Genomic selection in French dairy sheep: main results and design to implement genomic breeding schemes

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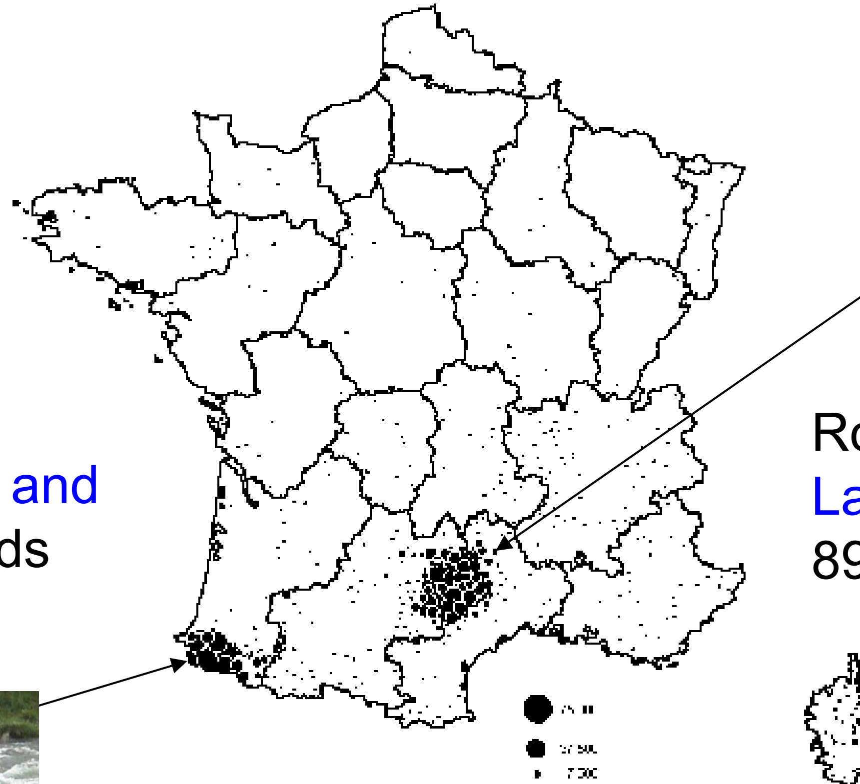
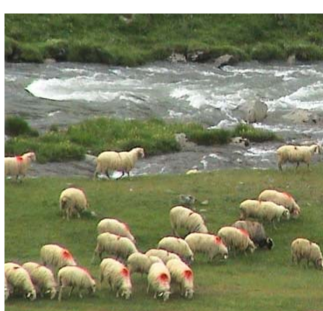
Sheep dairying in France



Western Pyrenean
Manech
(red and black faced) and
Basco-Béarnais breeds
432,000 ewes

