Genome-based inbreeding in French dairy sheep breeds

S. T. Rodríguez-Ramilo, A. Legarra
Introduction

Genetic diversity has been characterised and managed with pedigree-based inbreeding estimates.

**Constraints:**

(1) Pedigree completeness and quality are essential.

(2) Mendelian sampling variation is not considered.

(3) Does not take into account LD caused by selection.

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Introduction

The realised proportion of the genome that two individuals share can be estimated from genome-based information.

Alternatives:

1. SNP-by-SNP: unique alleles in the base population
2. Segment-based: fragments of homozygous SNP (ROH)
Introduction

Selection of French dairy sheep for each breed separately

Breeds:

(1) Lacaune: Confederation (LACCon) and Ovitest (LACOvi)

(2) Manech Tête Rousse (MTR)

(3) Manech Tête Noire (MTN)

(4) Basco-Béarnaise (BB)
Objective

To quantify the genetic diversity in five selected French dairy sheep subpopulations and breeds with several pedigree- and marker-based methods and to compare the results in terms of rate of inbreeding and on effective population size.
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**Material**

<table>
<thead>
<tr>
<th>Breed</th>
<th>Genotyped individuals</th>
<th>Individuals in pedigree</th>
<th>Equivalent number of complete generations</th>
</tr>
</thead>
<tbody>
<tr>
<td>BB</td>
<td>321</td>
<td>1,861</td>
<td>6.10</td>
</tr>
<tr>
<td>MTN</td>
<td>329</td>
<td>1,616</td>
<td>5.29</td>
</tr>
<tr>
<td>MTR</td>
<td>1,906</td>
<td>11,574</td>
<td>7.61</td>
</tr>
<tr>
<td>LACCon</td>
<td>3,030</td>
<td>29,255</td>
<td>10.84</td>
</tr>
<tr>
<td>LACOvi</td>
<td>3,114</td>
<td>28,497</td>
<td>11.69</td>
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**Total** = 8,700  **Total** = 72,803

Lacaune has since 1976 two subpopulations (separate breeding schemes): LACCon & LACOvi

Map of France showing distribution of French dairy sheep breeds.
Material

OvineSNP50 BeadChip: 38,287 autosomal SNP
Methods

**Pedigree**-based inbreeding estimates

Software **PEDIG**
Methods

**SNP-by-SNP** inbreeding estimates

Proportion of **homozygous SNP**
Methods

ROH-based inbreeding estimates

\[ F_{ROH_i} = \sum_{k=1}^{n_{ROH_i}} L_{ROH_{ik}} / l_g \]
Methods

\[ N_e = \frac{1}{2\Delta F} \]

- Pedigree
- SNP-by-SNP
- ROH

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## Results

Rate of inbreeding per generation ± standard error

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<tr>
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<th>$\Delta F_{\text{ROH}}$</th>
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<td>BB</td>
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<tr>
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Results

Effective population size. Bars indicate the 95% confidence interval.

(1) LACOvi
(2) LACCon
(3) MTR
(4) MTN
(5) BB
Summarising...

(1) $\Delta F$ and $N_e$ are empirically comparable across the three evaluated methods

(2) $N_e$ of these dairy sheep subpopulations and breeds are in the low hundreds

(3) Further research on ROH-based inbreeding is still required
Acknowledgements

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Thanks for your attention!