

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

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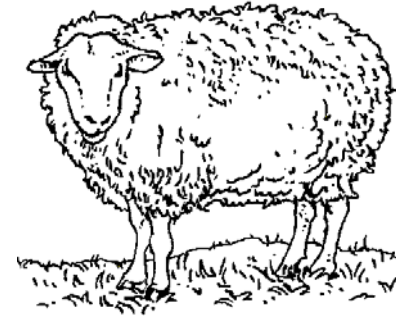
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Plan

- Context - Robustness
- Cluster analysis
 - Materials and methods
 - Results
- Genetic analysis
 - Materials and methods
 - Results
- Discussion – Conclusion
- Perspectives



Context - Robustness

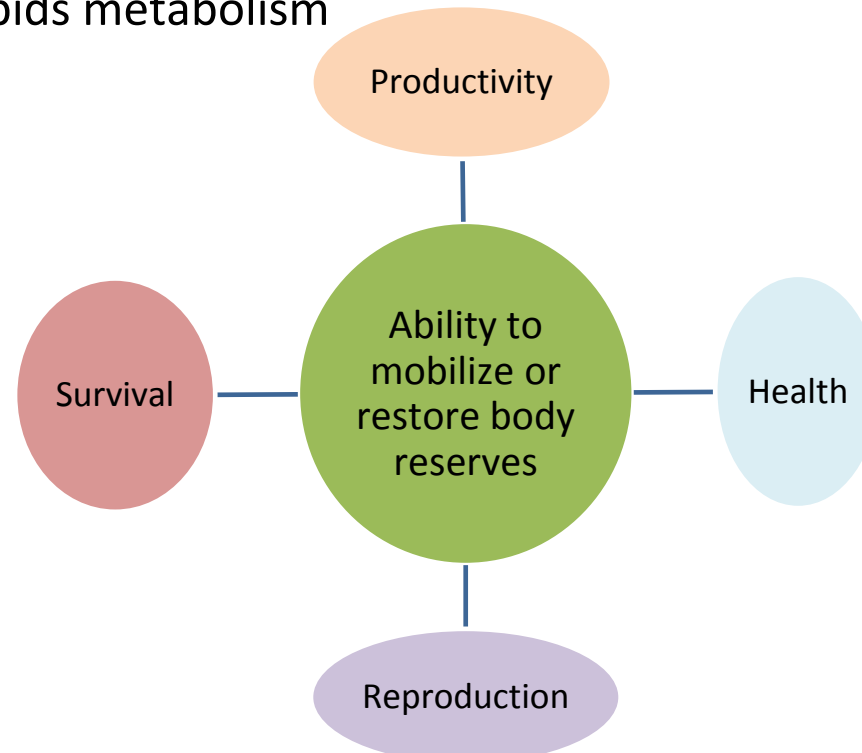
- Robust animals to assure the farm sustainability in harsh conditions or in more controlled conditions (sheepfold)
- One component of robustness: mobilization/accretion of body reserves (BR) through lipids metabolism

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 (successive measurements)

