



Benefits of genomic selection on genetic gain of French small ruminant breeding programs

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Nantes | August 28, 2013

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EAAP – 64th Annual Meeting, Nantes, France, 2013



Outline

- ❖ **Small ruminant selection designs**
- ❖ **Particular considerations for genomic selection in small ruminants**
- ❖ **Objectives**
- ❖ **Modeled schemes**
- ❖ **Results**
- ❖ **Conclusions**

Small ruminant selection designs (1/2)

Dairy breeding programs

Breeding goal: dairy traits

Selection modalities:

- Lambs on parents' EBVs
- Rams on their EBVs after progeny testing on dairy traits (Index)
- Females on their EBVs of their repeated record
(Optimal selection [across age classes])

Small ruminant selection designs (2/2)

Meat breeding programs

Breeding goal: Meat and Maternal traits

Selection modalities:

- Lambs on parents' EBVs
- Young males on EBV of their meat trait values
- Rams on their EBVs after progeny testing on meat and maternal traits (selection by independent culling methods). *[or no progeny testing]*
- Selection of females on their maternal traits (selection across age classes)

Particular considerations for genomic selection in small ruminants (1/2)

The Annual Genetic Gain (AGG):

$$AGG = \frac{\textit{selection intensity}(i) * \textit{accuracy}(r_{IH})}{\textit{generation interval}(L)} * \sigma_a$$

With genomic selection, the 3 terms (i , r_{IH} and L) are harder to change in favor of AGG in small ruminant than in dairy cattle breeding programs.

Particular considerations (2/2)

- **Reference populations** as known in dairy cattle are difficult to acquire due to very few or no reliable phenotypes
- **Effective population size** (N_e) is still large in small ruminants and would require denser maps
- The **generation interval** in small ruminants is already, relatively low
- **Genotyping costs** relative to the value of the candidates is higher
- Small ruminants breeding organizations use **limited funds**

Can genomic selection be beneficial in small ruminants ?

The Objectives

- ✓ **Model sheep & goats breeding programs as they operate to date, considering multiple traits.**
- ✓ **Include genomic information**
- ✓ **Optimize all modeled scenarios for a fair comparison**

Modeled schemes

With deterministic methods, we modeled:

- ✓ Meat breeding program (Mouton Ile de France sheep breed)
- ✓ Dairy breeding programs (Manech Tête Rousse sheep and Alpine goat breeds)

Inspired by the developments of Dekkers (2007) and Daetwyeler et al. (2008) and Goddard, (2009),

- ✓ Genomic information was included in the selection index
- ✓ We assumed reference population of non progeny tested individuals

Optimization

Decisional variables were optimized within certain constraints to maximize the total AGG

$$\text{Max } AGG_{tot}(x) = \alpha_b AGG_b(x) + \alpha_m AGG_m(x)$$

Under lower and upper limits : $x_l < x < x_u$

x was vector of the decisional variables

Some demographic parameters and decisional variables

Parameters	Value		
	Mouton Ile de France	Manech Tête Rouse	Alpine
<u>Demographic</u>			
No. of recorded females	14,000	70,000	90,000
Effective population size(Ne)	200	200	200
<i>Base reference population</i>	<i>2,000</i>	<i>2,000</i>	<i>2,000</i>
<u>Decisional variables (to be optimized)</u>			
Male selection candidates	300	-	-
Males to be progeny tested/year	20	150	40
No.of progeny/test sire	20	30	80
Total elite sires in breeding unit	~40	~110	~60
Natural service sires in breeding unit	~300	~300	~1500
Quantity of AI as % of recorded females	~35%	~47%	~40%
Relative weights between traits	0.5	-	-

