

Work in progress on genomic evaluation using GBLUP in French Lacaune dairy sheep breed

**G. Baloche, H. Larroque, J.M. Astruc, J.M. Babilliot,
M.Y. Boscher, P. Boulenc, C. Chantry-Darmon,
C. de Boissieu, G. Frégeat, B. Giral-Viala, P. Guibert,
G. Lagriffoul, C. Moreno, P. Panis, C. Robert-Granié, G. Salle,
A. Legarra, F. Barillet (*)**

**(*) corresponding author: francis.barillet@toulouse.inra.fr
INRA, UR 631, Station d'amélioration génétique des animaux
31326 Castanet-Tolosan, France**

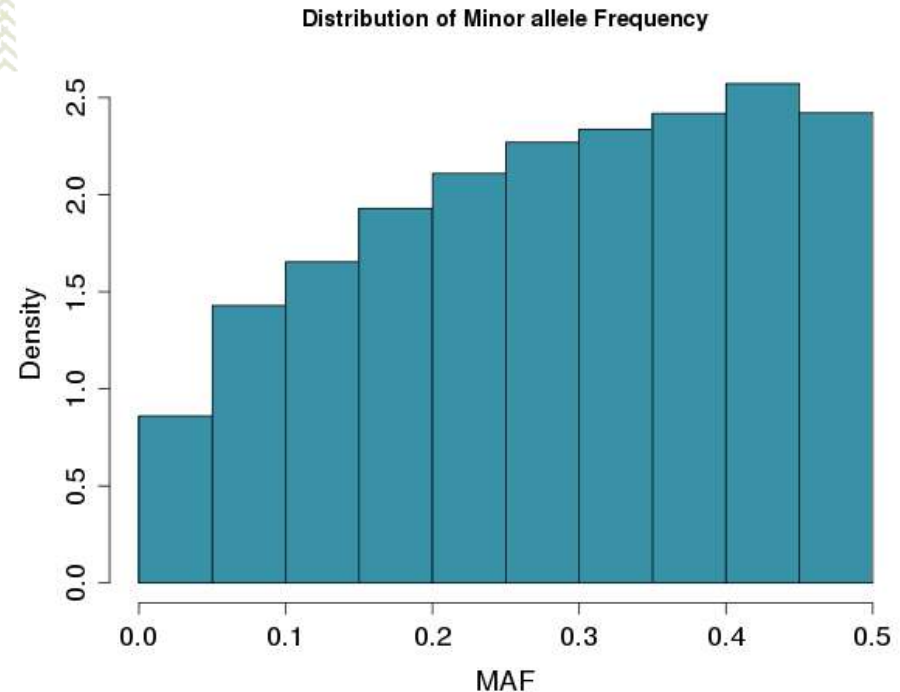
Reasons to think that genomic selection is possible in the Lacaune dairy sheep

- A Progeny-test based scheme (nucleus flocks):
 - 174,000 ewes recorded in 2010 in nucleus flocks
 - 420 AI rams progeny-tested each year (samples of 40 daughters)
- Recording and selection on milk yield and contents, SCS and udder type traits plus scrapie resistance on Prp gene
- Storage of DNA/blood of the Lacaune AI rams organized since the middle of the 90's
- Ovine SNP50 BeadChip available since 2009

=> Possibility of building a large reference population

Genotyping : quality control and frequency of SNPs

	Threshold	Exclusion
Call freq	0.98	4.4%
Call rate	0.97	8.4%
HWE	10^{-5}	4.7%
MAF	0.01	10%
Finally	-	19%



- Genotyping of rams born between 1998 and 2008
- 2,567 genotypes validated
- Numerous SNP retained : 43,929 out of 54,241

Structure of the Lacaune reference population (4,326 at the end of 2010)