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

Context - Robustness

➤ Objectives

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

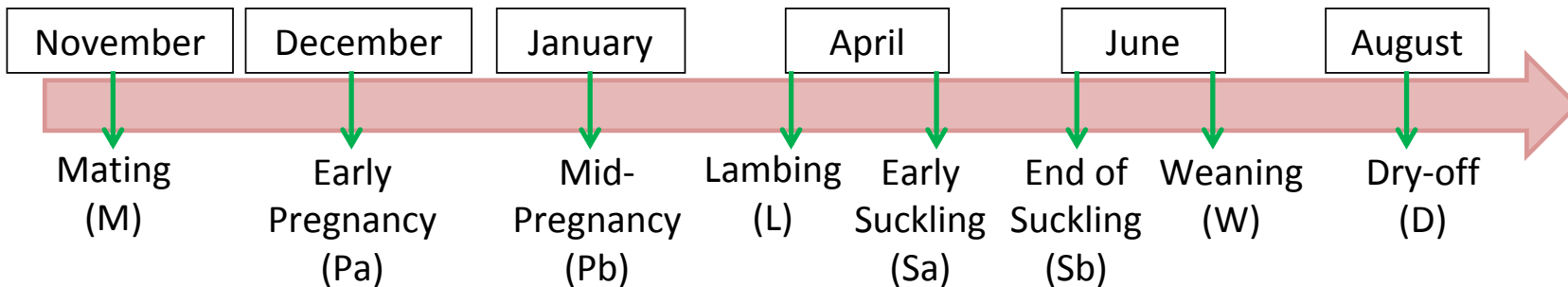
Materials and Methods

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



Materials and Methods

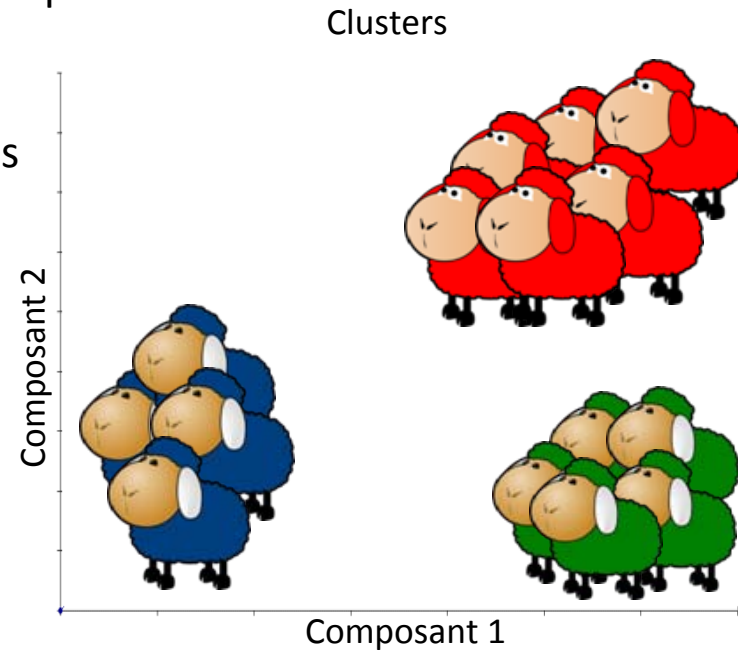
- Romane flock (n=250 ewes) reared exclusively outdoors in harsh conditions on a plateau (near Roquefort, La Fage)
- BCS measured on 1146 ewes from 78 sires (2002-2015)
 - Cycle 1: 1146
 - Cycle 2: 1068
 - Cycle 3: 414
- **8 BCS** measurements per productive cycle



Materials and Methods – Cluster analysis

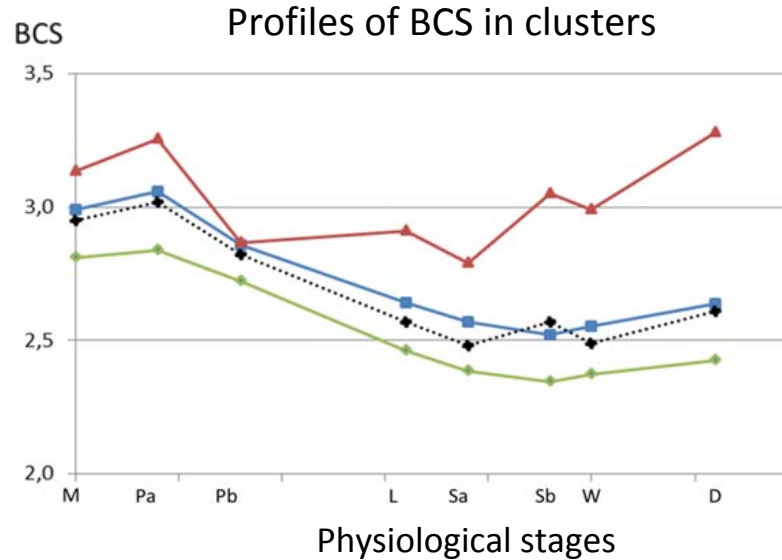
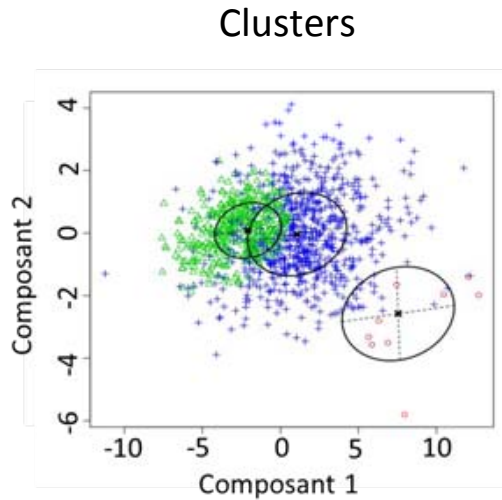
➤ Clustering

