French genomic experience: genomic for all ruminant species

E. Venot¹, D. Boichard¹, A. Legarra¹, S. Fritz³, H. Larroque¹, C. Robert-Granié¹, V. Ducrocq¹, A. Vinet¹, JM. Astruc², M. Barbat³, A. Baur³, P. Boulesteix², C. Carillier¹, MN. Fouilloux², P. Croiseau¹, A. Gion², C. Hoze³, A. Launay², F. Tortereau¹, R. Lefebvre¹, V. Loywyck², I. Palhière¹, F. Phocas¹, J. Promp², R. Rupp¹, R. Saintilan³, T. Tribout¹, A. Barbat¹, M-P Sanchez¹, S. Mattalia²

¹ INRA, ² IDELE, ³ ALLICE
French genomic experience:
genomics for all ruminant species
27th October 2016

French specificities

~ 1000 km

Source: www.CartesFrance.fr
French specificities
Large number of breeds

French genomic experience: genomics for all ruminant species
27th October 2016
Small ruminant breeds
A constructive and efficient French organization

- Inter-professional association for genetic improvement of all ruminants
- Common management quality system for all on-field organizations
- Centralized national database
- Close relationship between Industry partners and R & D

Win – Win situation

- Share of R & D between species

Example with the share of tools:

- In 2016 a common pipeline to impute & phase Dairy & Beef genomic information from different chips
- Implementation of dairy sheep in the same pipeline in progress
French genomic developments
led by Dairy cattle pioneers

IDEAL SITUATION

► large number of tested bulls and large use of AI
► large generation interval
► high cost of progeny testing
► small genetic size populations
► relative small genotyping cost / breeding animal price
► international breeds (Interbull evaluation and possible consortia)

ALL TOOLS TO IMPROVE:

\[
\Delta G = \frac{i.R.\sigma_g}{T}
\]
Reference population size & Accuracy (R)

Reference population per breed and reliability expected for candidates

<table>
<thead>
<tr>
<th>Breed</th>
<th>Nb Bulls</th>
<th>Nb Dams</th>
<th>Young candidate REL</th>
</tr>
</thead>
<tbody>
<tr>
<td>HOLSTEIN</td>
<td>33000</td>
<td>-</td>
<td>[0.55-0.70]</td>
</tr>
<tr>
<td>BROWN</td>
<td>6000</td>
<td>-</td>
<td>[0.45-0.70]</td>
</tr>
<tr>
<td>MONTBELIARDE</td>
<td>2800</td>
<td>31000</td>
<td>[0.55-0.70]</td>
</tr>
<tr>
<td>NORMANDE</td>
<td>2400</td>
<td>16000</td>
<td>[0.50-0.65]</td>
</tr>
</tbody>
</table>

December 2015
## Reference population size & Accuracy (R)

Reference population per breed and reliability expected for candidates

<table>
<thead>
<tr>
<th>Breed</th>
<th>Nb Bulls</th>
<th>Nb Dams</th>
<th>Young candidate REL</th>
</tr>
</thead>
<tbody>
<tr>
<td>HOLSTEIN</td>
<td>33000</td>
<td>-</td>
<td>[0.55-0.70]</td>
</tr>
<tr>
<td>BROWN</td>
<td>6000</td>
<td>-</td>
<td>[0.45-0.70]</td>
</tr>
<tr>
<td>MONTBELIARDE</td>
<td>2800</td>
<td>31000</td>
<td>[0.55-0.70]</td>
</tr>
<tr>
<td>NORMANDE</td>
<td>2400</td>
<td>16000</td>
<td>[0.50-0.65]</td>
</tr>
</tbody>
</table>

December 2015

**Genomic selection started in 2009 (QTL-GS)**

6 times / year with QTL and marker effects estimation

+ Weekly (without QTL effect estimation)
Reduction of generation interval and more efficient selection on functional traits

Before GS
- Birth
- Pedigree index
- 18 months
- Few AI
- Birth
- EBV based on progeny results
- 6 years
- 1st daughters in production
- Most AI

After GS
- Pedigree index
- Genomic breeding value
- 3 months
- Genotyping + GEBV computation
- Most/all AI

Milk production REL
- Before GS: 0.30
- After GS: 0.70

Fertility REL
- Before GS: 0.20
- After GS: 0.60

EBV based on progeny results
- Before GS: 0.75
- After GS: 0.95

Rel. values suggest improved efficiency and reduced generation interval.
Quick adoption of GS by breeders: more balanced selection

Genetic profile of the AI bulls used /year
Prim Holstein breed

Genomic selection

Milk yield
Udder Health
Fertility
Longevity

French genomic experience: genomics for all ruminant species
27th October 2016
Quick adoption of GS by breeders: use of young genomic bulls

AI % in France

- Proven bulls
- Bulls under progeny testing
- Proven bulls with genomic EBV
- Young bulls with genomic EBV without daughters
French genomic experience: genomics for all ruminant species
27th October 2016

Large increase of genotyping

Graph showing the increase in genotyping from 2011 to Jan-sept 2016, with a significant rise in commercial herds and breeding programs.