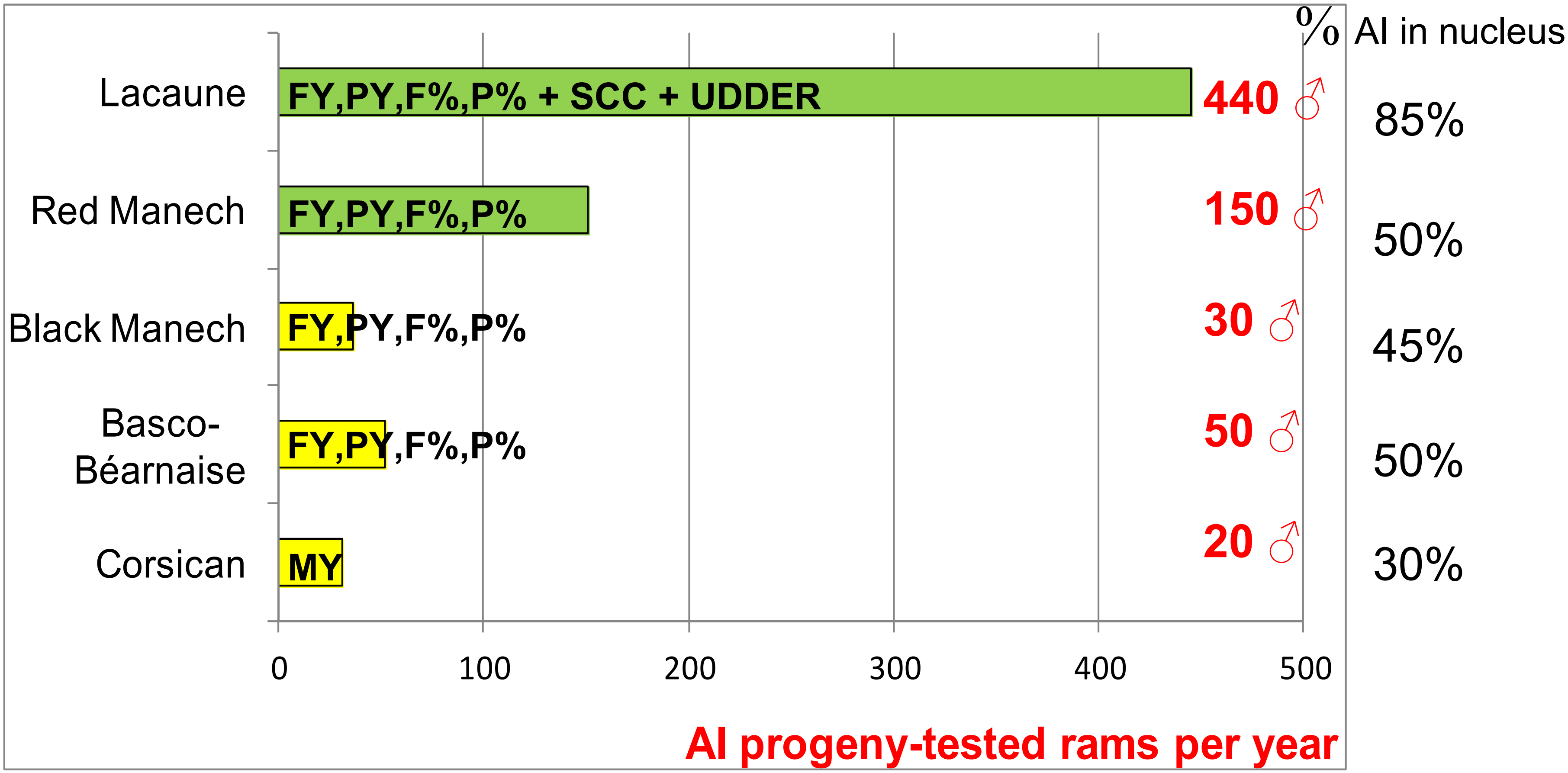


Roquefort area
Lacaune breed
890,000 ewes

Corsica island
Corsican breed
83,000 ewes

French dairy sheep breeding schemes

Breeding objectives and # AI rams progeny tested per breed and per year



Size of the reference populations (end of 2013)

AI rams phenotyped and genotyped
with the Illumina Ovine SNP50 beadchip

fundings : Roquefort'in, Genomia and Degeram projects

Breed	# AI genotyped rams	Years of birth	# SNP available for GEBV estimations
Lacaune	4,841 ♂	1999 to 2013	42,039
Basco-Béarnaise	509 ♂	2000 to 2012	38,287
Manech black faced	331 ♂	1999 to 2009	
Manech red faced	1,424 ♂	1999 to 2009	

Improvement of GEBV in French dairy sheep (from 2010 to 2013)

GBLUP

Evaluation in 2 steps

Pseudo-ss-GBLUP
(using all rams and daughter-yield-deviation)

Evaluation in 1 step

ss-GBLUP
(using all phenotypes and pedigrees as in animal model)

including unknown parent groups

Heterogeneity of variance within herd
(in progress)

GBLUP
Bayes Cπ
PLS
sPLS

Test of different GEBV methods

Duchemin et al, JDS 2012

Accuracy of GEBV using GBLUP or other methods in Lacaune breed (1,806 ♂ in training population, and 681 ♂ born in 2007-2008 in validation population)

Accuracy of EBV / GEBV				
Methods		Milk	Fat	SCS
EBV	BLUP (parent average)	0.37	0.46	0.39
GEBV	GBLUP 2 steps	0.42	0.56	0.44
	Bayes Cπ	0.44	0.57	0.45
	PLS	0.41	0.56	0.43
	sPLS	0.42	0.56	0.43

- ✓ GEBV (genomic) always better than EBV (parent average)
- ✓ Nearly no difference between GEBV methods

Duchemin et al, JDS 2012, 95

Improvement of GEBV in French dairy sheep (from 2010 to 2013)

GBLUP

Evaluation in 2 steps

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(using all rams and daughter-yield-deviation)

Evaluation in 1 step

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(using all phenotypes and pedigrees as in animal model)

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GBLUP
Bayes Cπ
PLS
sPLS
Duchemin et al, JDS 2012

Accuracy of EBV / GEBV in dairy sheep : comparison between BLUP and GBLUP estimates

✓ Lacaune breed

✓ 2,900 progeny tested rams :

- 1,593 in training population (born between 1999 & 2005)
- 707 excluded (born in 2006 & 2007)
- 592 (born in 2008 or 2009) in validation

