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


* INRA - Toulouse, France

francis.barillet@toulouse.inra.fr

Session S2 Dairy Sheep and Goats,
Berlin, Germany, 23 May 2014

39th ICAR Session, Berlin, Germany, 2014
Sheep dairying in France

Roquefort area
Lacaune breed
890,000 ewes

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

<table>
<thead>
<tr>
<th>Breed</th>
<th>FY, PY, F%, P% + SCC + UDDER</th>
<th>FY, PY, F%, P%</th>
<th>FY, PY, F%, P%</th>
<th>FY, PY, F%, P%</th>
<th>% AI in nucleus</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lacaune</td>
<td>440</td>
<td>150</td>
<td>30</td>
<td>20</td>
<td>50%</td>
</tr>
<tr>
<td>Red Manech</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>50%</td>
</tr>
<tr>
<td>Black Manech</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>45%</td>
</tr>
<tr>
<td>Basco-Béarnaise</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>50%</td>
</tr>
<tr>
<td>Corsican</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>30%</td>
</tr>
</tbody>
</table>
### 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**

<table>
<thead>
<tr>
<th>Breed</th>
<th># AI genotyped rams</th>
<th>Years of birth</th>
<th># SNP available for GEBV estimations</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lacaune</td>
<td>4,841 ♂️</td>
<td>1999 to 2013</td>
<td>42,039</td>
</tr>
<tr>
<td>Basco-Béarnaise</td>
<td>509 ♂️</td>
<td>2000 to 2012</td>
<td></td>
</tr>
<tr>
<td>Manech black faced</td>
<td>331 ♂️</td>
<td>1999 to 2009</td>
<td>38,287</td>
</tr>
<tr>
<td>Manech red faced</td>
<td>1,424 ♂️</td>
<td>1999 to 2009</td>
<td></td>
</tr>
</tbody>
</table>
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)*

**Test of different GEBV methods**

Duchemin et al, JDS 2012

GBLUP

Bayes $C\pi$

PLS

sPLS
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)

<table>
<thead>
<tr>
<th>Methods</th>
<th>Milk</th>
<th>Fat</th>
<th>SCS</th>
</tr>
</thead>
<tbody>
<tr>
<td>EBV</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>BLUP (parent average)</td>
<td>0.37</td>
<td>0.46</td>
<td>0.39</td>
</tr>
<tr>
<td>GEBV</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>GBLUP 2 steps</td>
<td>0.42</td>
<td>0.56</td>
<td>0.44</td>
</tr>
<tr>
<td>Bayes Cτ</td>
<td>0.44</td>
<td>0.57</td>
<td>0.45</td>
</tr>
<tr>
<td>PLS</td>
<td>0.41</td>
<td>0.56</td>
<td>0.43</td>
</tr>
<tr>
<td>sPLS</td>
<td>0.42</td>
<td>0.56</td>
<td>0.43</td>
</tr>
</tbody>
</table>

- 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
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)

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)

Baloche et al, JDS 2014, 97
### Accuracy gain in GBLUP (GEBV) over BLUP (EBV) in dairy sheep

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

- 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

<table>
<thead>
<tr>
<th>Trait</th>
<th>Cattle (France)</th>
<th>Sheep (France)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Holstein</td>
<td>Montbeliarde</td>
</tr>
<tr>
<td><strong>MILK YIELD</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Accuracy</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Parent average (EBV)</td>
<td>0.33</td>
<td>0.30</td>
</tr>
<tr>
<td>Genomic (GEBV)</td>
<td>0.60</td>
<td>0.47</td>
</tr>
<tr>
<td><strong>Accuracy gain</strong></td>
<td>0.33</td>
<td>0.27</td>
</tr>
<tr>
<td>Reference population</td>
<td>4,000</td>
<td>1,200</td>
</tr>
<tr>
<td>(training)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Effective size of the</td>
<td>45</td>
<td>125</td>
</tr>
<tr>
<td>Population (breed)</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
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

$$\Delta g \text{ per year} = \text{precision} \times \text{selection rate} \times \sigma_g$$

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

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 future)

- Sampling rams (240 rams)
- Lay-off (230 rams)
- 115 Progeny-tested rams

- Young rams
- Lay-off (230 rams)
- 115 Progeny-tested rams

Selection rate (r) at 2.5-year-old: 50%

Number of alive AI rams in the AI center

Classical AI scheme

Genomic AI scheme

- Selection rate (r1) at 3-4-month-old
- Selection rate (r2) at 2.5-year-old

Genomic selection rate (r1) at 3-4-month-old

Number of alive AI rams in the AI center:

Classical AI scheme

700 ♂

Genomic AI scheme

can be reduced thanks to suppression of lay-off at 15 year old
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)

Genomic AI scheme (near futur)

Candidate genotyped rams

8-months Young rams

1.5 year Young rams

2.5 years Progeny-tested rams

3.5 years (low) Selection rate (r2) at 2.5-year-old

4.5 years (genomic rams) at 3-4-month-old

# alive AI rams in the AI center

Genomic AI scheme 400 to 450 ♂ - 40 % versus 700 ♂ - 40 % in classical scheme
Modeling a genomic scheme in dairy sheep
(illustration with 1 Lacaune breeding company)

- Candidate genotyped rams
  - 130 Young rams
  - 110 Young rams

- 80 Progeny tested rams
  - 60 ♂️
  - 40 ♂️

Total: 420 AI ♂️ in the AI center

Genomic selection rate (r1) at 3-4 month old: {1/3; 1/4; 1/5; 1/6; 1/7}

Selection rate (r2) at 2.5-yr-old after progeny-test results: {1; 0.9; 0.8; 0.7}
Annual genetic gain (in genetic standard deviation) according to $r_1$ (genomic selection rate) and $r_2$ (selection after progeny test) for one Lacaune breeding scheme

- Impact of $r_1$ much higher than impact of $r_2$
- 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 ($r_1$)

Which decision?
1. **Scenario 1 with $r_1=1/3$** (current genotyping cost (115 €))
2. **Scenario 2 with $r_1=1/4$** (if genotyping cost (85 €))

$\Delta G : + 10$ to $+15$ %
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.
30 ram lamb per sire: 46 families and 928 genotyped candidates

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

Classical rams (CR)

18 ram lambs per sire

12 ram lambs per sire

± 1/3

6 ram lambs per sire

12 ram lambs to be progeny-tested per sire

1/2 1/2

3 ram lambs to be progeny-tested per sire

Genomic selection rate

standard & developpement
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 future in Pyrenean breeds (Basco-Béarnaise and Manech).
Collaborations and fundings

INRA                           Livestock Breeding Institute

F. Barillet                J.M. Astruc
G. Baloche                  G. Lagriffoul
D. Buisson
H. Larroque
A. Legarra

Dairy sheep breeding companies

C. Soulas, X. Aguerre, F. Fidele
B. Giral-Viala, P. Boulenc
P. Panis, P. Guibert
G. Frégeat