



Study of genetic progress in the context of disconnection between two originally connected populations

M. Wicki^{1,2}, A. Legarra³, J. Raoul^{1,2}

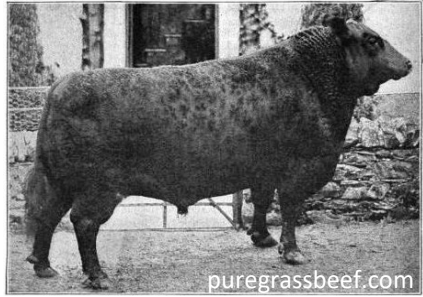
¹INRAE, INP, UMR 1388 GenPhySE, F-31326 Castanet-Tolosan, France

²Institut de l'Elevage, Castanet-Tolosan 31321, France

³Council on Dairy Cattle Breeding, Bowie, MD 20716, USA

Context

Many cases of divergence in livestock populations



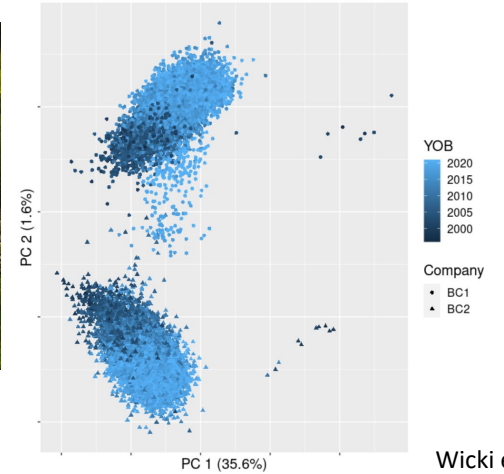
Aberdeen Angus (Scotland)



Angus (US, Australia, etc.)



French Lacaune Dairy breed



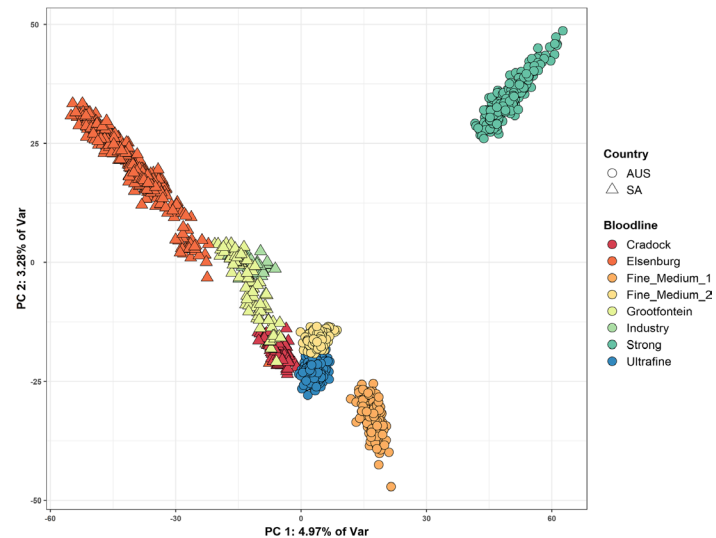
Wicki et al. 2023



Superfine wool Merino



Strong wool Merino



Nel et al. 2022

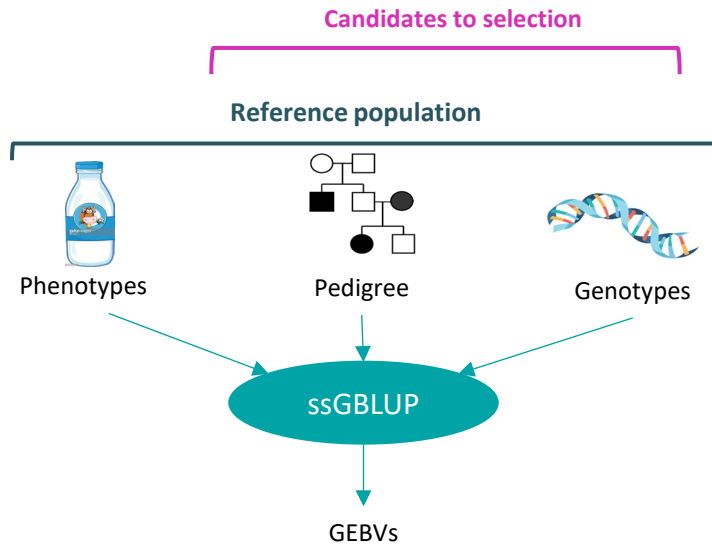
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Breeding scheme optimization: balancing breeding goal(s), genetic progress and diversity

