Genomic selection in French Lacaune and Manech dairy sheep breeds :
comparison of BLUP and GBLUP accuracies

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ALIMENTATION
AGRICULTURE
ENVIRONNEMENT

Aims of *in progress* research projets regarding **genomic selection in dairy sheep in France**

✓ Three breeding companies (2 in Lacaune and 1 in Manech breeds) managing the breeding schemes in these dairy sheep breeds

✓ Two research projects between INRA, Institut de l'Elevage and these 3 companies, **to build reference populations in Lacaune and Manech breeds,** in the aim

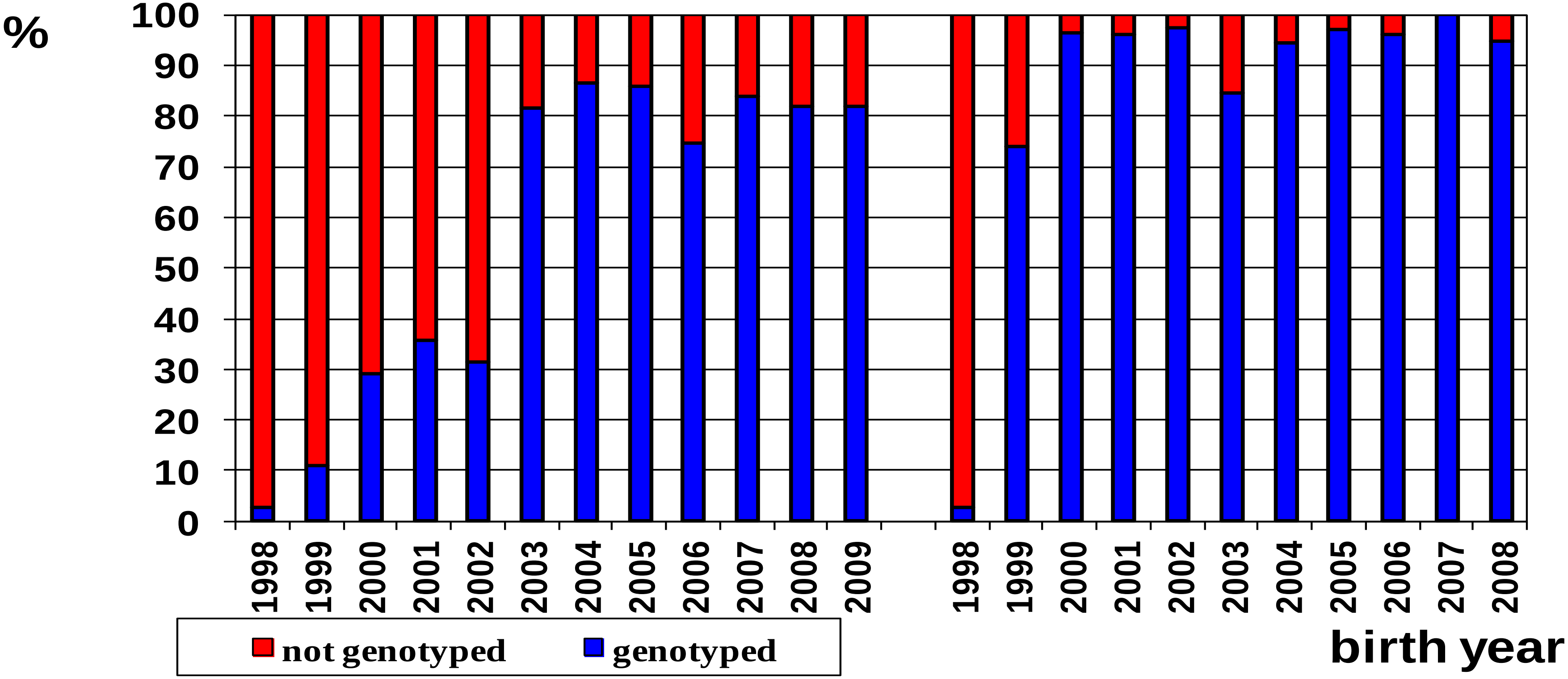
1. to produce technical and economical parameters of possible genomic selection schemes relevant for their dairy sheep breeds

2. to permit these companies **to decide or not to move to genomic selection** in the next future.