- Commercial herds
- Breeding programs
Larger panel of bulls used

% of AI done with the 5 most used bulls each year
Montbéliarde breed

Use of Genomic Selection for AI bulls

French genomic experience: genomics for all ruminant species
27th October 2016
Implementation in other breeds and species?

- Less favorable situation for Beef cattle breeds and Dairy regional breeds
  - same large generation interval
  - genetic population size larger
  - reference population more difficult to generate
    - less AI use for beef
    - phenotype less precise / DYD
    - smaller population size

Multi-breed option?
Multi-breed genomic evaluation for cattle?

HD genotyping of bulls from 18 cattle breeds in selection in France

Unsuccessful => very few common QTL found between breeds
=> no multi-breed genomic evaluation possible

Good basis to develop genomic selection for several breeds (imputation)

Implementation of Genomic Selection
  o in Dairy regional breeds
  o in large Beef cattle breeds (BLA, CHA & LIM)
### Genomic selection for regional dairy cattle breeds

Reference population per breed and reliability expected for candidates

<table>
<thead>
<tr>
<th>Breed</th>
<th>Nb Bulls</th>
<th>Nb Dams</th>
<th>Young candidate REL</th>
</tr>
</thead>
<tbody>
<tr>
<td>HOLSTEIN</td>
<td>33000</td>
<td>-</td>
<td>[0.55-0.70]</td>
</tr>
<tr>
<td>MONTBELIARDE</td>
<td>2800</td>
<td>31000</td>
<td>[0.55-0.70]</td>
</tr>
<tr>
<td>NORMANDE</td>
<td>2400</td>
<td>16000</td>
<td>[0.50-0.65]</td>
</tr>
<tr>
<td>BROWN</td>
<td>6000</td>
<td>-</td>
<td>[0.45-0.70]</td>
</tr>
<tr>
<td>ABONDANCE</td>
<td>350</td>
<td>1900</td>
<td>[0.35-0.55]</td>
</tr>
<tr>
<td>TARENTAISE</td>
<td>300</td>
<td>1300</td>
<td>[0.30-0.50]</td>
</tr>
<tr>
<td>SIMMENTAL</td>
<td>300</td>
<td>200</td>
<td>[0.20-0.50]</td>
</tr>
<tr>
<td>VOSGIENNE</td>
<td>60</td>
<td>1100</td>
<td>[0.20-0.50]</td>
</tr>
</tbody>
</table>

December 2015

Official in 2015
# Reference population for beef cattle breeds

<table>
<thead>
<tr>
<th></th>
<th>Charolais</th>
<th>Limousine</th>
<th>Blonde</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Direct genetic</strong> effect</td>
<td>Birth</td>
<td>Weaning</td>
<td>Carcass</td>
</tr>
<tr>
<td>Birth</td>
<td>15 000 / 1800</td>
<td>6 600 / 2 700</td>
<td>5 600 / 1 200</td>
</tr>
<tr>
<td>Weaning</td>
<td>12 500 / 2400</td>
<td>5 600 / 2 400</td>
<td>3 900 / 1 000</td>
</tr>
<tr>
<td>Carcass</td>
<td>2 400 / 600</td>
<td>1 750 / 400</td>
<td>720 / 300</td>
</tr>
<tr>
<td><strong>Maternal genetic effect</strong></td>
<td>Birth</td>
<td>Weaning</td>
<td></td>
</tr>
<tr>
<td>Birth</td>
<td>5 200 / 500</td>
<td>3 300 / 200</td>
<td>3 000 / 200</td>
</tr>
<tr>
<td>Weaning</td>
<td>4 500 / 450</td>
<td>2 400 / 500</td>
<td>2 100 / 200</td>
</tr>
</tbody>
</table>

Example of reliability gain for young Charolais calf

<table>
<thead>
<tr>
<th></th>
<th>EBV</th>
<th>Polygenic reliability</th>
<th>Genomic reliability</th>
</tr>
</thead>
<tbody>
<tr>
<td>Birth</td>
<td>0,30</td>
<td>0,40 (+33%)</td>
<td></td>
</tr>
<tr>
<td>Growth Total Merit Index</td>
<td>0,27</td>
<td>0,33 (+22%)</td>
<td></td>
</tr>
<tr>
<td>Maternal Total Merit Index</td>
<td>0,25</td>
<td>0,34 (+36%)</td>
<td></td>
</tr>
</tbody>
</table>

Different method used for beef cattle with blending of polygenic and genomic results  
(VanRaden et al., 2009)
## French genomic experience: genomics for all ruminant species