✓ EBV (polygenic) based on BLUP : pseudo-BLUP

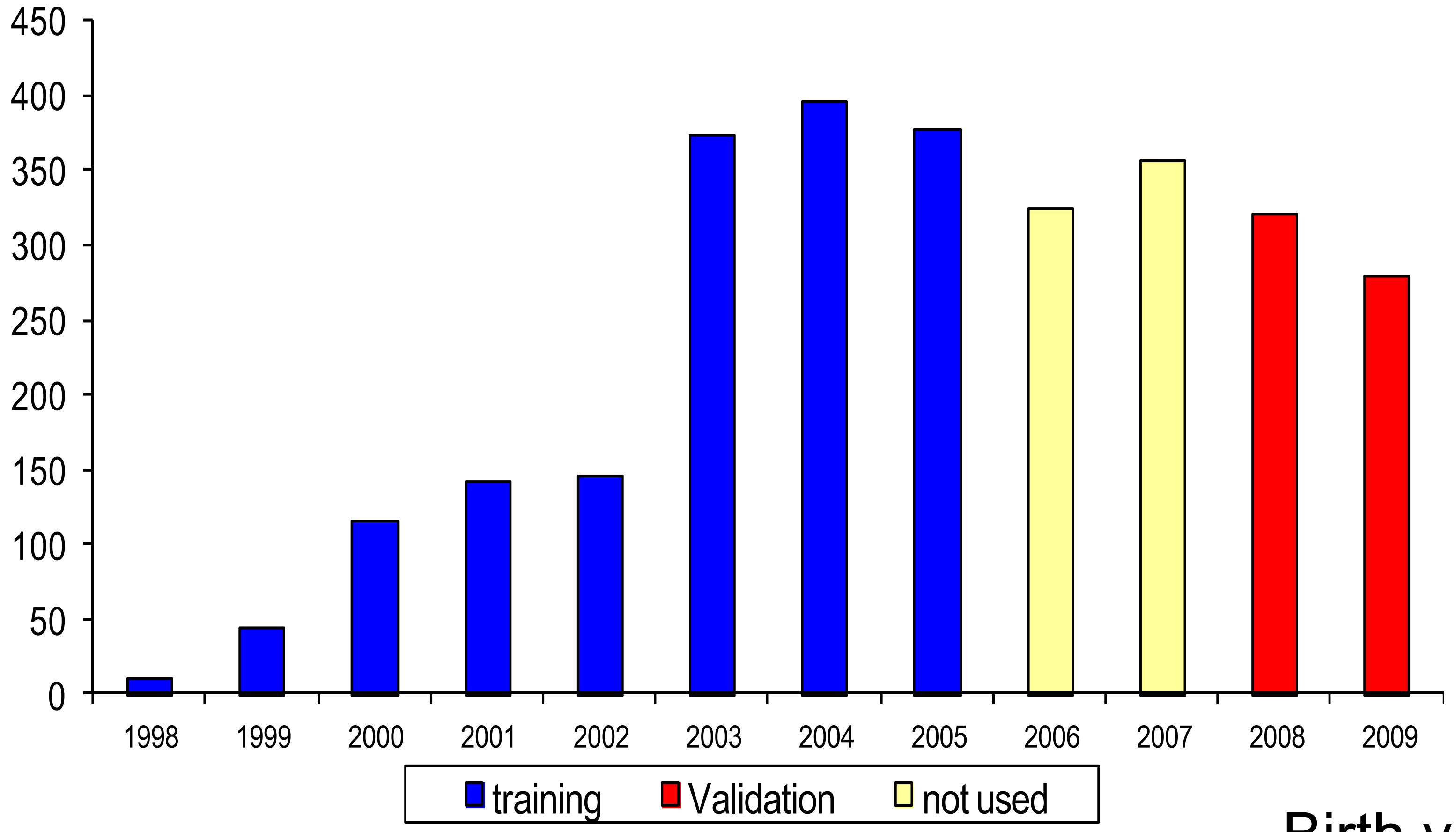
✓ GEBV (genomic) estimates

using pseudo-ss-GBLUP (2 steps) or ss-GBLUP (1 step)

Baloche et al, JDS 2014, 97

Use of reduced (2007) and full data sets (2011) to assess accuracy

(*according to Interbull recommendations*)



Birth year of the rams

Baloche et al, JDS 2014, 97

Accuracy gain in GBLUP (GEBV) over BLUP (EBV) in dairy sheep

Trait	Accuracy (reliability)			
	BLUP (PA)	GBLUP 2 steps	GBLUP 1 step	Accuracy gain in GEBV over EBV (PA)
Milk yield	0.32	0.43	0.47	0.15
Fat content	0.58	0.65	0.71	0.13
Protein content	0.54	0.62	0.70	0.16
SCS	0.49	0.59	0.59	0.10
Teat angle	0.47	0.58	0.66	0.19

✓ Genomic (GEBV) always better than pedigree (EBV)

✓ But accuracy gain lower than in dairy cattle (large pop)

Baloche et al, JDS 2014, 97

Summary of accuracy gain in (French) dairy cattle and sheep breeds

Trait	Cattle (France)		Sheep (France)	
MILK YIELD	Holstein	Montbeliarde	Lacaune	Manech red faced
Accuracy Parent average (EBV) Genomic (GEBV) **Accuracy gain**	 0.33 0.60 **0.33**	 0.30 0.47 **0.27**	 0.32 0.47 **0.15**	 0.29 0.43 **0.14**
Reference population (training)	4,000	1,200	1,900	1,000
Effective size of the Population (breed)	45	125	250	170

From conventional to genomic breeding scheme in French dairy sheep

- ✓ Lacaune breed : 1 breed and 2 breeding schemes (companies)

- ✓ Pyrenean breeds : 1 company and 3 breeding schemes / 3 breeds

  (Basco-Bearnaise, Manech black faced, Manech red faced)

Following presentation based on 1 Lacaune breeding scheme (1 company)

Objective (defined by the managers of the breeding scheme) :

is it possible to get at least a similar genetic gain without extra cost ?