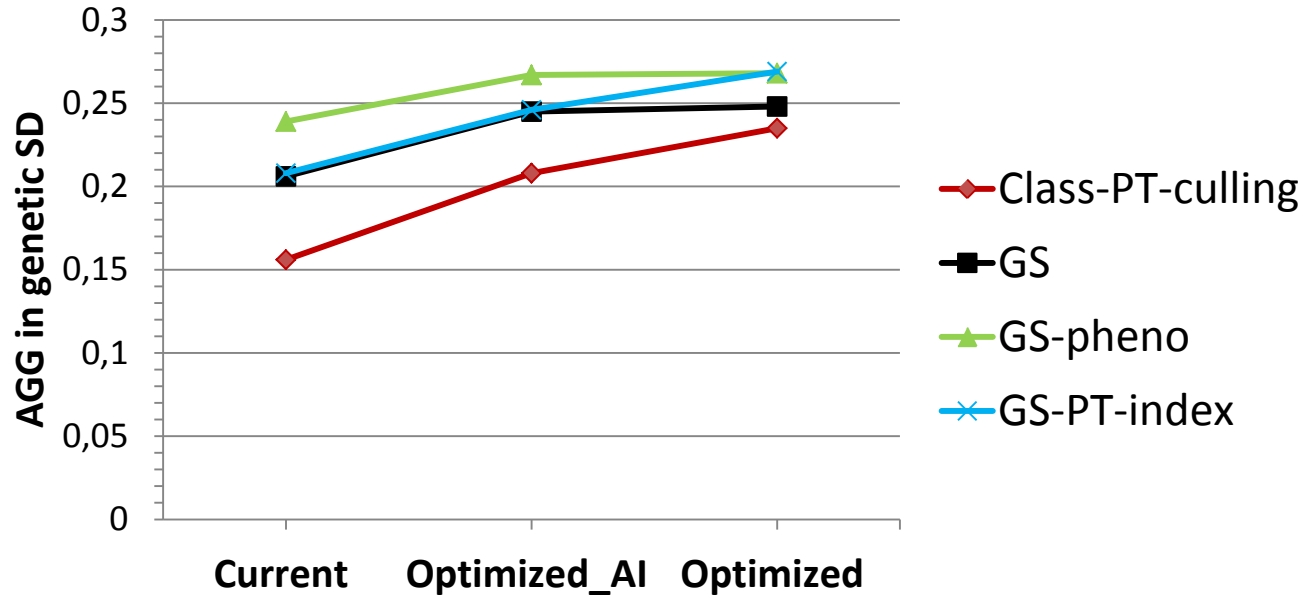
Some scenarios modeled, optimized and compared:

Scenario	Information on males candidates	
<i>Meat sheep scheme</i>		
1. Class-PT-culling	Meat phenotype on young lambs Meat and Maternal progeny test records	→ Conventional
2. GS	Genotypes on young lambs	
3. GS-pheno	Genotypes on young lambs Meat phenotype on young lambs	
4. GS -PT-index	Genotypes on young lambs Meat and Maternal progeny test records	
<i>Dairy schemes</i>		
1. Class-PT-index	Dairy progeny test records	→ Conventional
2. GS-PT-index	Genotypes on young lambs Dairy progeny test records	
3. GS	Genotypes on young lambs	

Results (1/2)

Expected total AGG

Mouton Ile de France breeding program

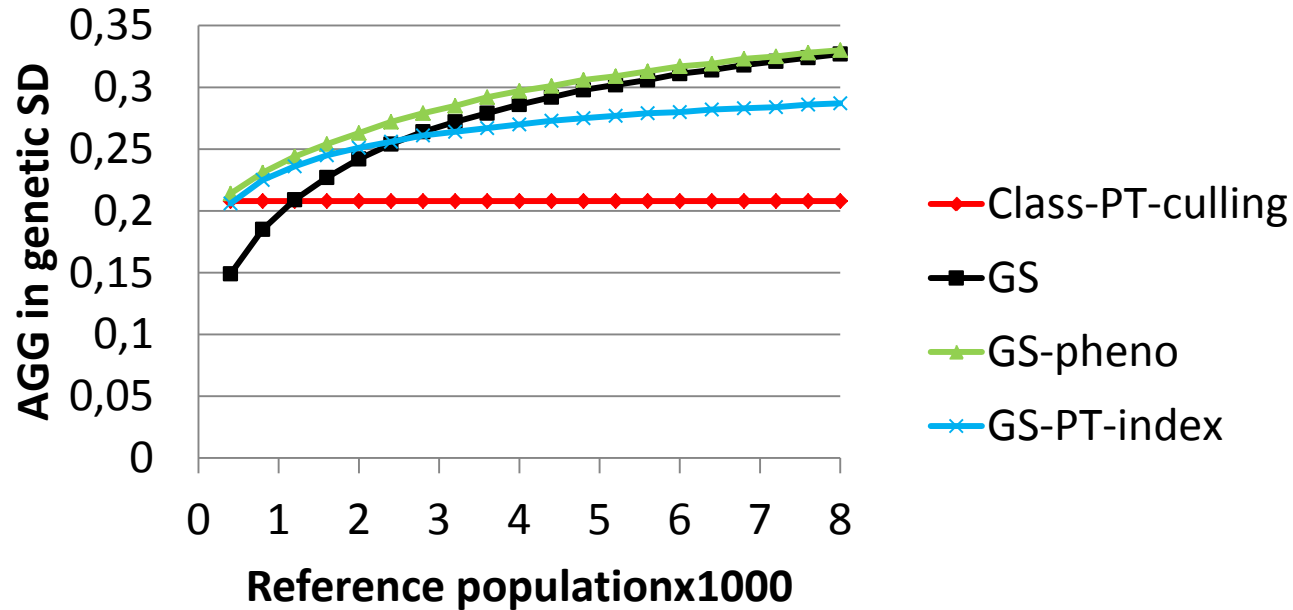


- Optimization Increased AGG, & conventional schemes are less optimal
- Genomic information increased AGG
- ~ same trend for all breeds

