

# Comparison of genomic evaluation in Lacaune dairy sheep using single or multiple step GBLUP

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# Turning into genomic breeding scheme

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- Apply early and accurate selection/strong selection intensity on « Sire to Son » path
- Accounting for pre-selection of candidates required (Patry, 2011)
- Either multiple-step or single-step genomic predictions to get GEBV

# Objectives

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- Apply **Multiple-Step(MS) GBLUP**, **Single-Step(SS) GBLUP** and pedigree-based(PA) BLUP
- To compare their ability to predict genetic merit
- Computation tested on 4 traits : milk yield, protein and fat content and somatic cell count

# Available Data : Genotypes and phenotypes

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- 2,868 genotyped rams with 41,501 SNPs
  - Rams genotyped using the OVINESNP50 illumina chip
- Phenotypes extracted from official French ovine evaluation
  - Full data from 2011 evaluation (4,341,830 lactations)
  - Reduced data from 2007 evaluation (3,738,475 lactations)
  - **DYD weighted by EDC**(repartition of daughters accross flocks)
  - **Ewes performances**

# Composition of datasets

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	Full data		Learning rams		Candidates rams
	Rams with DYD	Genotyped with DYD	Rams with DYD	Genotyped with DYD	
# of rams	9,340	2,868	7,587	1,593	595
Year of birth	1990-2009	1998-2009	1990-2005	1998-2005	2008-2009

# H<sup>2</sup>, EDC

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	H <sup>2</sup>	EDC Learning Rams	EDC Candidates Rams
Milk yield	0.3	103	45
Fat Content	0.35	83	44
Protein Content	0.45	83	44
SCS	0.13	94	45

# Method of computation : G-BLUP(F90)

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- Computation of a scaled genomic matrix:
  - Tuned as Vitezica et al., 2011 (Fst adjustment)
- Blended with the Numerator relationship Matrix:
- $W=0.95$ , assuming 5% of total genetic variance due to polygenic effects
- H matrix input in BLUP

$$G = \frac{Z'Z}{2 \sum p_i(1-p_i)}$$

$$G_w = w \times G + (1 - w) \times A_{22}$$

$$H^{-1} = A^{-1} + \begin{bmatrix} 0 & 0 \\ 0 & G_w^{-1} - A_{22}^{-1} \end{bmatrix}$$

# MS vs SS GBLUP

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- $Y = DYD$  weighted by EDC
- $Y = \mu + ram + e$
- Only rams included in evaluation
- Output DGV
- $Y = Ewes$  performances
- $Y = cg + pe + animal + e$ 
  - Cg=contemporary group
  - Pe=permanent environment
- Entire population included in evaluation
- Output GEBV



# Validation on candidate rams

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- Regression of DYD 2011 to DGV or GEBV
- $R^2_{\text{interbull}} = R^2(1 + k/\overline{\text{EDC}})$ 
  - $k = (4 - h^2)/h^2$
- Expected prediction bias (b1)  $\sim 1$
- Comparison of  $R^2_{\text{interbull}}$  and b1 between methods

# Time of computation

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- Most computing time devoted to build and inverse matrix in both cases
- Faster convergence with **MS-GBLUP** related to the size of the Mixed Model Equations (\*17 for **SS-GBLUP**)
- Inability to obtain standard error from **SS-GBLUP**
  - Too large system of equations

# Results of regression

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	Milk		Fat		Protein		SCS	
	b1	R <sup>2</sup>	b1	R <sup>2</sup>	b1	R <sup>2</sup>	b1	R <sup>2</sup>
PA	0.63	0.07	1.1	0.27	0.85	0.25	0.81	0.11
MS-GBLUP	<b>0.70</b>	<b>0.15</b>	<b>1.0</b>	<b>0.34</b>	<b>0.86</b>	<b>0.32</b>	<b>0.74</b>	<b>0.20</b>
SS-GBLUP	<b>0.75</b>	<b>0.18</b>	<b>0.93</b>	<b>0.41</b>	<b>0.90</b>	<b>0.42</b>	<b>0.73</b>	<b>0.20</b>

# Performance of SS-GBLUP

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- Gain of 10-30% accuracy of genomic predictions over PA
- Inflation of predictions for most traits ( $b_1 < 1$ )
- **SS-GBLUP** slightly outperforms **MS-GBLUP** in terms of inflation and  $R^2$

# Conclusion

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- **SS-GBLUP** more efficient than **MS-GBLUP**
- No differences in global (EDC,DYD vs direct computation) time of computation for EBV
- Advantage of accounting for pre-selection of candidates
- Approximation required to compute reliability in **SS-GBLUP**
- Correction of inflation?

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