Context



Reference population

→ **Size** (Daetwyler et al., 2008 ; Liu et al., 2011)

→ **Design**

- Relatedness within the reference population (Pszczola et al., 2012)
- Relatedness between candidates to selection and the reference population (Zhang et al., 2018 ; de Roos et al., 2009 ; Habier et al., 2010)

→ How divergence of populations can be problematic ?

- Separate evaluation → reduction in the reference population size
- Common evaluation → reduction in relatedness between candidates and reference across sub-populations

Context

Future problematic case :

- High use of artificial insemination in **French dairy sheep**
- **Organic farming** prohibits the use of synthetic hormones to induce œstrus

→ Split of conventionnal vs organic breeding program ?



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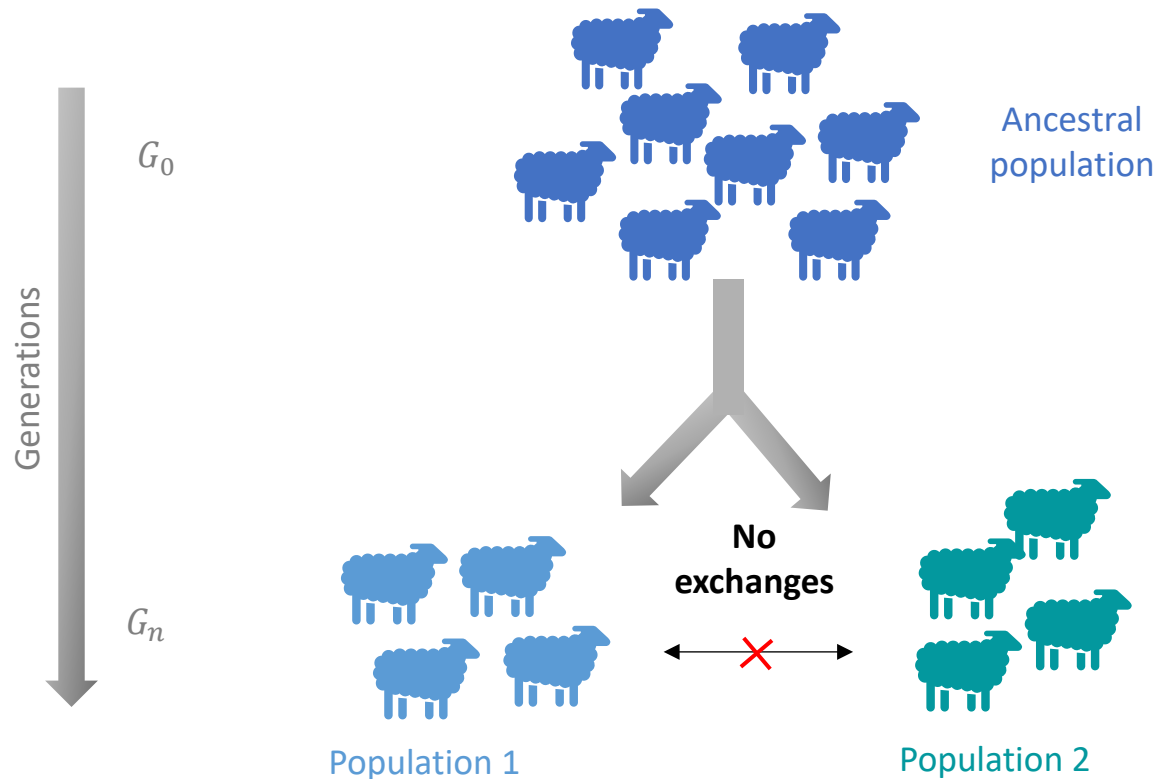
Breeding scheme optimization: balancing breeding goal(s), genetic progress and diversity