From conventional to genomic breeding scheme in French dairy sheep

$$\text{precision} = \sqrt{\text{accuracy}}$$

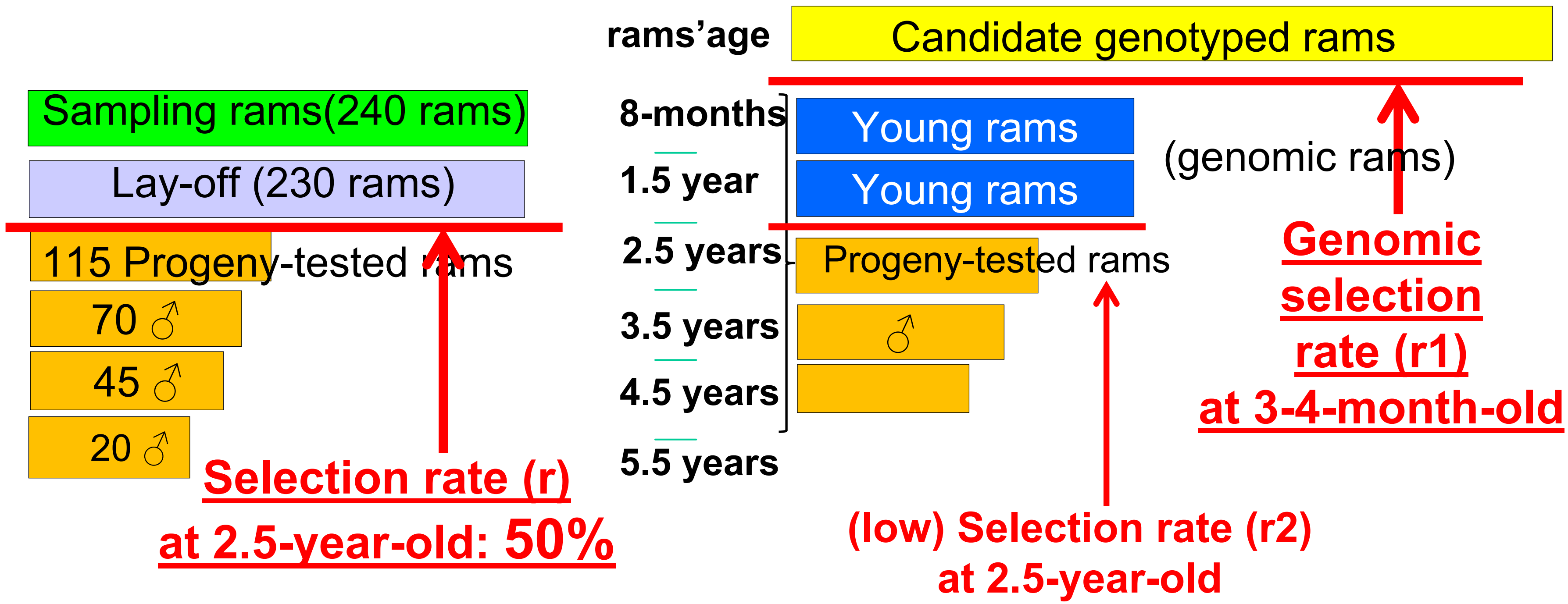
$$\Delta g \text{ per year} = \frac{\text{precision} \times \text{selection rate} \times \sigma g}{\text{generation interval}}$$

- ✓ Precision : comparable for conventional and genomic scheme
- ✓ Generation interval : quite similar for conventional and genomic scheme

- ✓ **Selection rate :** Objective to be reached comes mostly from possible selection rate in genomic **versus** conventional situation (breeding scheme), given the constraint of no-extra costs.

Classical AI scheme (present)

Genomic AI scheme (near futur)



Number of alive AI rams in the AI center

Classical AI scheme **Genomic AI scheme**

700 ♂

can be reduced thanks to suppression of lay-off

Objective : is it possible to get at least a similar genetic gain without extra costs ?

Annual genetic gain (Δg / year) in genomic versus classical scheme
depending on possible genomic selection rate (r1)

given the constraint of no extra-costs

NEW COSTS

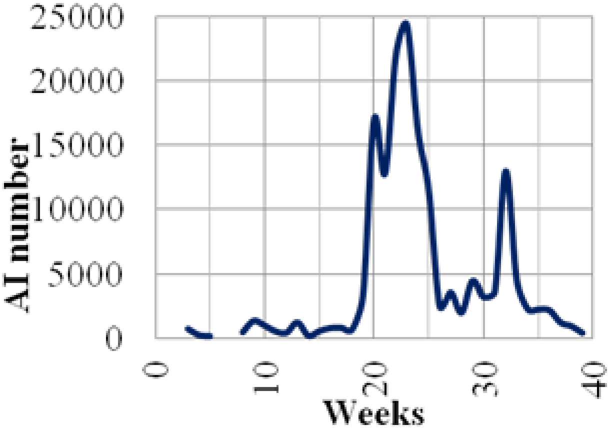
Breeding and **genotyping** of a number of young candidate rams (1 to 4 month-old) suitable for **genomic selection rate (r1)**

