

Genome-based inbreeding in French dairy sheep breeds



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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



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: Confedration (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**

Material

	Genotyped individuals	Individuals in pedigree	Equivalent number of complete generations
BB	321	1,861	6.10
MTN	329	1,616	5.29
MTR	1,906	11,574	7.61
LACCon	3,030	29,255	10.84
LACovi	3,114	28,497	11.69

Total = 8,700 Total = 72,803



Lacaune (LAC)

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



Basco-Béarnaise (BB)



Manech Tête Rousse (MTR)

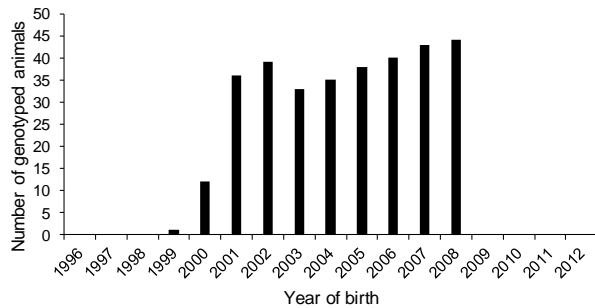


Manech Tête Noire (MTN)

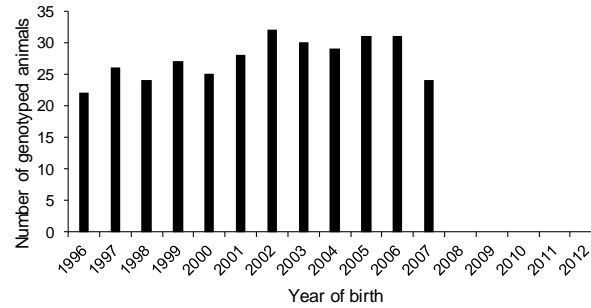


Material

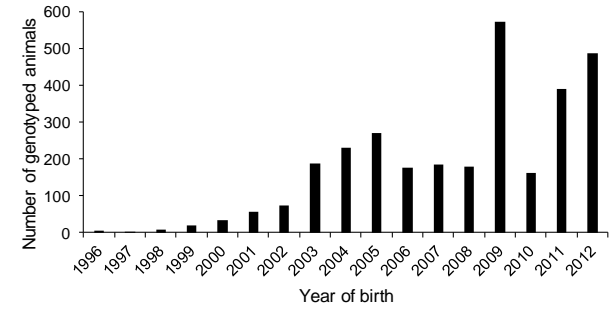
BB



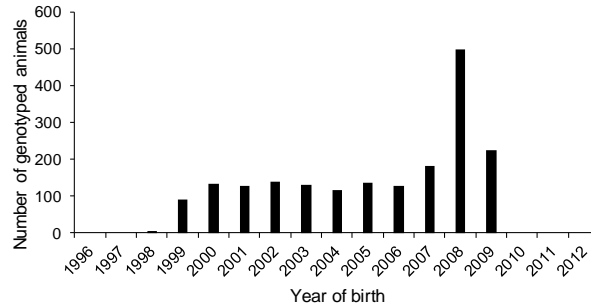
MTN



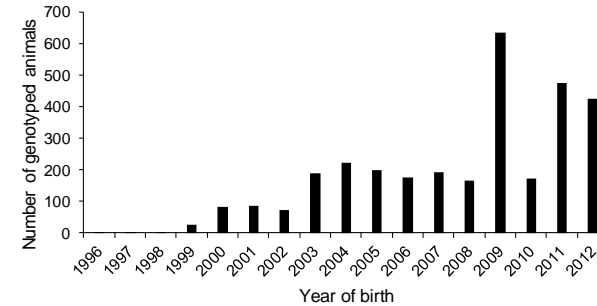
LACCon



MTR



LACovi



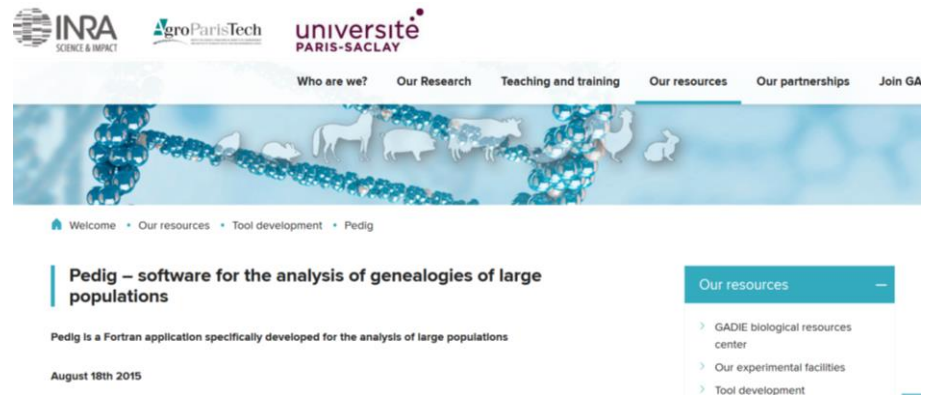
OvineSNP50 BeadChip: 38,287 autosomal SNP