- 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

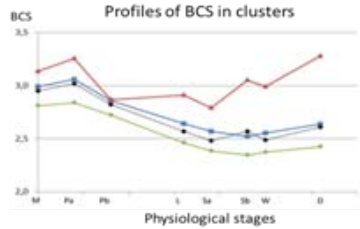
Cycle 1



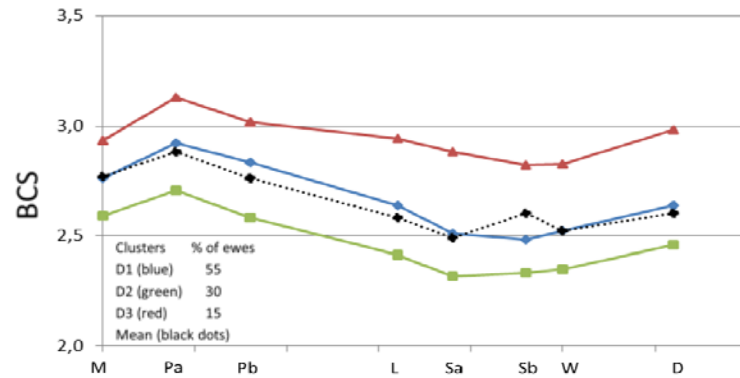
Clusters	% of ewes
B1 (blue)	63
B2 (green)	36
B3 (red)	1
Mean (black dots)	

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

Results - Cluster analysis

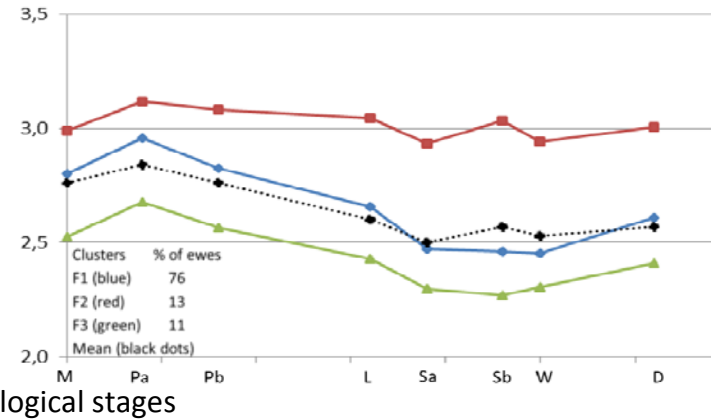


Profiles of BCS in cluster at cycle 2



- ✓ 56 % of D1 came from B1
- ✓ 53 % of D2 came from B2
- ✓ 64 % of D3 came from B1