COST DECREASE

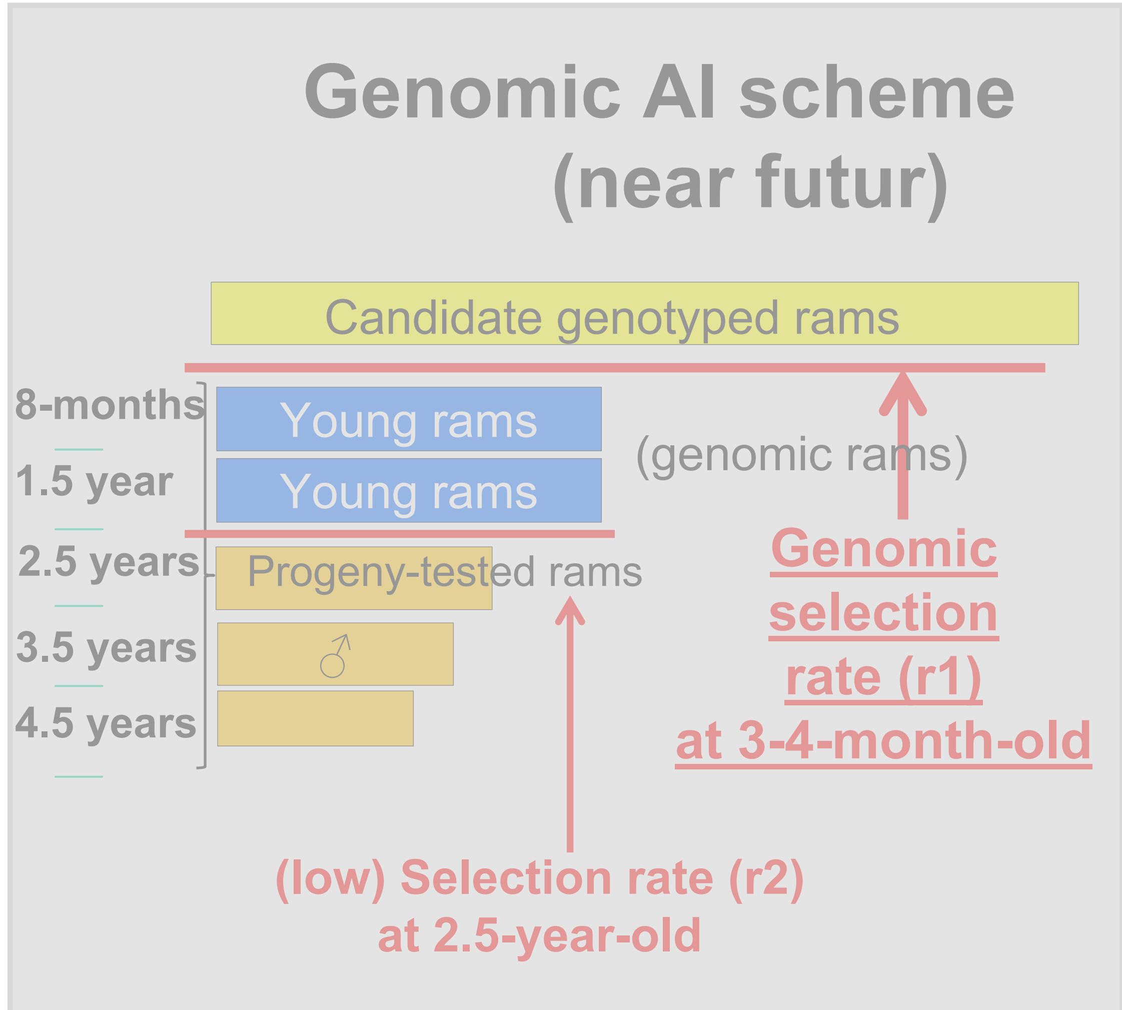
Which reduction of the number of alive AI rams in the AI center (thanks to suppression of lay-off) ?

Fine modelling of physiological constraints

in the framework of
extensive use of AI
in fresh semen
with highly seasoned
period



allows us to define a range of total alive AI rams
(given the age structure in genomic situation)