### 27th October 2016

<table>
<thead>
<tr>
<th></th>
<th>Charolais</th>
<th>Limousine</th>
<th>Blonde</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Direct genetic effect</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Birth</td>
<td>15 000 / 1800</td>
<td>6 600 / 2 700</td>
<td>5 600 / 1 200</td>
</tr>
<tr>
<td>Weaning</td>
<td>12 500 / 2400</td>
<td>5 600 / 2 400</td>
<td>3 900 / 1 000</td>
</tr>
<tr>
<td>Carcass</td>
<td>2 400 / 600</td>
<td>1 750 / 400</td>
<td>720 / 300</td>
</tr>
<tr>
<td><strong>Maternal genetic effect</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Birth</td>
<td>5 200 / 500</td>
<td>3 300 / 200</td>
<td>3 000 / 200</td>
</tr>
<tr>
<td>Weaning</td>
<td>4 500 / 450</td>
<td>2 400 / 500</td>
<td>2 100 / 200</td>
</tr>
</tbody>
</table>

### Maternal effects

Different method used for beef cattle with blending of polygenic and genomic results (VanRaden et al., 2009)

Official since end 2015 for BLA, CHA and LIM

2 national runs / year

+ Weekly computation for new candidates (without re-estimation of marker effects)
What about sheep?

- Less favorable situations for small ruminants
  - high relative cost of genotyping
  - generation interval already short
  - fresh semen use for AI in sheep
  - AI demand highly concentrated in time

- already familiar with the use of molecular information (scrapie)

- Different cases:

<table>
<thead>
<tr>
<th>Breed</th>
<th>Number of milk recorded ewes</th>
<th>Genotyped rams with daughters</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lacaune</td>
<td>156,491</td>
<td>4,716</td>
</tr>
<tr>
<td>Manech TR</td>
<td>66,020</td>
<td>1,879</td>
</tr>
<tr>
<td>Basco-Béarnaise</td>
<td>21,620</td>
<td>562</td>
</tr>
<tr>
<td>Manech TN</td>
<td>9,302</td>
<td>475</td>
</tr>
<tr>
<td>Corse</td>
<td>14,028</td>
<td>197</td>
</tr>
</tbody>
</table>

(2015)
Different research programs and funding to test GS interest and feasibility in Dairy sheep

- Illumina OvineSNP50 chip available since 2009

- Different goals:
  - build up reference population
  - check interest of GS for sheep (with no additional cost)
  - define the best method to apply on sheep data
  - test GS in experimental conditions
  - include new traits
  - foresee potential impact on selection scheme
Results for dairy sheep

- QTL detection study: no big QTL found (limited power detection)
- ssGBLUP with phantom group
  => reliability gain: [ 0.13 ; 0.20 ]
- Lacaune experimental study:
- Modeling of different genomic selection pressures on young rams
  => with 1/3 selection pressure, + 15 % genetic gain without extra cost
  => cost of genotyping balanced by reduction of number of rams in AI Center.
Results for dairy sheep

 ► Lacaune breed:
  => Studies showed interest of GS for Lacaune breed
  => GS official in 2015 + end of ram progeny testing
  => 7 genomic evaluations / year

 ► Other dairy sheep breeds:
  o reference population smaller
  o test of multi-breed evaluations with LATXA Spanish breed
  => GS should take place in 2017.
Meat sheep

- limited or no progeny testing and limited AI => No GS planned
- Genotyping first for parentage verification and assignation
- Research to include major gene in genetic evaluation (prolificacy...)

Goats

- Goat chip available in 2010
- 2 kind of populations for reference population:
  2 400 females (G + P) and 800 AI bucks
- Research in progress on:
  - combination of the 2 breeds (Alpine and Saanen) + international coll.
  - major gene inclusion in genetic evaluation

Goal: GS in 2017
CONCLUSION

► It has been a real genomic revolution these last years

► large impact on selection scheme organization
  => early use of breeding animals for higher genetic gain on all traits

► thanks to the French professional organization structure closely linked to R & D, genomic selection have been adapted to the different specificities of ruminant species and breeds

Genomic evaluation in place in 14 cattle and 1 sheep breeds

In the very next future for 4 sheep and 2 goat breeds
END OF THE STORY? ...

... NO! JUST THE BEGINNING!

➤ several challenges:
  o Private initiatives
  o Organizational reforms
  o Reference population maintenance
  o Competition on new phenotypic recording
  o Integration of sequence information

...
REFERENCES

- http://en.france-genetique-elevage.org
- www.idele.fr
- www.allice.fr
- http://www.jouy.inra.fr/gabi_eng

D. Boichard¹, V. Ducrocq¹, P. Croiseau¹, S. Fritz³,
A. Baur³, R. Saintilan³, T. Tribout¹, M-P Sanchez¹,
P. Boulesteix², JM. Astruc², A. Legarra¹, C. Robert-Granié¹,
C. Carillier¹, I. Palhière¹, F. Tortereau¹, R. Rupp¹,
H. Larroque¹, V. Loywyck², S. Mattalia²

¹ INRA, ² IDELE, ³ ALLICE