Reference populations (AI rams) **available in 2011 for genomic evaluation tests** in French Lacaune and Manech red faced breeds

Lacaune
Genotyped : 2.885 AI rams

Manech red faced
1.295 AI rams



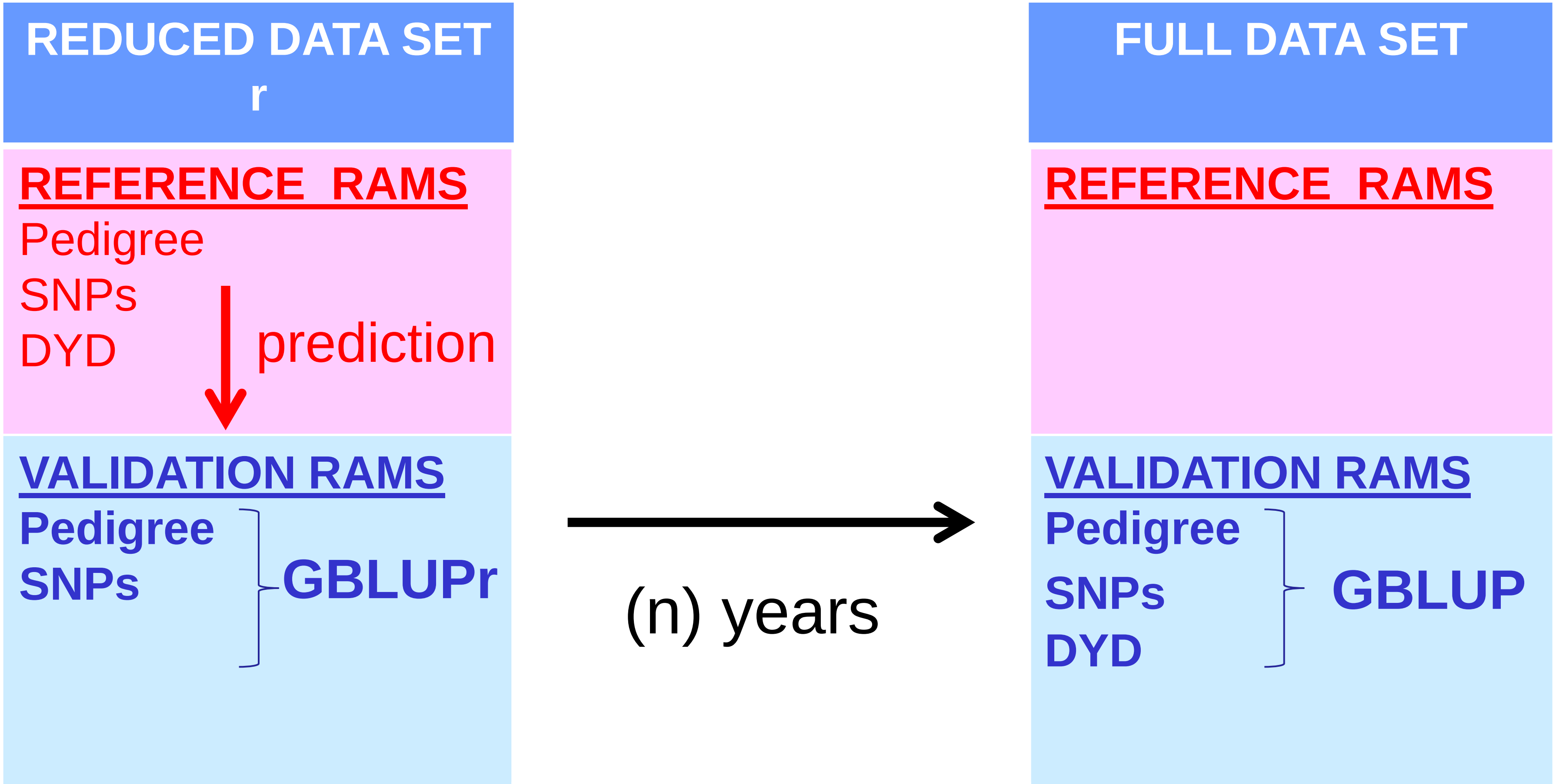
SNP genotypes : quality control

- ✓ Illumina Ovine SNP50 Beadchip *(available since 2009)*

- ✓ Genotyping performed by LABOGENA Lab

	# SNP
Total number	54,241
Causes of elimination - non autosomal SNP - MAF, HWE, Call-rate - parent-progeny conflicts	12,720
Available SNP on the 26 autosomes	41,511

Material and method : genomic evaluation test (Interbull GEBV test)



REDUCED DATA SET r

<u>REFERENCE RAMS</u>

Pedigree
SNPs
DYD

prediction

<u>VALIDATION RAMS</u>

Pedigree
SNPs

GBLUPr

(n) years

FULL DATA SET

<u>REFERENCE RAMS</u>

<u>VALIDATION RAMS</u>

Pedigree
SNPs
DYD

GBLUP

Material and method : criteria of comparison of a genomic evaluation test

EBV of VALIDATION RAMS	**DATA** (n) years between		**CRITERIA of comparison**
	Reduced data set	Full data set	
1. Conventional genetic evaluation	BLUPr EDCr	BLUP EDC DYD	correlation (expected (a)) r1 (DYD, BLUPr) r2 (DYD, GBLUPr) regression (expected (b)) DYD=a1 + b1*BLUPr + e1 [1] DYD=a2 + b2*GBLUPr + e2 [2]
2. Genomic evaluation	GLUPr	GBLUP	

expected (a) : r2 > r1

expected (b) : R^2 model [2] > R^2 model [1] and b1=b2=1 if representative sample of the validation rams in the corresponding birth years

