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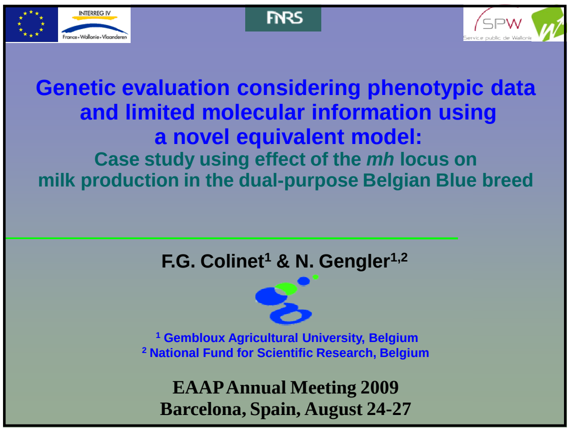

Genetic evaluation considering phenotypic data and limited molecular information using a novel equivalent model:
Case study using effect of the *mh* locus on milk production in the dual-purpose Belgian Blue breed

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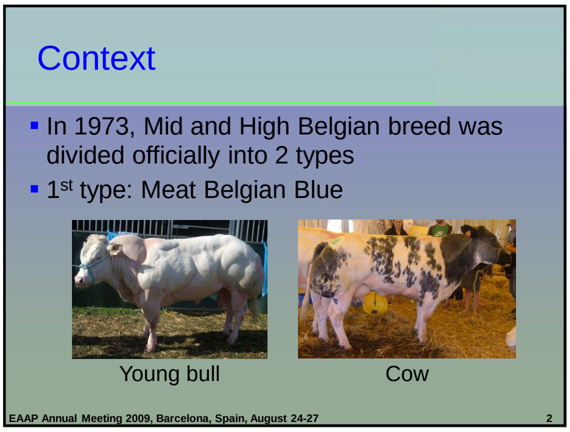
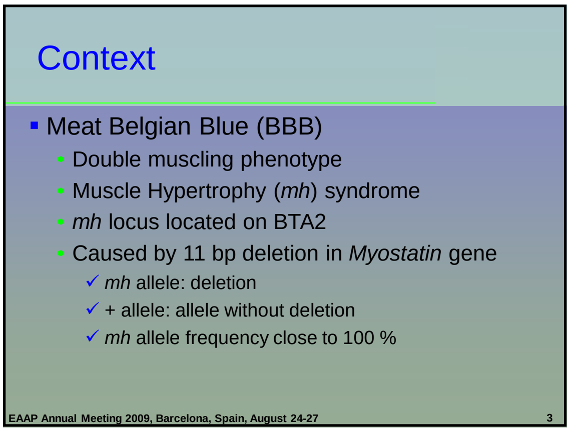


