MAS using a dense SNP markers map:
Application to the Normande and Montbéliarde breeds

Guillaume F., Fritz S. , Ducrocq V., Croiseau P. and Boichard D.




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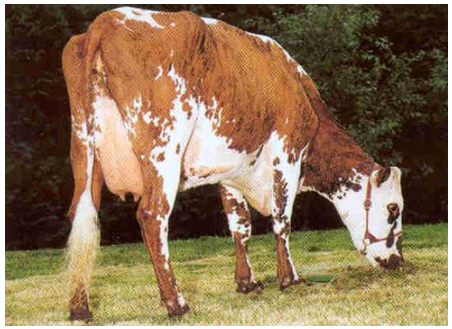
Introduction

- France has run a MAS program since 2001 in the three main dairy breeds (Holstein, Normande and Montbeliarde)
- In 2008, 54k SNP chip available
- Find a solution convenient for all breeds, in a short time.
  - QTL detection
  - Simple haplotype based model
- Promising results in Holstein

➔ **What are the results in « smaller » breeds ?**

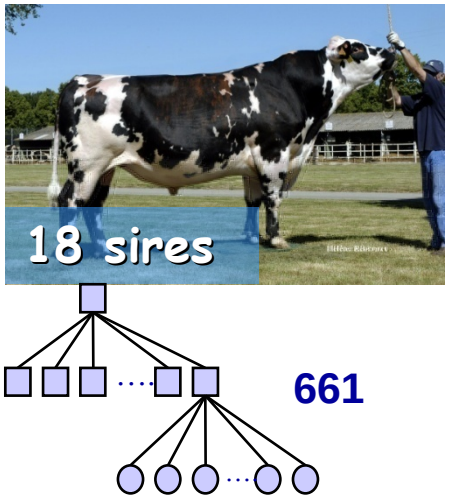
Normande and Montbéliarde, two medium size breeds

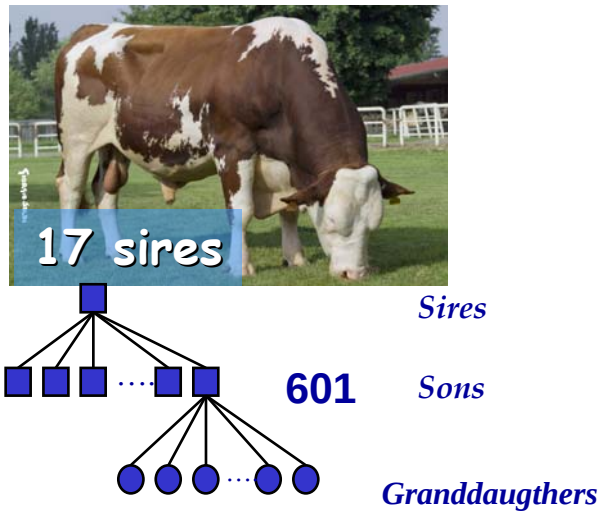
- Normande
  - 387 000 recorded Cows
  - ~150 progeny tested Bulls /year



- Montbeliarde
  - 263 000 recorded Cows
  - ~150 progeny tested Bulls /year

Fine-mapping resource population





- ~600 sires/breed genotyped with the 54k SNP chip
- 15 traits
- LD-LA analysis

➔ Confirm and Fine Map QTL

➔ Identify Haplotypes in LD with QTL

QTL detection : Results

- **Numerous QTL** have been found for each traits
- Most QTL are **breed specific**
- QTL detection more **problematic in smaller population**

➔From 40 to 50 % of Genetic Variance can be explained by « reliable» QTL => MA-Evaluation

French MAS Model

- Haplotype based model

$$y_i = \mu + u_i + x_i' h + e_i$$

  - y_i is the phenotype of individual i (DYD)
  - μ is an intercept
  - u_i is the polygenic effect of individual i
  - h is a vector of hapotypes' effects (IBS)
  - x_i is an incidence vector
  - e_i is a random residual

- Variance component:
  - From 31% to 44 % of genetic variance explained by 17 to 38 QTL in Normande breed
  - From 33 % to 43 % of genetic variance explained by 15 to 27 QTL in Montbeliarde breed

Validations samples (October 2008)

- 152 Normands and 144 Montbeliards candidates
- 2004 information of these candidates available
- Ending progeny test in 2008

For these candidates, correlation between :

- **DYD** observed in 2008
- **Polygenic or MA-EBV** based on available phenotypes in 2004
- (Weighted by 2008 DYD's EDC)

First results

	Normande		Montbeliarde	
Traits	Correlation (DYD2008 x MA-EBV2004)	Increase Compared to polygenic EBV	Correlation (DYD2008 x MA-EBV2004)	Increase Compared to polygenic EBV
Milk Yield	0,560	0,274	0,550	**0,289**
Fat Yield	0,543	**0,123**	**0,480**	0,236
Prot Yield	0,523	0,263	0,494	0,266
F%	0,699	0,139	0,664	0,187
P%	0,584	**0,289**	0,638	0,161
SCC	0,587	0,187	0,599	**0,131**
FER	**0,434**	0,173	0,496	0,224

- Correlations are improved
- …Improvement are lower than in Holstein
- Validation sample remain small…

Second validation

- January 2009 (New MAS program running for 3 months)
  - Montbeliarde population increase :
    - 601 -> 921 genotyped population
    - 144 ->277 candidates
- Validation :

	Milk Yield	Fat Yield	Prot Yield	F%	P%
MAS Oct08 (144)	0.55	0.48	0.49	0.66	0.63
MAS Jan09 (144)	0.56	0.56	0.51	0.65	0.53
MAS Jan09 (227)	**0.42**	**0.44**	**0.38**	**0.58**	**0.54**

- Figures getting lower, mostly due to the newly genotyped candidates

Second validation

- New genotyped candidates :
  - Less related to animal used in QTL detection
  - Coming from smaller family

➔The model needs to better fit the structure of the population

  - Frequent fine mapping study to update model
  - Lowering significance threshold ?

➔Due to population size, validation of the model remains hazardous

➔Are the challenges faced by smaller population the same as in the Holstein population ?

Comparisons

- Compared to Holstein :
  - Correlations are lower ➔ Less QTL included , less variance explained by them in the model
  - Validation is more hazardous
  - Computing time lower
- Comparisons with genome wide evaluation (work still in progress):
  - Results are of the same order
    - Cf P.Croiseau's

    (presentation (session 28))
  - Compatible with monthly evaluation

Conclusions

- Haplotype-based model may provide a first solution to small population needs
  ➔ **Use of SNP can enhance evaluation** even in smaller population

- Time to reach a critical population size will take longer than for bigger population

- Validation of the model will also take longer

Acknowledgements

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- Institut de l'élevage
- INRA
- UNCEIA
- Labogena

Thank you for your attention

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