CLUSTERING AND GENETIC ANALYSIS OF BODY RESERVES CHANGES THROUGHOUT PRODUCTIVE CYCLES IN MEAT SHEEP

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Plan

- Context - Robustness

- Cluster analysis
  - Materials and methods
  - Results

- Genetic analysis
  - Materials and methods
  - Results

- Discussion – Conclusion

- Perspectives
Context - Robustness

- Robust animals to assure the farm sustainability in harsh conditions or in more controlled conditions (sheepfold)
- One component of robustness: mobilization/accretion of body reserves (BR) through lipids metabolism

Russel et al., 1971
Blanc et al., 2006
Context - Robustness

- Robust animals to assure the farm sustainability in harsh conditions or in more controlled conditions (sheepfold)
- One component of robustness: mobilization/accretion of body reserves (BR) through lipids metabolism

Russel et al., 1971
Blanc et al., 2006
Context - Robustness

- Body Condition Score use to characterize robustness
  - Score from 1 to 5: lean to fat
  - Optimum between 2.5 and 3.5

- Heritability of BCS when considered as a punctual measurement
  - From 0.10 to 0.45 for ruminants

- No study in ruminants on genetic for BCS when considering variations along productive cycle (successful measurements)

Russel et al., 1971
Borg et al., 2005
Loker et al., 2011
Shackell et al., 2011
Objectives

- To investigate temporal changes and profiles of BR dynamics throughout productive cycles
- To analyze the genetic variability of BR dynamics in meat sheep
Materials and Methods

- Romane flock (n=250 ewes) reared exclusively outdoors in harsh conditions on a plateau (near Roquefort, La Fage)
Materials and Methods

- Romane flock (n=250 ewes) reared exclusively outdoors in harsh conditions on a plateau (near Roquefort, La Fage)
- BCS measured on 1146 ewes from 78 sires (2002-2015)
  - Cycle 1: 1146
  - Cycle 2: 1068
  - Cycle 3: 414
- 8 BCS measurements per productive cycle
Materials and Methods – Cluster analysis

- Clustering
  - To investigate variability in individual BCS profiles
  - Smoothing (51 nodes)
  - Functional Principal Component Analysis (FPCA)
  - Clusters construction
    - Three first components of FPCA
    - Expectation-Maximization Algorithm
    - Repeatability and stability of clusters (n=2 to 7 clusters)
Results - Clusters analysis

Cycle 1

- Three clusters identified at cycle 1
- Two main clusters with similar profiles but differing in level of BCS
Results - Cluster analysis

- Three clusters identified at cycles 2 and 3
- Majority of clusters showed similar profiles along cycle but differed in BCS levels
- Biological effects
Materials and Methods – Genetic Analysis

- Trait = Difference in BCS between two physiological stages
- Example of four traits

Univariate and multivariate analysis: Heritabilities and correlations estimation with animal model (ASReml, all cycles considered)

\[ Y = \text{mu} + \text{animal} + \text{perm} + \text{age} + \text{parity} + \text{litter} + \text{year} + e \]

- \( Y \): trait
- \( \text{mu} \): mean of the trait
- \( \text{animal} \): additive genetic effect of the ewe
- \( \text{perm} \): environmental permanent effect of the ewe
- \( \text{age of the ewe, parity, litter, year of measurements} \) as fixed effects
- \( e \): residual
## Results - Genetic Analysis

### Variables BCS

<table>
<thead>
<tr>
<th>Variables BCS</th>
<th>Early pregnancy to Weaning</th>
<th>Lambing to Suckling</th>
<th>Early dry-off</th>
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<tr>
<td>Early pregnancy to Weaning</td>
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<td><strong>0.11</strong> (0.04)</td>
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- Low to medium heritabilities (0.07 ± 0.02 to 0.15 ± 0.02)
Results - Genetic Analysis

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- Positive correlation between periods characterizing BR mobilization
### Results - Genetic Analysis

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<td>0.75 (0.10)</td>
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<td>Weaning to Mating</td>
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- Positive correlation between periods characterizing BR accretion
Results - Genetic Analysis

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<td>Early pregnancy to Weaning</td>
<td><strong>0.14</strong> (0.02)</td>
<td>0.49 (0.12)</td>
<td><strong>-0.71</strong> (0.08)</td>
<td><strong>-0.73</strong> (0.14)</td>
</tr>
<tr>
<td>Lambing to Suckling</td>
<td>0.07 (0.02)</td>
<td><strong>-0.46</strong> (0.12)</td>
<td><strong>-0.52</strong> (0.18)</td>
<td></td>
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- Negative correlations between periods characterizing BR accretion and mobilization
Discussion - Conclusion

- Variability in BR dynamics
  - Three clusters at each cycle
  - Most of profiles with similar dynamic but differing in BR levels
  - Variation due to biological factors (litter size) AND individual differences

- BCS variations heritable: possibility of using it for selection

- Accretion and mobilization processes of BR linked at the genetic level
  - Common genes?
Discussion - Conclusion

 Perspectives

- Link with zootechnical performances (lamb growth, ewe reproduction...)