Context

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

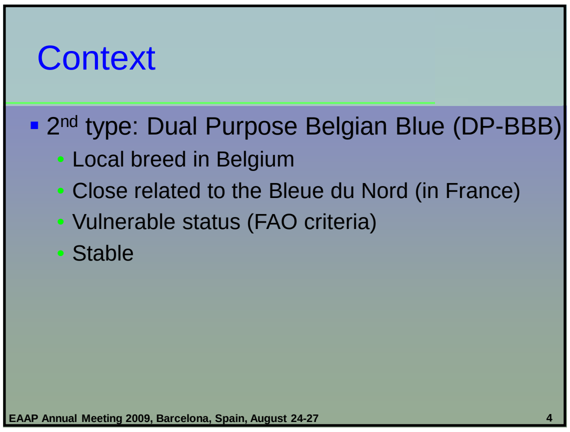
Young bull

Cow



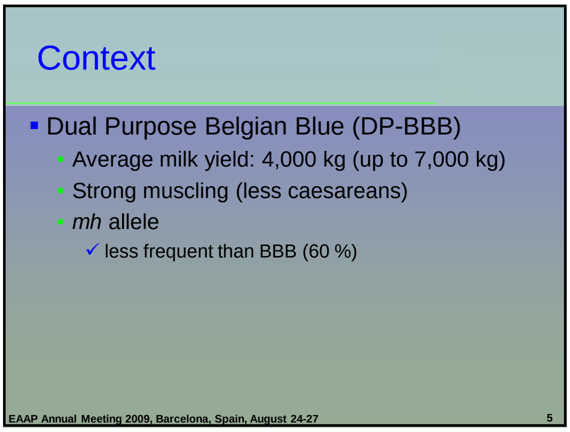
Context

- 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 %



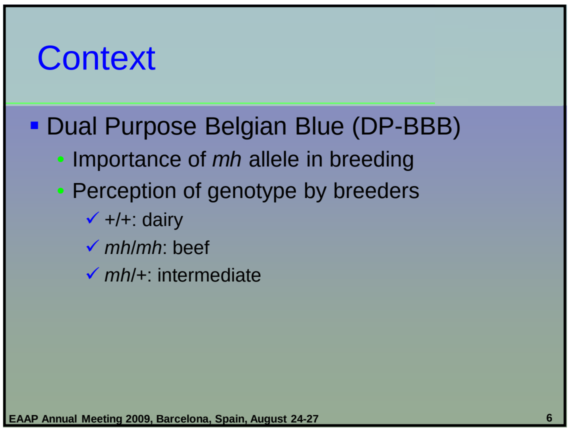
Context

- 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



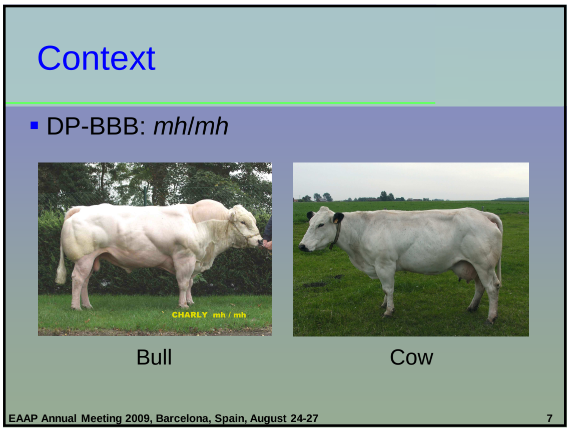
Context

- 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 %)



Context

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

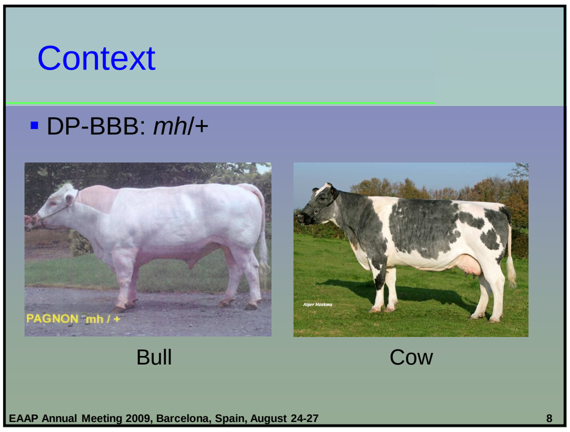


Context

- DP-BBB: *mh/mh*

Bull

Cow

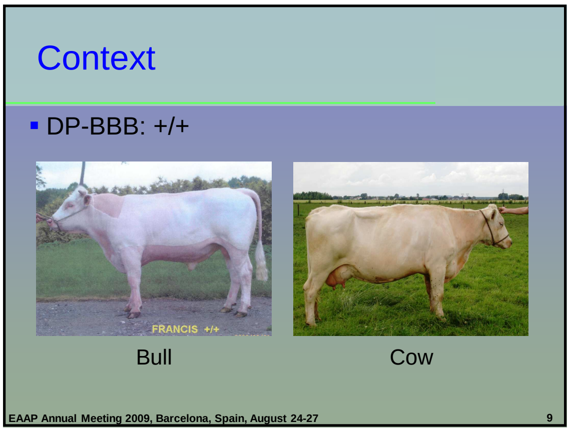


Context

- DP-BBB: *mh*/+

Bull

Cow



Context

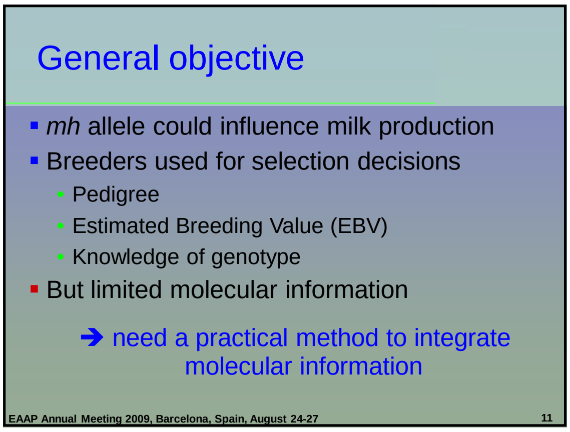
- DP-BBB: +/+

Bull

Cow

Context

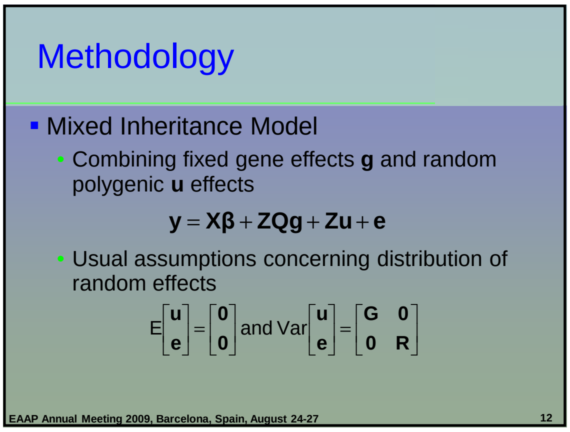
- Dual Purpose Belgian Blue (DP-BBB)
  - Cows of 3 genotypes recorded
  - Cows evaluated during routine run



