

Genetic evaluation considering phenotypic data and limited molecular information using a novel equivalent model:
Case study using effect of the *mh* locus on milk production in the dual-purpose Belgian Blue breed

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Context

- In 1973, Mid and High Belgian breed was divided officially into 2 types
- 1st type: Meat Belgian Blue



Young bull Cow

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Context

- Meat Belgian Blue (BBB)
 - Double muscling phenotype
 - Muscle Hypertrophy (*mh*) syndrome
 - *mh* locus located on BTA2
 - Caused by 11 bp deletion in *Myostatin* gene
 - ✓ *mh* allele: deletion
 - ✓ + allele: allele without deletion
 - ✓ *mh* allele frequency close to 100 %

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Context

- 2nd type: Dual Purpose Belgian Blue (DP-BBB)
 - Local breed in Belgium
 - Close related to the Bleue du Nord (in France)
 - Vulnerable status (FAO criteria)
 - Stable

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Context

- Dual Purpose Belgian Blue (DP-BBB)
 - Average milk yield: 4,000 kg (up to 7,000 kg)
 - Strong muscling (less caesareans)
 - *mh* allele
 - ✓ less frequent than BBB (60 %)

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Context

- Dual Purpose Belgian Blue (DP-BBB)
 - Importance of *mh* allele in breeding
 - Perception of genotype by breeders
 - ✓ +/+ : dairy
 - ✓ *mh/mh* : beef
 - ✓ *mh/+* : intermediate

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Context

- DP-BBB: *mh/mh*



CHARLY *mh/mh*

Bull




Cow

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Context

- DP-BBB: *mh/+*



PAGNON *mh/+*

Bull

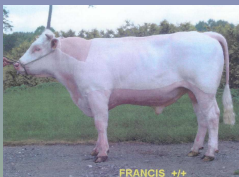


Cow

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Context

- DP-BBB: *+/+*



FRANCIS *+/+*

Bull



Cow

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Context

- Dual Purpose Belgian Blue (DP-BBB)
 - Cows of 3 genotypes recorded
 - Cows evaluated during routine run

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General objective

- mh* allele could influence milk production
- Breeders used for selection decisions
 - Pedigree
 - Estimated Breeding Value (EBV)
 - Knowledge of genotype
- But limited molecular information
 - need a practical method to integrate molecular information

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Methodology

- Mixed Inheritance Model
 - Combining fixed gene effects **g** and random polygenic **u** effects

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{ZQg} + \mathbf{Zu} + \mathbf{e}$$
 - Usual assumptions concerning distribution of random effects

$$E \begin{bmatrix} \mathbf{u} \\ \mathbf{e} \end{bmatrix} = \begin{bmatrix} \mathbf{0} \\ \mathbf{0} \end{bmatrix} \text{ and } \text{Var} \begin{bmatrix} \mathbf{u} \\ \mathbf{e} \end{bmatrix} = \begin{bmatrix} \mathbf{G} & \mathbf{0} \\ \mathbf{0} & \mathbf{R} \end{bmatrix}$$

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Methodology

- Equivalent Mixed Inheritance Model
 - Fixed gene effects and random polygenic effects replaced by a combined genetic effect u^*

$$y = X\beta + Zu^* + e \text{ where } u^* = Qg + u$$
 - Modification of assumptions

$$E \begin{bmatrix} u^* \\ e \end{bmatrix} = \begin{bmatrix} Qg \\ 0 \end{bmatrix} \text{ and } \text{Var} \begin{bmatrix} u^* \\ e \end{bmatrix} = \begin{bmatrix} G & 0 \\ 0 & R \end{bmatrix}$$

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Methodology

- Associated Mixed Model Equations
 - Following Quaas (*J. Dairy Sci.* 1988, 71, 1338-1345)
 - Same strategy to integrate genetic groups
 - Joint estimation of β , u^* and g

$$\begin{bmatrix} X'R^{-1}X & X'R^{-1}Z & 0 \\ Z'R^{-1}X & Z'R^{-1}Z + G^{-1} & -G^{-1}Q \\ 0 & -Q'G^{-1} & Q'G^{-1}Q \end{bmatrix} \begin{bmatrix} \hat{\beta} \\ \hat{u}^* \\ \hat{g} \end{bmatrix} = \begin{bmatrix} X'Ry \\ Z'Ry \\ 0 \end{bmatrix}$$