Results (2/2)

Effect of Reference population size on total AGG

Mouton Ile de France breeding program

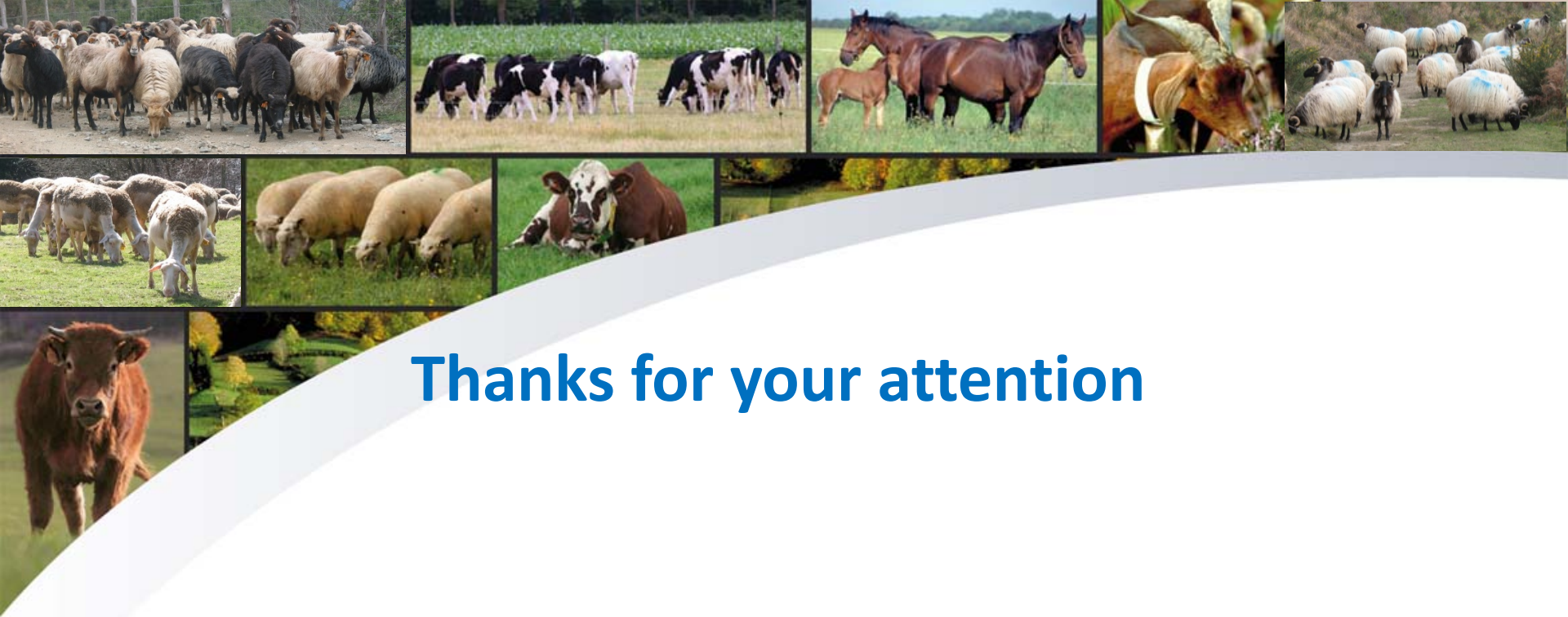


- As ref. increases, phenotype is less important (GS-pheno)
- In GS-PT-index, long generation offset the importance of r_{GBV}

Conclusions

- The optimization increased annual genetic gain in all scenarios
- With the reference population of 2000 individuals, genomic selection was superior to classical selection
- When a phenotype is recorded in early age (e.g. growth), combining it with genomic information greatly increase the AGG, especially when the reference population is small
- AGG was sensitive to genetic correlations between traits
- *The economic evaluation of these selection strategies is under study*

Shumbusho et al., (2013). Potential benefits of genomic selection on genetic gain of small ruminant breeding programs. J Anim Sci 91: 3644-3657.



Thanks for your attention

This study is funded by the French Ministry of Agriculture, via CASDAR GENOVICAP project and Institut de l'Elevage.



Avec la contribution financière
du compte d'affectation spéciale
«développement agricole et rural»