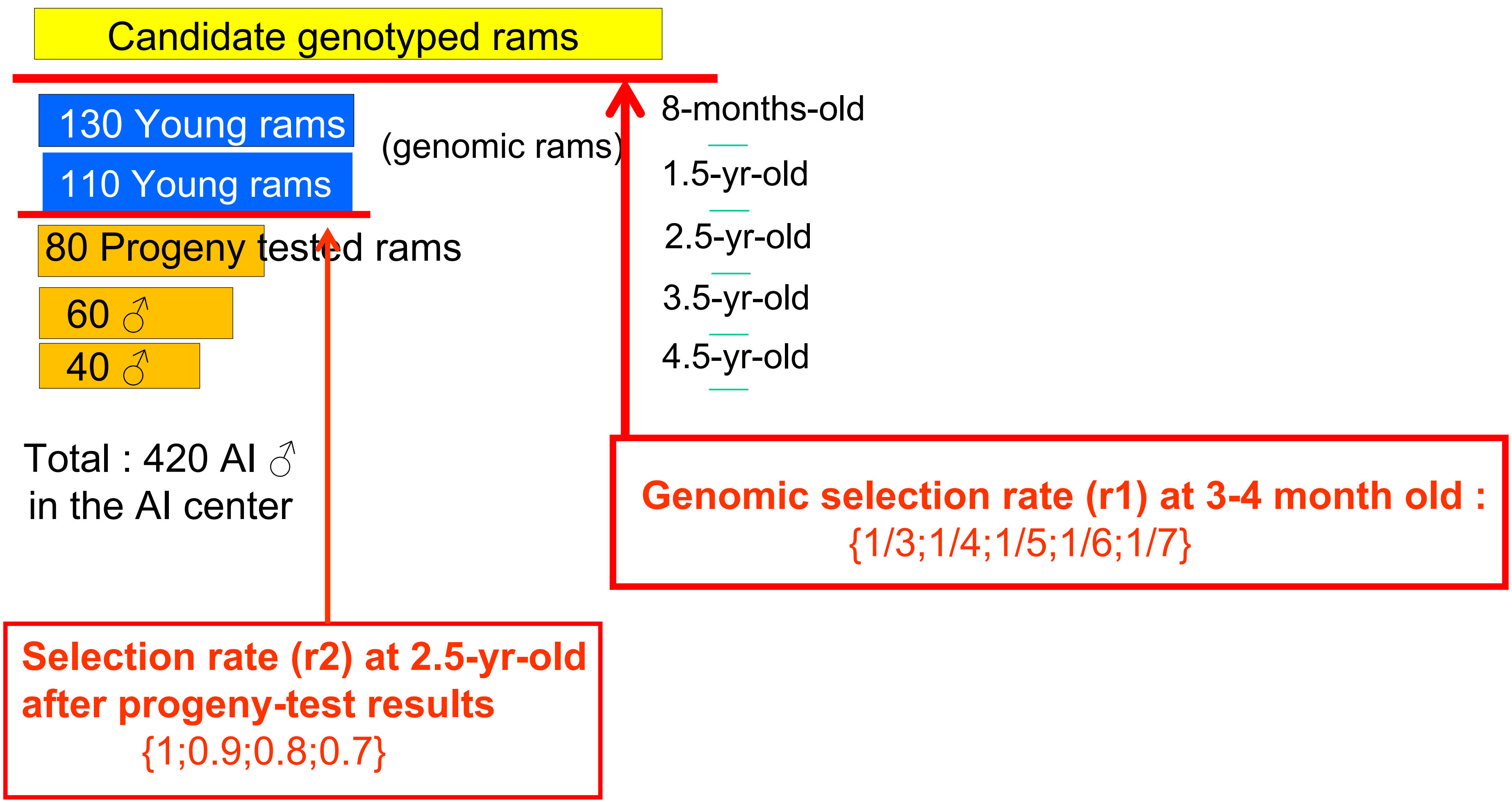
alive AI rams in the AI center

Genomic AI scheme

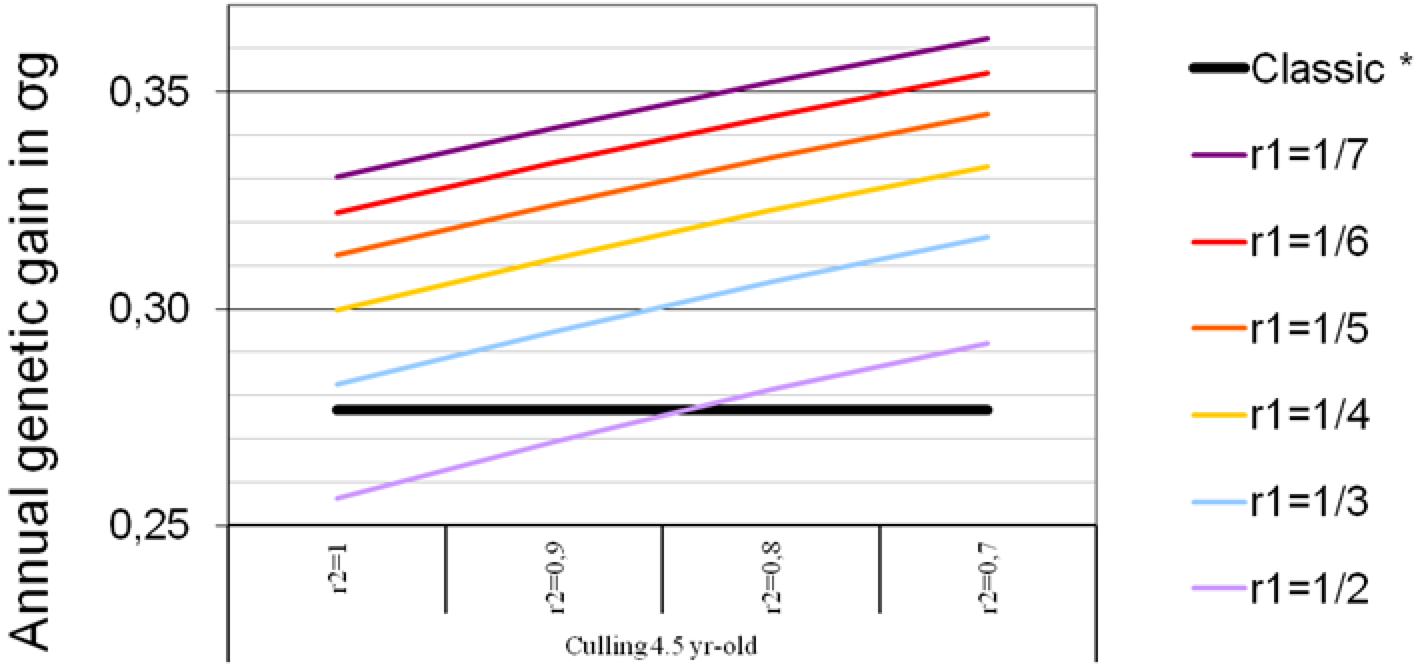
400 to 450 ♂ - 40 %

versus 700 ♂
in classical scheme

Modeling a genomic scheme in dairy sheep
(illustration with 1 Lacaune breeding company)