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Methodology

- Associated Mixed Model Equations

$$\begin{bmatrix} X'R^{-1}X & X'R^{-1}Z & 0 \\ Z'R^{-1}X & Z'R^{-1}Z + G^{-1} & -G^{-1}Q \\ 0 & -Q'G^{-1} & Q'G^{-1}Q \end{bmatrix} \begin{bmatrix} \hat{\beta} \\ \hat{u}^* \\ \hat{g} \end{bmatrix} = \begin{bmatrix} X'Ry \\ Z'Ry \\ 0 \end{bmatrix}$$
 - Solving of whole system is equivalent of solving iteratively two systems of equations
 - ✓ 1st, solving for the third row

$$Q'G^{-1}Q\hat{g} = Q'G^{-1}\hat{u}^*$$

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Methodology

- Associated Mixed Model Equations

$$\begin{bmatrix} X'R^{-1}X & X'R^{-1}Z & 0 \\ Z'R^{-1}X & Z'R^{-1}Z + G^{-1} & -G^{-1}Q \\ 0 & -Q'G^{-1} & Q'G^{-1}Q \end{bmatrix} \begin{bmatrix} \hat{\beta} \\ \hat{u}^* \\ \hat{g} \end{bmatrix} = \begin{bmatrix} X'Ry \\ Z'Ry \\ 0 \end{bmatrix}$$
 - Solving of whole system is equivalent of solving iteratively two systems of equations
 - ✓ 2nd, solving the system

$$\begin{bmatrix} X'R^{-1}X & X'R^{-1}Z \\ Z'R^{-1}X & Z'R^{-1}Z + G^{-1} \end{bmatrix} \begin{bmatrix} \hat{\beta} \\ \hat{u}^* \end{bmatrix} = \begin{bmatrix} X'R^{-1}y \\ Z'R^{-1}y + G^{-1}Q\hat{g} \end{bmatrix}$$

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Methodology

- Associated Mixed Model Equations
 - Solving iteratively until relative differences in estimation of $g < 10^{-5}$
- Advantages
 - Could allow solving when only limited number of genotyped animals
 - Gene effect could be estimated from limited known genotypes

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Material

- Data used for official January 2009 genetic evaluations in the Walloon Region of Belgium
 - Pedigree: 1,606,024 animals
 - Data: 11,117,505 Test Day (TD) records (2009)
10,019,460 TD recorded before 2003
 - 689,057 cows with production records

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Material

- Molecular information
 - *mh* genotypes available
 - ✓ 108 DP-BBB bulls
 - ✓ 1,891 DP-BBB cows with production records
 - Offspring of genotyped animals
 - ✓ 11,768 cows with production records

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Model

- Random regression test-day model
 - Official Walloon Model used for routine run
 - 4 evaluation runs

	TD recorded before 2003	TD recorded before 2009
Genotypes NOT integrated	2003	2009
Genotypes integrated	2003mh	2009mh

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Results

- *mh* allele substitution effect estimated with the equivalent model

Trait	Based on data recorded before	
	2009 (11,117,505 TD)	2003 (10,019,460 TD)
Milk yield (kg/305 d of lact)	-158.7	-149.9
Fat yield (kg/305 d of lact)	-8.93	-8.23
Protein yield (kg/305 d of lact)	-5.64	-5.16

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Results

- Correlations between EBVs for Milk Yield
 - All animals

Category	N	2009mh vs. 2009	2009mh vs. 2003mh	2009 vs. 2003
		All evaluated	1,606,024	1.000
DP-BBB	18,254	0.852	0.860	0.823
Offspring of genotyped DP-BBB	11,768	0.796	0.865	0.570

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Results

- Correlations between EBVs for Milk Yield
 - Cows with TD only recorded since 2003

Category	N	2009mh vs. 2009	2009mh vs. 2003mh	2009 vs. 2003
		All evaluated	58,695	0.997
DP-BBB	3,536	0.841	0.629	0.416
Offspring of genotyped DP-BBB	1,464	0.717	0.593	0.468

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Results

- Coefficients of Regression between EBVs for Milk Yield
 - All animals

Category	N	2003mh on 2009mh	2003 on 2009
		All evaluated	1,606,024
DP-BBB	18,254	0.832	0.698
Offspring of genotyped DP-BBB	11,768	0.885	0.752

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Results

- Coefficients of Regression between EBVs for Milk Yield
 - Cows with TD only recorded since 2003

Category	N	2003mh	2003
		on	on
		2009mh	2009
All evaluated	58,695	0.785	0.767
DP-BBB	3,536	0.547	0.201
Offspring of genotyped DP-BBB	1,464	0.606	0.290

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Conclusion

- Equivalent mixed inheritance model
 - We can use incomplete genotyped population
- Estimation of allele substitution effects
 - Results as expected

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Conclusion

- For all animals
 - Great majority is unrelated to genotyped animals
 - Minimal changes compared to original model
- For DP-BBB animals
 - Higher correlations and coefficients of regression

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Thank you for your attention

- Study related to two European projects



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