1998

Learning Population

428 rams

1,526 rams

1,458 rams

233 rams

	# daughters
Mean	89
Range	25-1,683
CV	59%

2006

Validation Population

681 rams

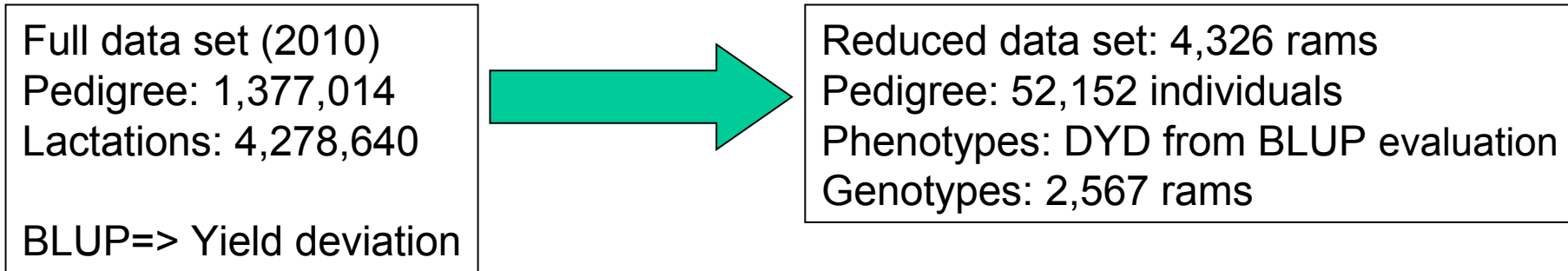
	# daughters
Mean	37
Range	10-79
CV	26%

2008

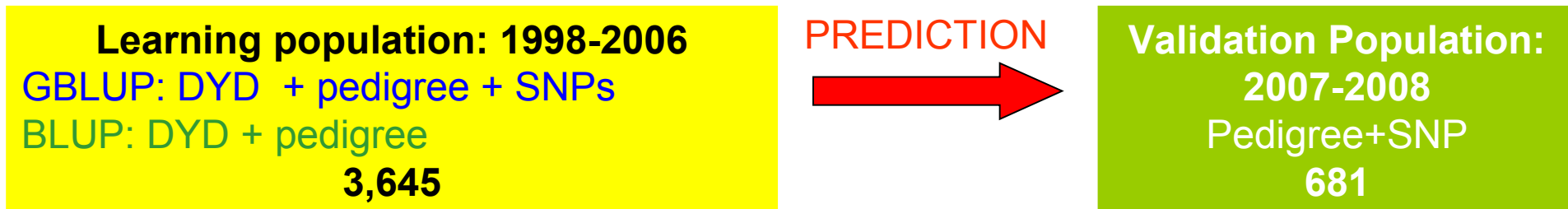
- Learning set: Rams with reliable estimate of their genetic merit
- Validation set: Considered as candidate for selection in our approach (although already progeny-tested)

Material and Methods

- Data: aggregation of information on rams of interest

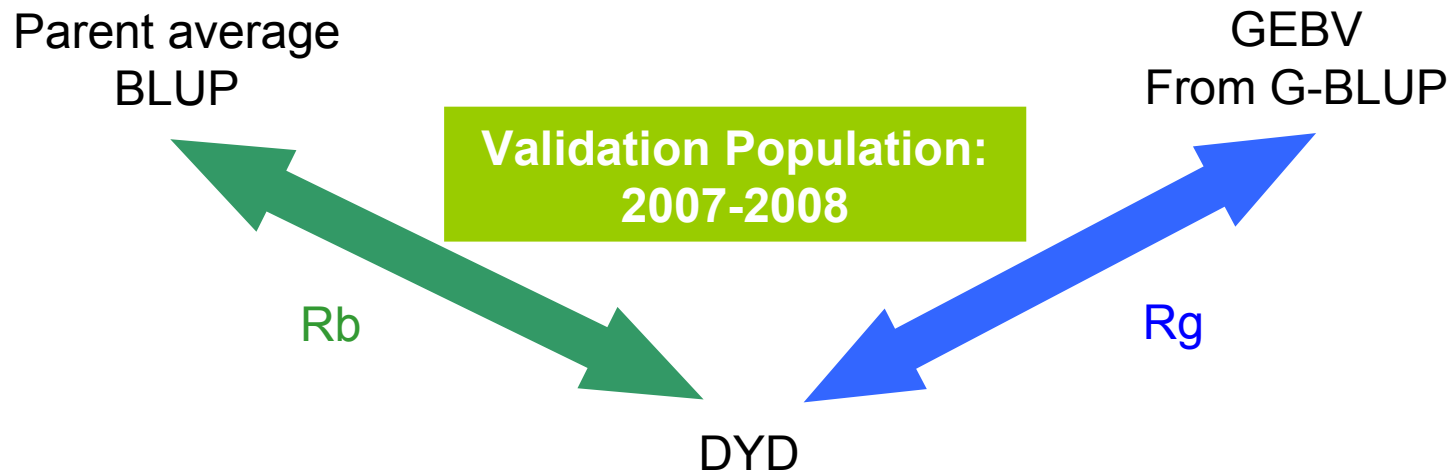


- Method: cross-validation



Material and Methods

- Quantifying accuracy of **genomic prediction** vs **parent average**
- DYD =>reference to assess accuracy of genomic prediction or parent average
- Correlation between **DYD and GEBV (R_g)** and **between DYD and Parent average**



