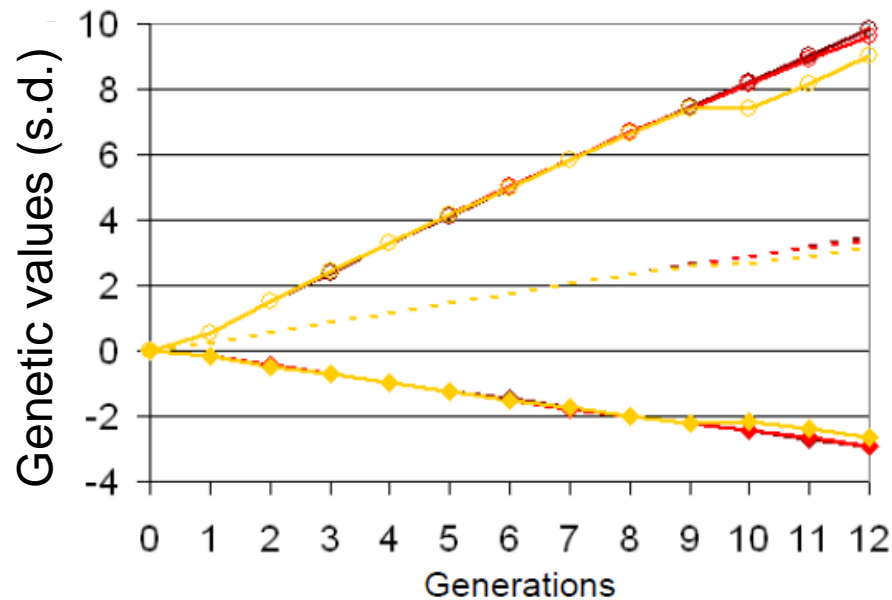
Black: No use of cryobank (scenario b2)

o: genetic value for A; \blacklozenge : genetic value for B; x: kinship ϕ

Impact of cryobank bulls only in case of large change of breeding objectives

Scenario d

Evolution of genetic values (a) and average kinship (b), according to scenario aiming at improving diversity



d1= use of cryobak bulls without change in selection scheme

d2= no use of cryobank bull, conservation of male lines

d3= no use of cryobank bull, conservation of male lines

o: genetic value for trait A; \blacklozenge : genetic value for trait B; dotted line: average genetic value between A and B; x: kinship ϕ

Evolution of cryobank bulls contribution to the population genepool

Objective	Selection stage 2 and scenario	Cryobank bulls contribution generation 10	Cryobank bulls contribution generation 10
Improve trait b	a / b1	3.6%	2.8%
	ab / b3	7.3%	6.5%
Maintaining genetic diversity	a / d1	0%	0%
	a / d3	8.8%	6.8%



Conclusions of the study

- Rapid elimination of cryobank bulls genes if their use is not combined with changes in breeding schemes
- In practice, the use of cryobank bulls seems to have little interest unless a dramatic change in selection goals.
- More interest in breeds with lower selection intensity or where management of genetic diversity becomes crucial
- Example in the Abondance breed, where a cryobank bull was successfully used as a bull sire

Cryoconservation and genome wide information use

Potential changes in sampling procedure (when existing)

- In relation to genomic selection
- Question of the rare specific alleles (prioritization)
- Need to develop practical methodologies to identify interesting bulls from the “genome wide” point of view

Cryoconservation and genome wide information use

How could be used those cryobank bulls

- More accurate genetic evaluation of cryobank bulls and new selection traits
- Need to develop methods to reintroduce interesting alleles without affecting global genetic level of the breed.
- When the aim is to reintroduce diversity : differentiation between global originality and genes of interest

Question about area of genome whose diversity have depleted

- Due to selection or drift
- Desirable or not (inbreeding purge effects?)

*Thanks for
your attention*



Gotlib