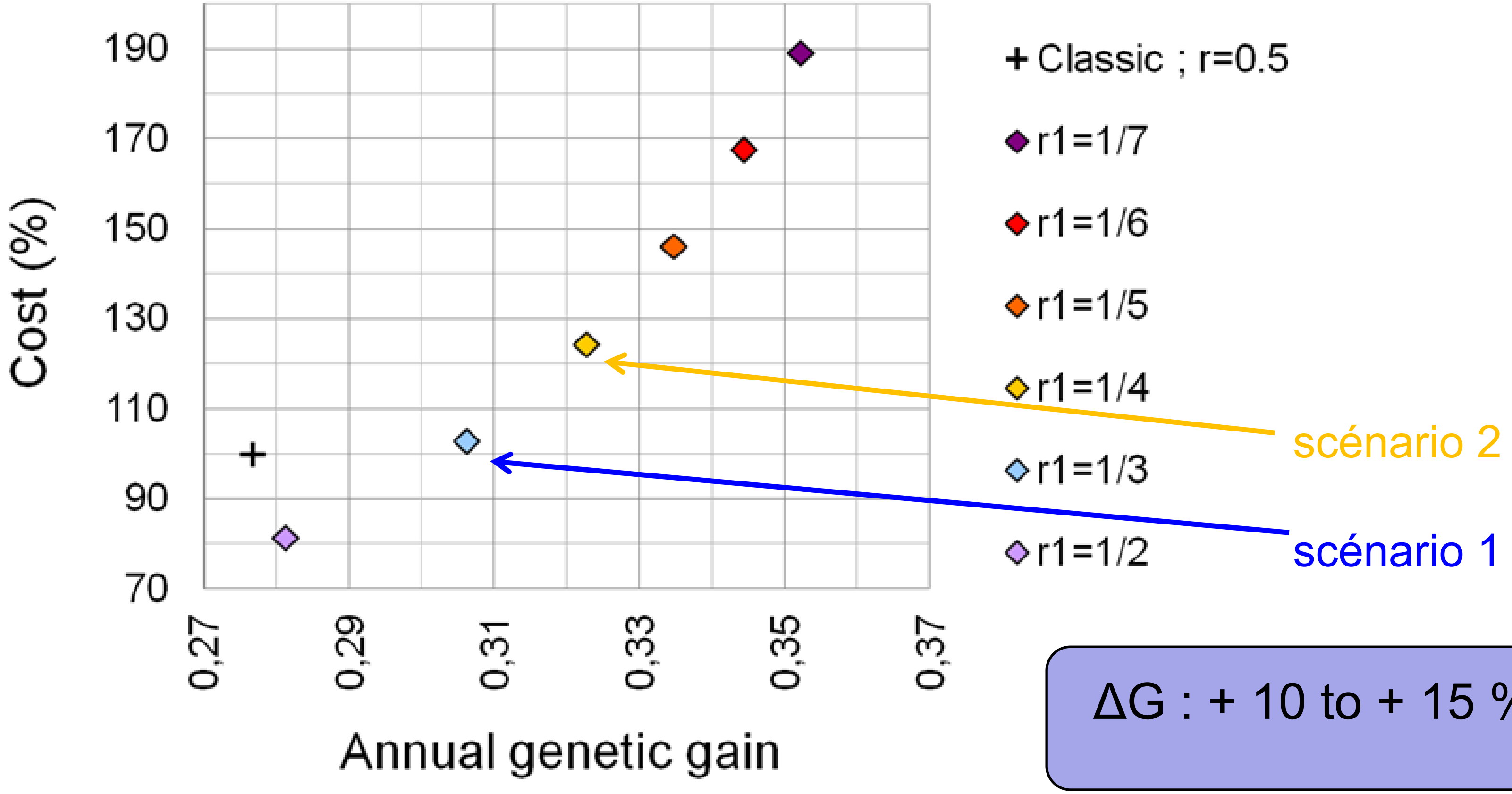
Annual genetic gain (in genetic standard deviation) according to **r1 (genomic selection rate) and r2 (selection after progeny test)** for one Lacaune breeding scheme



- ✓ impact of r1 much higher than impact of r2
- ✓ annual genetic gain (nearly) always higher with genomic selection
- ✓ extra genetic gain much lower than in dairy cattle

Buisson et al EAAP 2013, p.369

Co-evolution of annual genetic gain and costs according to the genomic selection rate (r1)



ΔG : + 10 to + 15 %

Which decision ?

1. **Scenario 1 with r1=1/3** (current genotyping cost (115 €)
2. **Scenario 2 with r1=1/4** (if genotyping cost (85 €)

To take the decision to move to genomic selection in French dairy sheep

- ✓ Efficient current (classical) French dairy sheep schemes: close to their optimum.

- ✓ Are we confident in our modelling of French dairy sheep genomic schemes and expected annual genetic gain ?

- ✓We performed a genomic experiment to check / validate it.