Profiles of BCS in cluster at cycle 3

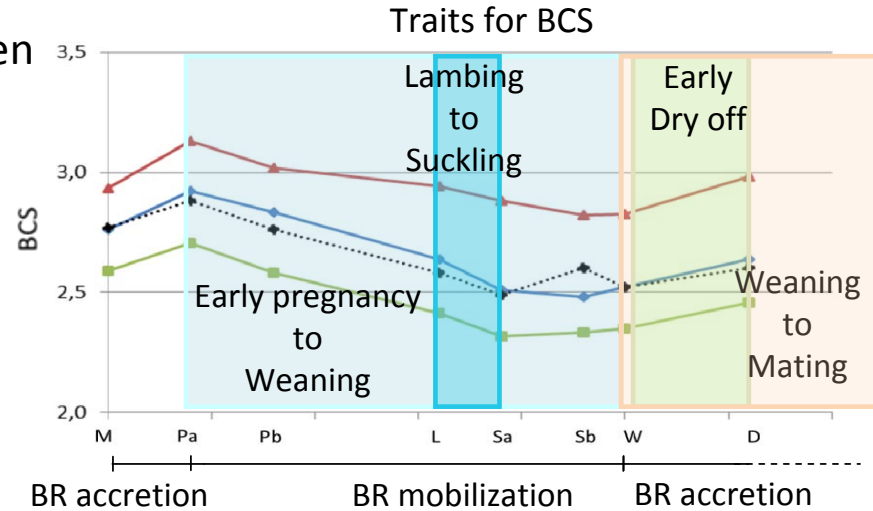


- ✓ 56 % of F1 came from D1
- ✓ 47 % of F2 came from D1
- ✓ 74 % of F3 came from D2

- 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)

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

Y: trait

μ: mean of the trait

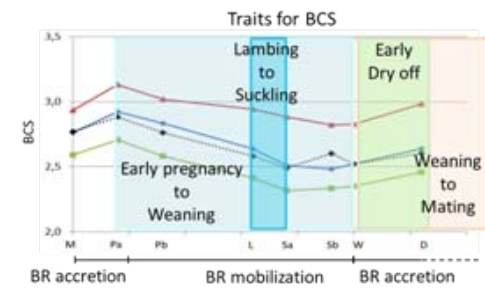
animal: additive genetic effect of the ewe

perm: environmental permanent effect of the ewe

age of the ewe, parity, litter, year of measurements as fixed effects

e: residual

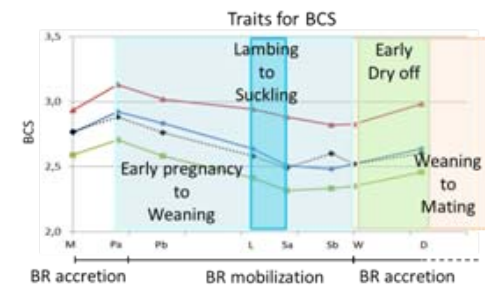
Results - Genetic Analysis



Variables BCS	Early pregnancy to Weaning	Lambing to Suckling	Early dry-off	Weaning to Mating
Early pregnancy to Weaning	0.14 (0.02)			
Lambing to Suckling		0.07 (0.02)		
Early dry-off			0.15 (0.02)	
Weaning to Mating				0.11 (0.04)

➤ Low to medium heritabilities (0.07 ± 0.02 to 0.15 ± 0.02)

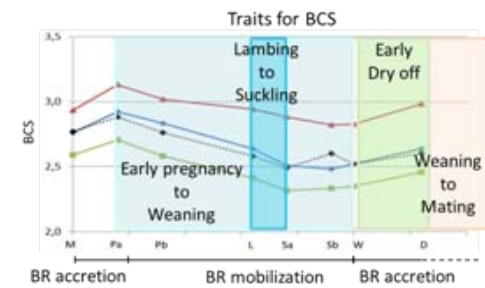
Results - Genetic Analysis



Variables BCS	Early pregnancy to Weaning	Lambing to Suckling	Early dry-off	Weaning to Mating
Early pregnancy to Weaning	0.14 (0.02)	0.49 (0.12)		
Lambing to Suckling		0.07 (0.02)		
Early dry-off			0.15 (0.02)	
Weaning to Mating				0.11 (0.04)