Research question

What would be the **loss, in terms of genetic gain, of such a split ? To what extent is **combined vs separate genomic evaluation** more advantageous ?**



Objective : Simulation of disconnection between two originally connected populations



→ Study of **genetic gain**

→ Combined evaluation

→ Separate evaluation

→ Hypothesis: genetic gain is affected by

the level of differentiation

→ Population size

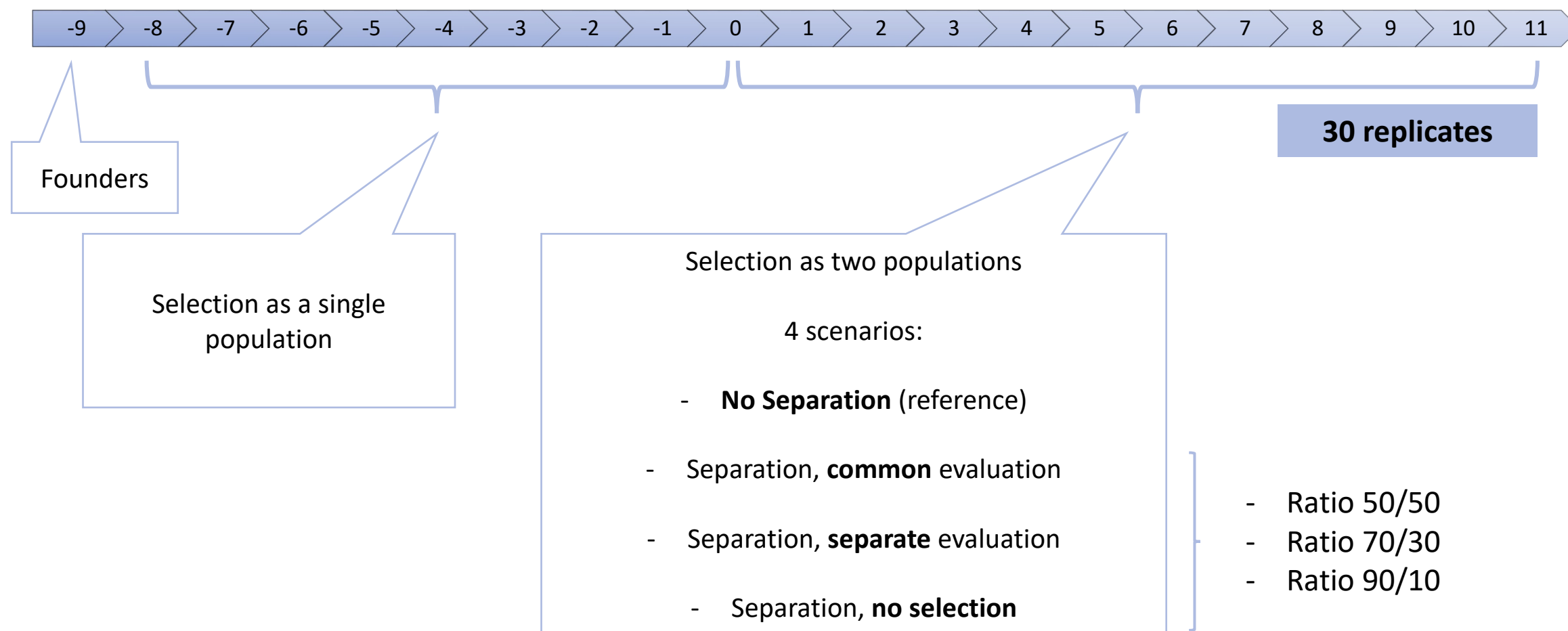
Method – mating, reproduction and selection

- Breeding program inspired by dairy sheep
- Stochastic simulation program coded in Fortran adapted from Raoul et al., 2017
- 9 discrete generations of single populations followed by 12 discrete generations of divergence
- 1 phenotype per female: $y_i = TBV_i + c_i + e_i$