Methods

Pedigree-based inbreeding estimates

Software **PEDIG**



INRA SCIENCE & IMPACT AgroParisTech universit  PARIS-SACLAY

Who are we? Our Research Teaching and training Our resources Our partnerships Join GA

Welcome • Our resources • Tool development • Pedig

Pedig – software for the analysis of genealogies of large populations

Pedig is a Fortran application specifically developed for the analysis of large populations

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Our resources

- > GADIE biological resources center
- > Our experimental facilities
- > Tool development



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



Results

Rate of inbreeding per generation \pm standard error

	ΔF_{PED}	ΔF_{SNP}	ΔF_{ROH}
BB	0.0099 \pm 0.0017	0.0044 \pm 0.0010	0.0085 \pm 0.0024
MTN	0.0094 \pm 0.0012	0.0028 \pm 0.0007	0.0062 \pm 0.0017
MTR	0.0045 \pm 0.0004	0.0025 \pm 0.0002	0.0046 \pm 0.0006
LACCon	0.0019 \pm 0.0002	0.0016 \pm 0.0001	0.0022 \pm 0.0003
LACovi	0.0022 \pm 0.0002	0.0014 \pm 0.0001	0.0014 \pm 0.0003



Results

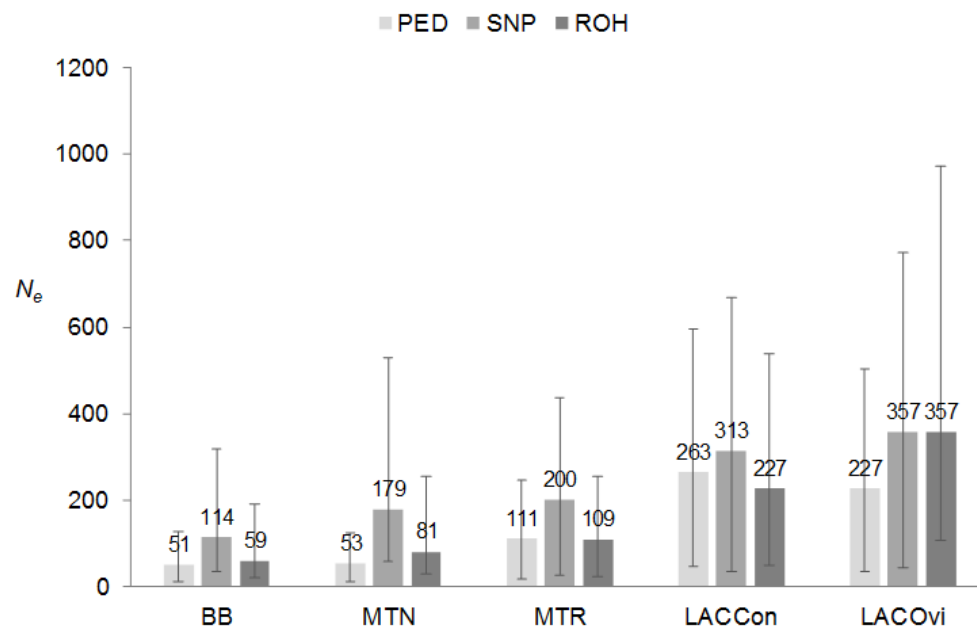
Rate of inbreeding per generation \pm standard error

	ΔF_{PED}	ΔF_{SNP}	ΔF_{ROH}
BB	0.0099 \pm 0.0017	0.0044 \pm 0.0010	0.0085 \pm 0.0024
MTN	0.0094 \pm 0.0012	0.0028 \pm 0.0007	0.0062 \pm 0.0017
MTR	0.0045 \pm 0.0004	0.0025 \pm 0.0002	0.0046 \pm 0.0006
LACCon	0.0019 \pm 0.0002	0.0016 \pm 0.0001	0.0022 \pm 0.0003
LACovi	0.0022 \pm 0.0002	0.0014 \pm 0.0001	0.0014 \pm 0.0003



Results

Effective population size. Bars indicate the 95% confidence interval



- (1) LACovi
- (2) LACCon
- (3) MTR
- (4) MTN
- (5) BB





Summarising...

- (1) ΔF 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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FEDER

Fondo Europeo de
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Thanks for your attention!