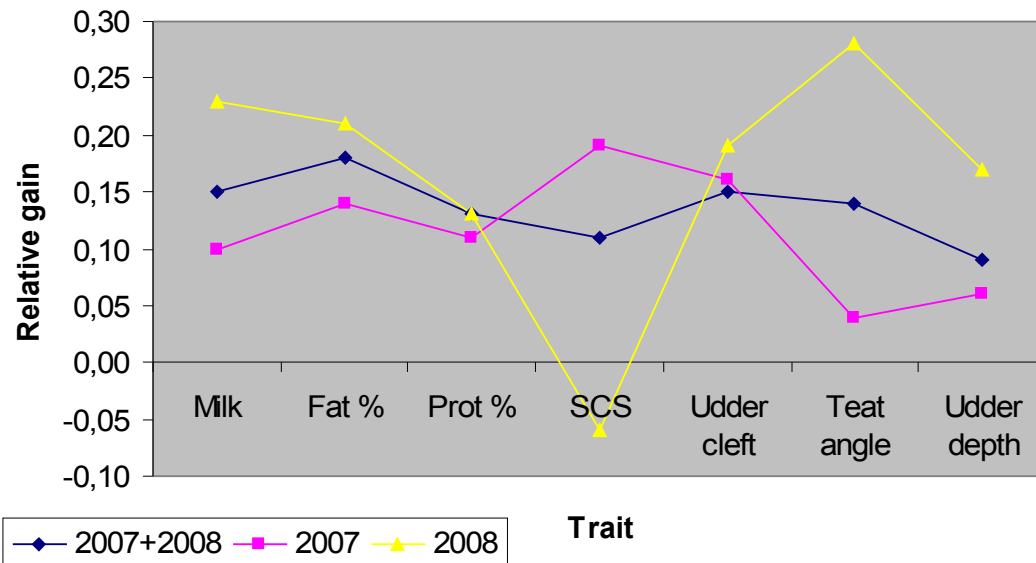
- Hypothesis $R_g \gg R_b$

Efficiency of genomic prediction accross traits

	Milk	Fat %	Prot %	SCS	Udder cleft	Teat Angle	Udder depth
Rb	0.39	0.49	0.53	0.41	0.46	0.44	0.43
Rg	0.45	0.57	0.59	0.45	0.53	0.50	0.47

- On average 14% higher correlations with genomic prediction
- Variation among traits and birth of year of validation rams
- Usually relative gain about 2 times higher for 2008 rams (1st evaluation) than 2007 rams (2nd evaluation), mainly due to Rb.

Relative gain in correlation accross traits



Effect of modifying the learning population

- Removing either ungenotyped rams (Rg1) (Duchemin et al.)
- or rams born before 2003 (Rg2)
- or closely related rams of validation rams (Rg3)

	Milk	%difference	SCS	%difference	Size of population
Rg	0.45		0.45		100%
Rg1	0.42	-9%	0.44	-3%	52%
Rg2	0.40	-11%	0.42	-9%	40%
Rg3	0,33	-27%	0,37	-18%	85%

- In agreement with with Habier *et al.*
- =>necessity of maintaining performance recording
- Moderate positive impact of adding ungenotyped or eldest rams

Comparison with dairy cattle results

Correlations	<i>Lacaune</i>	Montbéliarde (France) (1)	Holstein (France) (1)
	<i>Milk</i>	<i>Milk</i>	<i>Milk</i>
<i>R_b : Blup-DYD</i>	0.39	0.28	0.38
<i>R_g : G-blup-DYD</i>	0.45	0.42	0.56
Relative gain	15 %	50 %	47%
<i>Reference population</i>	2,567	1,172	3,940

- Smaller relative gain :
 - Better parent average correlations (R_b)
 - larger size of contemporary groups (flocks) and lack of preferential treatment
 - Too much information (DYD in 2010) included regarding 2007/2008 rams

(1) Bayes CT vs GBLUP, PLS regression, Sparse PLS and Elastic Net: Genomic Selection in French dairy cattle, C. Colombani et al.

Conclusions and perspectives

- Performances and genomic evaluation
 - Need to maintain performance recording to continuously update reference population (sires of sons needed)
 - Compared to cattle, smaller relative gain in correlation for genomic prediction
 - Better parent average correlations in sheep : size of contemporary groups and lack of preferential treatment in sheep ?
 - Too much information included relative to 2008/2007 rams in 2010 ?
 - Further methodological development needed (Bayes, non-parametric)
- Application
 - potential gain on generation interval : smaller in sheep / cattle
 - relative gain in accuracy : appears smaller in dairy sheep compared to dairy cattle...may be partly due to validation test to be improved (design of reduced data set)

Conclusions and perspectives

Savings

- Avoiding progeny-testing



- Reducing the size of the AI ram livestock

Costs

- High selection intensity at birth



- Genotyping Costs

Acknowledgements

- financial support provided by
 - ANR and ApisGene ([SheepSNPQTL project](#)) managed by INRA
 - and FUI, Midi-Pyrenées Region, Aveyron & Tarn departements, and Rodez town ([Roquefort'in project](#)) managed by Confédération Générale de Roquefort.
- technical cooperation/support from
 - genotyping platform [Labogena](#), Jouy-en-Josas, France
 - bio-informatics support of [Sigenae](#), Toulouse, France
 - computing facilities of [CTIG](#), Jouy-en-Josas, France
 - bio-informatics platform [Genotoul](#), Toulouse, France
- collaboration with the 7 partners of Roquefort'in project



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