Experimental design : AI rams born in 2011 from 46 sires

30 ram lamb per sire : 46 families et 928 genotyped candidates

Genomic rams (GR) : chosen on their GBLUP ***at 3 month-old***

Genomic rams (GR)

18 ram lambs per sire

± 1/3

6 ram lambs per sire

1/2

3 ram lambs to be progeny-tested per sire

genomic selection rate

standard & developpement

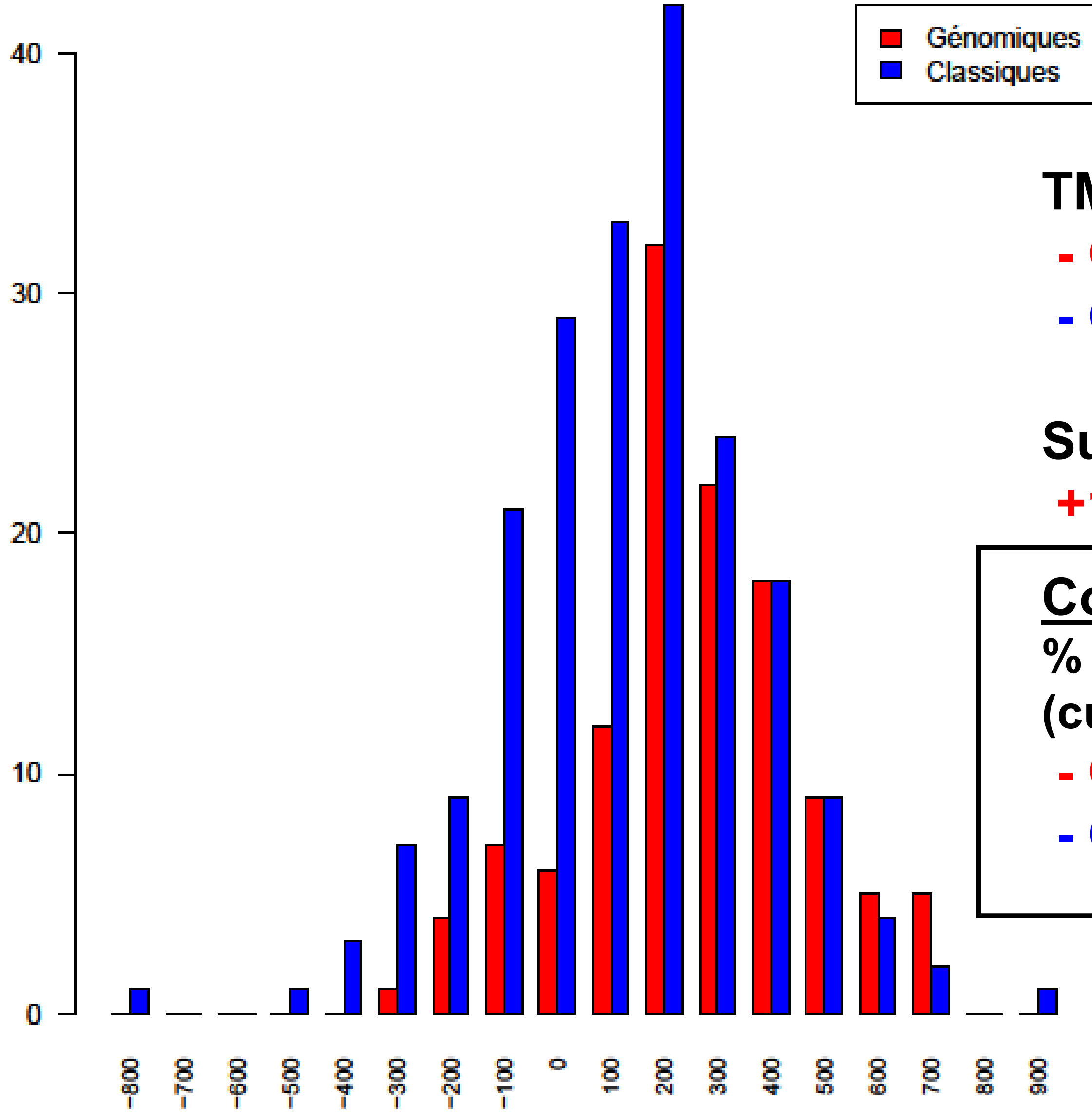
Classical rams (CR)

12 ram lambs per sire

1/2

6 ram lambs to be progeny-tested per sire

Distribution of total merit index (TMI) ssGBLUP for CR and GR - **at 2.5-year-old** -



TMI mean :

- GR : + 201 points

- CR : + 79 points

Superiority of GR :

+122 points (0.50 TMI std)

Consequences :

% rams above TMI 100 points (culling rate at 2.5-yr-old)

- GR : 24 %

- CR : 48 %

Conclusion

Significant reduction (by 30 % to 40 %) of the number of alive AI rams in the case of genomic selection (GS) versus classical selection .

More flexible GS breeding scheme allowing, at the same cost, an annual genetic gain increased by 10%-15 %, with a genomic selection rate (r1) at 3-month-old between 1/3 and ¼.

The genomic selection experiment performed for AI rams born in 2011 confirms the relevance of selection rate (r1) and (r2) equal respectively to 0.3 and 0.80 in this GS situation experiment.

Genomic selection will be implemented in 2015 in the French Lacaune breed and in a near futur in Pyrenean breeds (Basco-Béarnaise and Manech).

Collaborations and fundings

INRA

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