Different validation tests for genomic evaluations carried out since 2011

Test	**Breed**	**Year for each data set**		**Reference rams**		**Validation rams (birth year)**
		Reduced (learning) set	Full (validation) set	Rams with DYD	Genotyped rams with DYD	
Test 1	Lacaune	2010	2010	3,645 (<= 2006)	1,886	681 (2007-2008)
Test 2	Lacaune	2007	2011	4,073 (<=2005)	1,593	681 (2007-2008)
Test 3	Manech red faced	2008	2011	1,207 (<=2006)	1,002	293 (2007-2008)

Results of validation tests 1 & 2 in Lacaune

Criteria	Test and breed : n 1 Lacaune				
	Milk	Fat content	Protein content	SCS	Udder cleft
correlation					
DYD - BLUPr	0.39	0.49	0.53	0.41	0.46
DYD - GBLUPr	0.45	0.57	0.59	0.45	0.53
Relative gain	**15 %**	**16 %**	**11 %**	**10 %**	**15 %**

Criteria	Test and breed : n 2 Lacaune				
	Milk	Fat content	Protein content	SCS	Udder cleft
correlation					
DYD - BLUPr	0.35	0.44	0.52	0.39	
DYD - GBLUPr	0.42	0.50	0.57	0.45	
Relative gain	**20 %**	**14 %**	**10 %**	**15 %**	

Comparison between different genomic methods in Lacaune breed (test n 1)

(from Duchemin et al., JDS, 2012, 95:2723-2733)

Criteria	Test and breed : n 1 Lacaune		
	Milk	Fat content	SCS
correlation			
DYD - GBLUPr	0.42	0.56	0.44
DYD - Bayes Cπ	0.44	0.57	0.45
DYD - PLS	0.41	0.56	0.43
DYD - sPLS	0.42	0.56	0.43

Influence of the genetic structure of the reference rams population in Lacaune breed

Criteria	Test and breed : n 1 Lacaune		
	Milk	Loss of relative gain	Size of the reference population
correlation			
DYD – GBLUP - total	0.45	0 %	100 %
DYD – GBLUP & (1)	0.42	- 9 %	52 %
DYD – GBLUP & (2)	0.40	-11 %	40 %
DYD – GBLUP & (3)	0.33	- 27 %	85 %

total : all the 3.645 rams of the reference rams population

(1) removing ungenotyped reference rams

(2) removing reference rams born before 2003

(3) removing closely related reference rams of validation rams (fathers…)

Results of validation tests n 2 and 3

Criteria	Test and breed : n 2 Lacaune				
	Milk	Fat content	Protein content	SCS	
correlation					
DYD - BLUPr	0.35	0.44	0.52	0.39	
DYD - GBLUPr	0.42	0.50	0.57	0.45	
Relative gain	**20 %**	**14 %**	**10 %**	**15 %**	

Criteria	Test and breed : n 3 Manech red faced				
	Milk	Fat content	Protein content		
correlation					
DYD - BLUPr	0.27	0.32	0.43		
DYD - GBLUPr	0.38	0.37	0.48		
Relative gain	**41 %**	**16 %**	**12 %**		

Comparison of main factors of variation of genomic selection efficiency between (French) dairy cattle and dairy sheep