- Longitudinal genetic modeling (Random Regression) of the BCS variations profiles

- Joint analysis with climatic data (reaction norm model)

- Further phenotyping for BR variations (key metabolites /hormones /ultra sound measurements...)

Macé Tiphaine – WCGALP 2018
Take home message

- Variability in BR dynamics
- BCS variations heritable: possibility of selection
- Accretion and mobilization of BR linked at the genetic level
Results – Genetic Analysis

Estimates (± standard errors) of variance components for BCS.

<table>
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<tr>
<th>Variables</th>
<th>$h^2$</th>
<th>$c^2$</th>
<th>$e^2$</th>
<th>$r$</th>
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<tr>
<td>BCS-M</td>
<td>0.35 (0.04)</td>
<td>0.03 (0.03)</td>
<td>0.62 (0.02)</td>
<td>0.38 (0.02)</td>
<td>0.04 (0.00)</td>
</tr>
<tr>
<td>BCS-Pa</td>
<td>0.37 (0.04)</td>
<td>0.04 (0.03)</td>
<td>0.60 (0.02)</td>
<td>0.40 (0.02)</td>
<td>0.05 (0.00)</td>
</tr>
<tr>
<td>BCS-Pb</td>
<td>0.32 (0.03)</td>
<td>0.04 (0.03)</td>
<td>0.64 (0.02)</td>
<td>0.36 (0.02)</td>
<td>0.05 (0.00)</td>
</tr>
<tr>
<td>BCS-L</td>
<td>0.26 (0.04)</td>
<td>0.10 (0.03)</td>
<td>0.64 (0.02)</td>
<td>0.36 (0.02)</td>
<td>0.04 (0.00)</td>
</tr>
<tr>
<td>BCS-Sa</td>
<td>0.27 (0.03)</td>
<td>0.04 (0.03)</td>
<td>0.69 (0.02)</td>
<td>0.31 (0.02)</td>
<td>0.04 (0.00)</td>
</tr>
<tr>
<td>BCS-Sb</td>
<td>0.26 (0.05)</td>
<td>0.05 (0.05)</td>
<td>0.69 (0.04)</td>
<td>0.31 (0.04)</td>
<td>0.05 (0.00)</td>
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<tr>
<td>BCS-W</td>
<td>0.33 (0.04)</td>
<td>0.05 (0.03)</td>
<td>0.61 (0.02)</td>
<td>0.39 (0.02)</td>
<td>0.05 (0.00)</td>
</tr>
<tr>
<td>BCS-D</td>
<td>0.33 (0.04)</td>
<td>0.06 (0.03)</td>
<td>0.61 (0.02)</td>
<td>0.39 (0.02)</td>
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$h^2$: heritability; $c^2$: proportion of total phenotypic variance due to ewe permanent environmental effect; $e^2$: proportion of total phenotypic variance due to temporary environmental effects; $r$: repeatability; $\sigma^2_p$: total phenotypic variance.
Results – Genetic Analysis

Estimates (± standard errors) of variance components for BCS variations.

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<td>BCS-M:Pa</td>
<td>0.07 (0.02)</td>
<td>0.00 (0.02)</td>
<td>0.92 (0.02)</td>
<td>0.08 (0.02)</td>
<td>0.041 (0.001)</td>
</tr>
<tr>
<td>BCS-Pa:W</td>
<td>0.16 (0.03)</td>
<td>0.02 (0.03)</td>
<td>0.83 (0.02)</td>
<td>0.17 (0.02)</td>
<td>0.056 (0.002)</td>
</tr>
<tr>
<td>BCS-Pa:L</td>
<td>0.10 (0.02)</td>
<td>0.02 (0.02)</td>
<td>0.88 (0.02)</td>
<td>0.12 (0.02)</td>
<td>0.055 (0.001)</td>
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<tr>
<td>BCS-L:Sa</td>
<td>0.04 (0.02)</td>
<td>0.04 (0.02)</td>
<td>0.92 (0.02)</td>
<td>0.08 (0.02)</td>
<td>0.030 (0.001)</td>
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<tr>
<td>BCS-W:D</td>
<td>0.10 (0.03)</td>
<td>0.01 (0.03)</td>
<td>0.89 (0.03)</td>
<td>0.11 (0.03)</td>
<td>0.032 (0.001)</td>
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<td>BCS-W:M</td>
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Results – Genetic Analysis

CV
BCS-Pa:W 22%
BCS-L:Sa 32%
BCS-W:D 52%
BCS-W:M 25%