➤ Positive correlation between periods characterizing BR mobilization

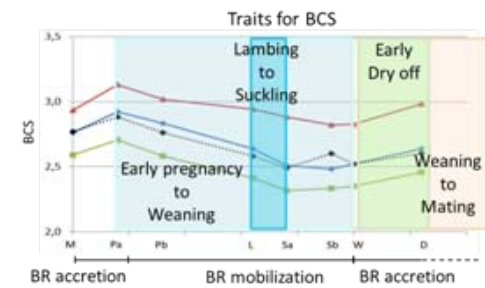
Results - Genetic Analysis



Variables BCS	Early pregnancy to Weaning	Lambing to Suckling	Early dry-off	Weaning to Mating
Early pregnancy to Weaning	0.14 (0.02)	0.49 (0.12)		
Lambing to Suckling		0.07 (0.02)		
Early dry-off			0.15 (0.02)	0.75 (0.10)
Weaning to Mating				0.11 (0.04)

➤ Positive correlation between periods characterizing BR accretion

Results - Genetic Analysis



Variables BCS	Early pregnancy to Weaning	Lambing to Suckling	Early dry-off	Weaning to Mating
Early pregnancy to Weaning	0.14 (0.02)	0.49 (0.12)	-0.71 (0.08)	-0.73 (0.14)
Lambing to Suckling		0.07 (0.02)	-0.46 (0.12)	-0.52 (0.18)
Early dry-off			0.15 (0.02)	0.75 (0.10)
Weaning to Mating				0.11 (0.04)

- 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...)

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 (\pm standard errors) of variance components for BCS.

Variables	h^2	c^2	e^2	r	σ_p^2
BCS-M	0.35 (0.04)	0.03 (0.03)	0.62 (0.02)	0.38 (0.02)	0.04 (0.00)
BCS-Pa	0.37 (0.04)	0.04 (0.03)	0.60 (0.02)	0.40 (0.02)	0.05 (0.00)
BCS-Pb	0.32 (0.03)	0.04 (0.03)	0.64 (0.02)	0.36 (0.02)	0.05 (0.00)
BCS-L	0.26 (0.04)	0.10 (0.03)	0.64 (0.02)	0.36 (0.02)	0.04 (0.00)
BCS-Sa	0.27 (0.03)	0.04 (0.03)	0.69 (0.02)	0.31 (0.02)	0.04 (0.00)
BCS-Sb	0.26 (0.05)	0.05 (0.05)	0.69 (0.04)	0.31 (0.04)	0.05 (0.00)
BCS-W	0.33 (0.04)	0.05 (0.03)	0.61 (0.02)	0.39 (0.02)	0.05 (0.00)
BCS-D	0.33 (0.04)	0.06 (0.03)	0.61 (0.02)	0.39 (0.02)	0.04 (0.00)

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; σ_p^2 : total phenotypic variance.

Results – Genetic Analysis

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

Variables	h^2	c^2	e^2	r	σ_p^2
BCS-M:Pa	0.07 (0.02)	0.00 (0.02)	0.92 (0.02)	0.08 (0.02)	0.041 (0.001)
BCS-Pa:W	0.16 (0.03)	0.02 (0.03)	0.83 (0.02)	0.17 (0.02)	0.056 (0.002)
BCS-Pa:L	0.10 (0.02)	0.02 (0.02)	0.88 (0.02)	0.12 (0.02)	0.055 (0.001)
BCS-L:Sa	0.04 (0.02)	0.04 (0.02)	0.92 (0.02)	0.08 (0.02)	0.030 (0.001)
BCS-W:D	0.10 (0.03)	0.01 (0.03)	0.89 (0.03)	0.11 (0.03)	0.032 (0.001)
BCS-W:M	0.10 (0.04)	0.01 (0.05)	0.89 (0.05)	0.11 (0.05)	0.039 (0.002)

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; σ_p^2 : total phenotypic variance.

Results – Genetic Analysis

CV

BCS-Pa:W 22%

BCS-L:Sa 32%

BCS-W:D 52%

BCS-W:M 25%