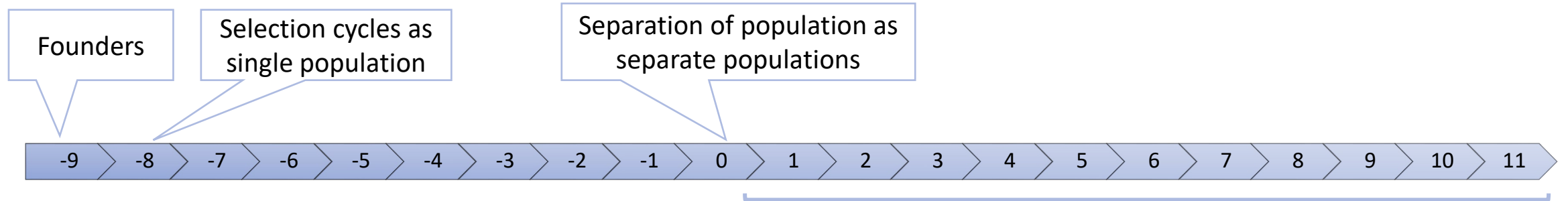
With y_i phenotype, TBV_i True Breeding Value = sum of QTL effects, c_i contemporary effect, e_i residuals effect

- QTL effects are assumed to be constant (no GxE, no GxG)
- Estimation of GEBVs (ssGBLup) with Blupf90+ software
- Only males are selected and genotyped
- 5400 females and 90 males per generation
- 2 progeny per female

Method – simulation steps



Method – simulation outputs



Fst → Indicator of genetic differentiation between 2 populations

Accuracy : correlation TBVs and GEBVs of males of 1 year old (Intra-population)

Genetic gain: regression of TBVs of females of 1 year old over time from generation 7 to 11 (Intra-population)



Results – Fst in final generation



	No selection	Common evaluation	Separate evaluation
50/50	0.032	0.054	0.059
70/30	0.038	0.063	0.068
90/10	0.085	0.124	0.134



→ The more unbalanced the ratio, the faster the divergence

→ Selection speeds up divergence

→ Common evaluation slows down divergence compared with separate evaluation

Results - Accuracy

Scenario	No Separation	Common	Common	Separate	Separate
		Evaluation	Evaluation	Evaluation	Evaluation
		pop 1	pop 2	pop 1	pop 2
50/50	0.60	98.3%	100%	95.0%	98.3%
70/30	0.60	100%	100%	100%	96.7%
90/10	0.61	98.4%	93.4%	100%	86.9%

pop 1 = largest population
pop 2 = smallest population

→ Lower accuracy for the smallest population (pop 2), particularly with a separate evaluation



Results – Genetic Gain

Scenario	No Separation	Common	Common	Separate	Separate
		Evaluation	Evaluation	Evaluation	Evaluation
		pop 1	pop 2	pop 1	pop 2
50/50	0.414	94.5%	98.5%	94.5%	98.6%
70/30	0.414	99.5%	96.4%	99.0%	92.8%
90/10	0.406	102%	85.7%	102%	83.4%



pop 1 = largest population
pop 2 = smallest population

- For balanced separation, the genetic gain in both populations is not impacted
- For unbalanced separation :
 - Genetic gain of the smallest population (pop 2) negatively impacted
 - No effect for the biggest population
 - The effect is even bigger when the population is small and the evaluation is separate

Conclusion

- Populations divergence negatively affects genetic gain
- The effect is potentially important if the population size is small and the evaluation is separate (loss of genetic gain of -16% per generation)
- Common evaluation may be a way to slow down this divergence but for small populations the effect on genetic gain is not totally offset
- Selection for different breeding goals between populations or GxE interactions may lead to greater loss in genetic gain





Nathalie Mathieu Photo/vidéo/drone St Affrique



Thank you !

Nathalie Mathieu
PHOTOGRAPHIE



1st September 2024 –Marine Wicki
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