



Using genomic information provided by selection schemes to assess French dairy breeds diversity

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Introduction

▶ Loss of diversity in selected ruminant breeds

- Selection strategies/IA = very small number of male breeders
- Genomic selection => generation interval reduced
- Loss of heterozygosity and allelic richness, bottleneck => close monitoring needed

▶ Use of molecular information

- Pedigree data usually preferred to molecular data to analyze genetic variability
- However huge improvement of genotyping techniques (SNPs / 54K chip mostly)
=> tremendous increase **(1)** N° of molecular markers **(2)** N° of animal genotyped

VARUME project: using **available** genotypes in dairy cattle/sheep breeds to monitor their **genetic variability**

Data available

(after quality control)

▶ Montbeliard breed

1,199 males - 33,973 SNPs

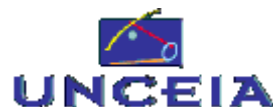


▶ Lacaune breed

1,615 males - 39,776 SNPs

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Genetic variability indicators calculated in our project

▶ Heterozygosity observed and expected

▶ “Molecular inbreeding” and “molecular coancestry”

$$F_{gen} = \frac{1}{n} \sum_{L=1}^n \left(1 - \frac{H_{ol}}{H_{el}}\right) \quad (\text{Baumung and al., 2003})$$

▶ Effective size (N_e) :

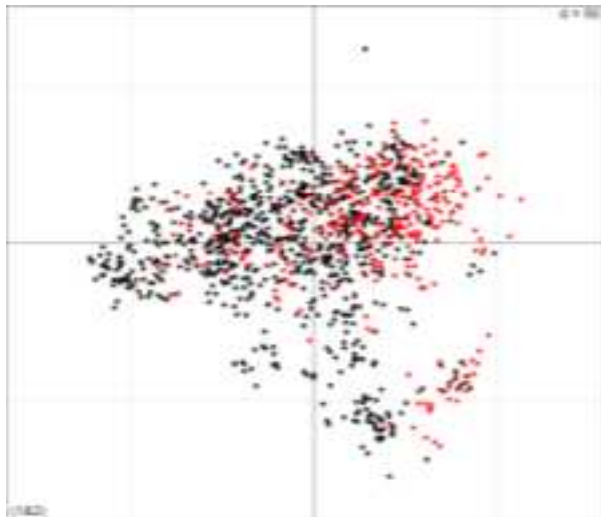
✓ Linkage disequilibrium : $d^2 \approx \frac{1}{3N_e} + \frac{1}{2n}$, with SNPs from different chromosomes (*Hill and al., 1988 ; Mangin and al., 2012*)

✓ Comparison with N_e based on **pedigree data**, based on inbreeding (*Gutiérrez and al., 2009*) and coancestry (*Cervantés and al., 2011*)

Results (1)

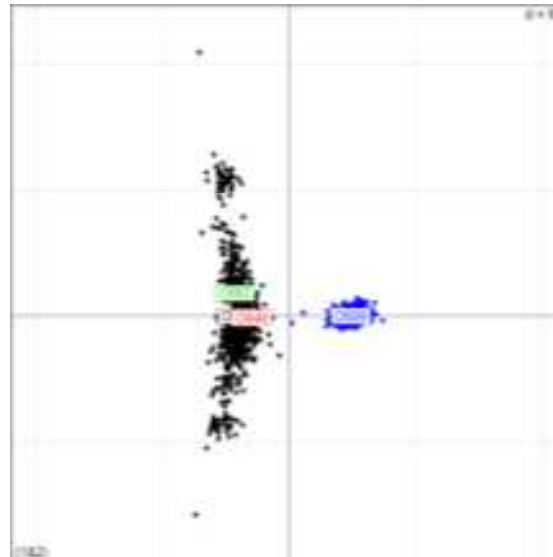
► Relationship matrix (*multi dimensional scanning*)

Montbéliard



Selection firm	Black	Red
N° of indiv.	853	312

Lacaune



Selection firm	Black	Blue
N° of indiv.	862	728

=> Grouping by selection firm mostly in the Lacaune breed

Results (2)

► Variation of the effective size values

Montbeliard

Indicator	Effective size
Coancestry (pedigrees)	55
Inbreeding (pedigrees)	78
LD	81

Lacaune

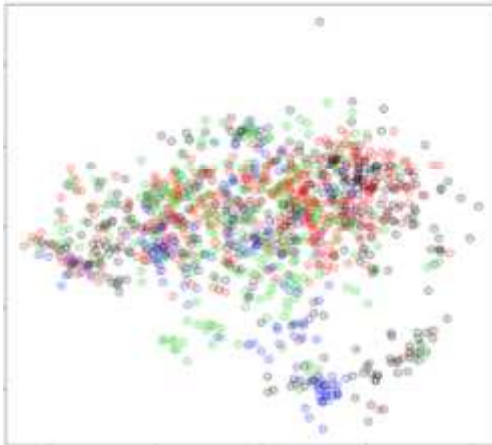
Indicator	Effective size
Coancestry (pedigrees)	231
Inbreeding (pedigrees)	182
LD	216

► Genetic diversity more important in the Lacaune breed (900 000 ewes in 2010) than in the Montbeliard breed (666 000 cows in 2010)

► Whatever the method, similar order of magnitude within a given breed

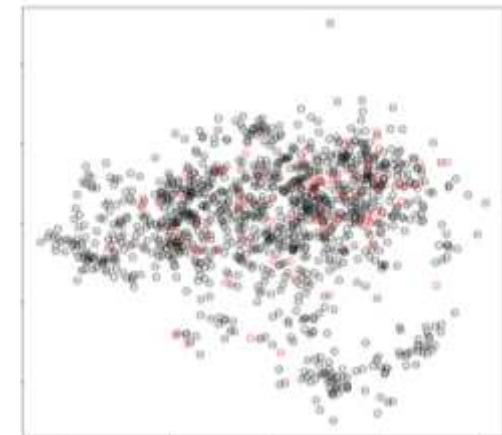
Other results for the Montbeliard breed

- Impact of external genes on the grouping of the coancestry matrix ?



Red Holstein genes (%)	<=0]0-5]]5-10]]10-15]]15-25]
Frequency	32.9%	29.0%	25.6%	11.9%	0.6%
Color	Black	Red	Green	Blue	Blue

=> External genes are a significant factor, however grouping not very consistent



- AI bulls in the French National Cryobank (red dots)

Discussion and perspectives

▶ Sampling issues

- ✓ Genotyped animals with various birthdates (Montbeliard: from 1982 to 2004; Lacaune: from 1996 to 2005).
- ✓ Last birth date = 2004, i.e. **before** genomic selection => need to an update for the genetic variability indicators.
- ✓ Study only based on **males**. However, in dairy breeds natural service is almost non existent to create reproducers.

▶ Perspectives

- ✓ Use of SNP genotypes to characterize the genetic variability of a breed = **feasible** + **coherent results** with indicators obtained with pedigree data.
- ✓ Study to be continued to all dairy breeds with numerous SNP data (i.e. two more dairy cattle breeds and three more dairy sheep breeds).
- ✓ Use of all available genotyped data, i.e. including young males.



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