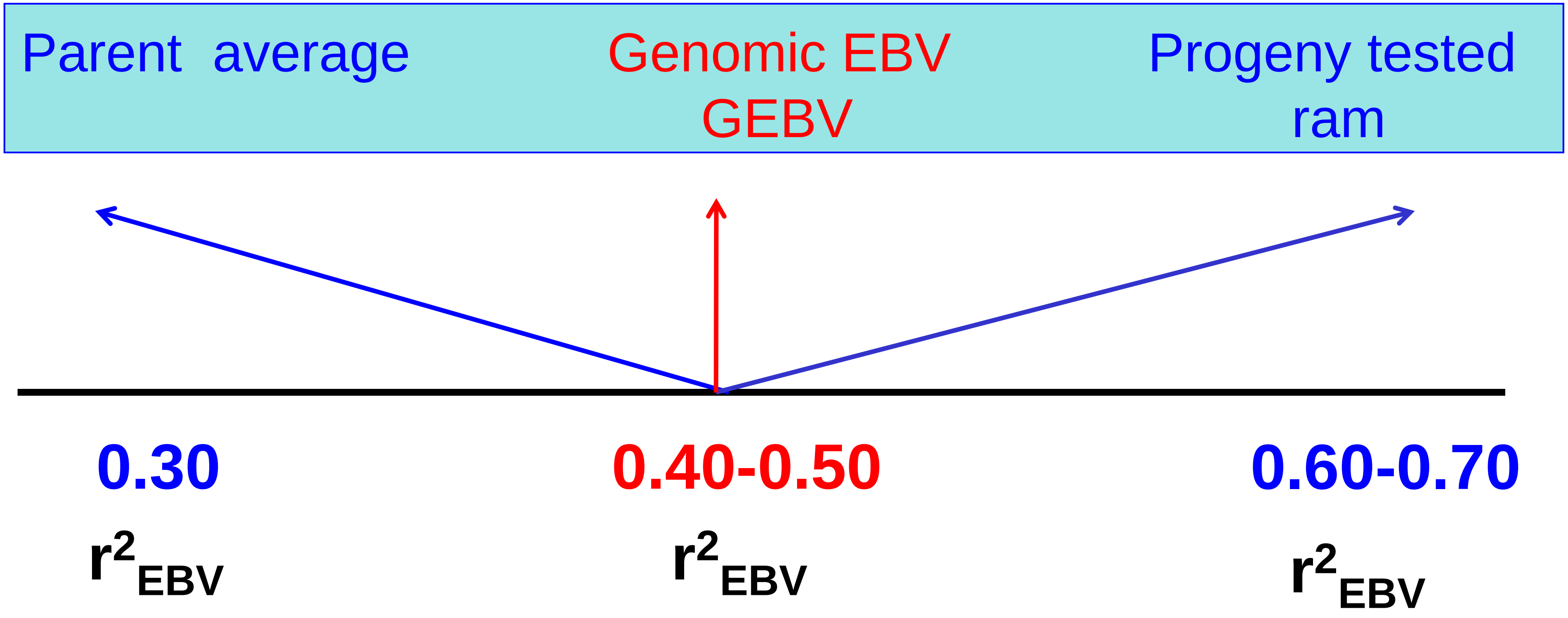
Species and breed	Size of reference population	Number of daughters per validation sire (progeny test)	Number of daughters per reference sire	Effective size of the population (breed)
Holstein (France)	4,000	80	thousands	45
Montbéliarde	1,200	80	thousands	125
Lacaune (lait)	1,900	40	110	230
Manech red faced	1,000	30	80	170

Summary of genomic selection results in (French) dairy cattle and sheep breeds

Criteria	Cattle		Sheep	
FOR MILK YIELD	Holstein	Montbeliarde	Lacaune	Manech red faced
Correlation				
DYD - BLUPr	0.33	0.30	0.35	0.27
DYD - GBLUPr	0.60	0.47	0.42	0.38
Relative gain	**82 %**	**57 %**	**20 %**	**41 %**
Reference population	4,000	1,200	1,900	1,000
Effective size of the Population (breed)	45	125	230	170

To summarise

Present estimates in French dairy sheep breeds : reliability (r^2_{EBV}) of **conventional** or **genomic** EBV



Parent average

Genomic EBV
GEBV

Progeny tested
ram

0.30
r^2_{EBV}

0.40-0.50
r^2_{EBV}

0.60-0.70
r^2_{EBV}

according to the trait

From conventional to genomic breeding scheme in French dairy sheep ?

$r^2_{GEBV} < r^2_{EBV}$ (proven ram)

$$\Delta g \text{ per year} = \frac{\text{EBV reliability} \times \text{selection pressure} \times \sigma g}{\text{generation interval}}$$

limited reduction in dairy sheep

Balance ?

Key point : genomic selection pressure

breeding and genotyping candidates : ↗ costs

reduction of livestock AI rams (*fresh semen*): ↘ costs

Conclusions (1/2)

- reference populations available in 2012 in French Lacaune and Manech dairy sheep breeds

- genetic structures of the reference populations more important than genomic methods used to compute GEBV : *in favor of polygenic determinism for analysed traits*
- r^2 parent average $_{\mathrm{EBV}} < \mathbf{r^2}_{\mathbf{GEBV}} < r^2$ proven ram $_{\mathrm{EBV}}$

  (large effective size of the populations (breeds) compared to dairy cattle; or low linkage desequilibrium in dairy sheep breeds compared to dairy cattle breeds)

Conclusions (2/2)

- in progress research to improve GEBV
  - bias (overestimation) of young rams
  - two steps / one step approaches
  - calibration between conventional / genomic data
  - multi-breeds Manech/Latcha, Manech/Lacaune

- ….and finally to permit the 3 French breeding companies involved in Lacaune and Manech breeding schemes **to decide or not to move to genomic selection** in the next future.

Collaborations and fundings

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Dairy sheep breeding companies

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