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



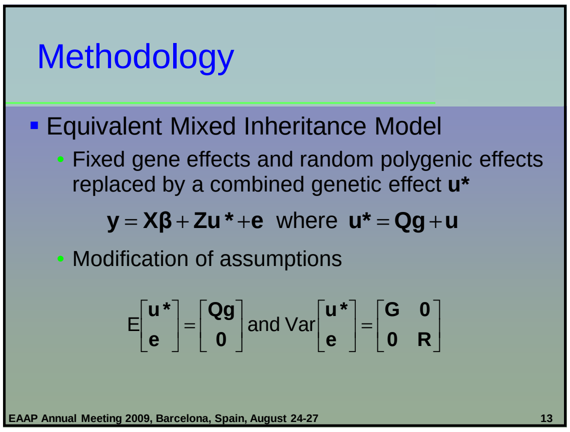
Methodology

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

$$\mathbf{y} = \mathbf{X\beta} + \mathbf{ZQg} + \mathbf{Zu} + \mathbf{e}$$

  - Usual assumptions concerning distribution of random effects

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



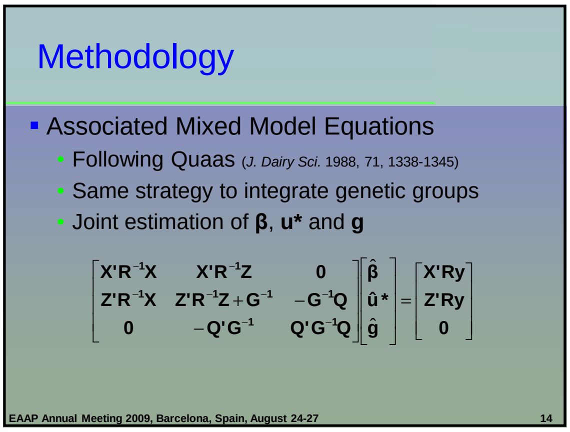
Methodology

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

$$\mathbf{y} = \mathbf{X\beta} + \mathbf{Zu^*} + \mathbf{e} \quad \text{where} \quad \mathbf{u^*} = \mathbf{Qg} + \mathbf{u}$$

  - Modification of assumptions

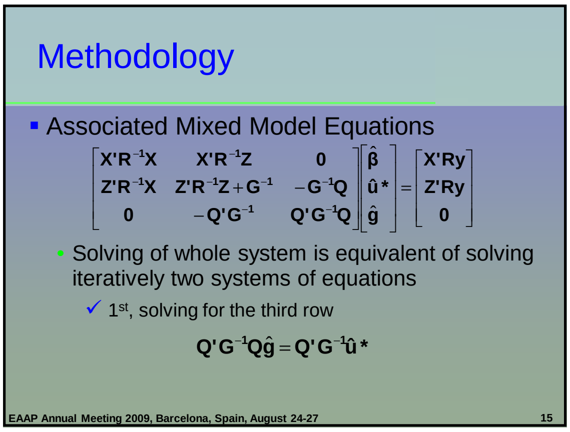
$$\mathrm{E}\begin{bmatrix}\mathbf{u^*}\\ \mathbf{e}\end{bmatrix} = \begin{bmatrix}\mathbf{Qg}\\ \mathbf{0}\end{bmatrix} \text{ and } \mathrm{Var}\begin{bmatrix}\mathbf{u^*}\\ \mathbf{e}\end{bmatrix} = \begin{bmatrix}\mathbf{G} & \mathbf{0}\\ \mathbf{0} & \mathbf{R}\end{bmatrix}$$



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**

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



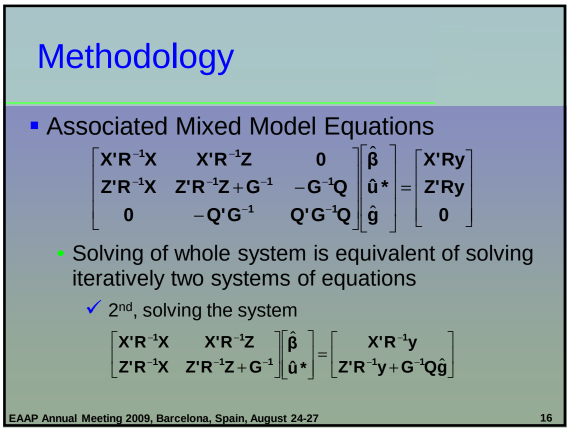
Methodology

- Associated Mixed Model Equations

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

  - Solving of whole system is equivalent of solving iteratively two systems of equations
    - ✓ 1st, solving for the third row

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



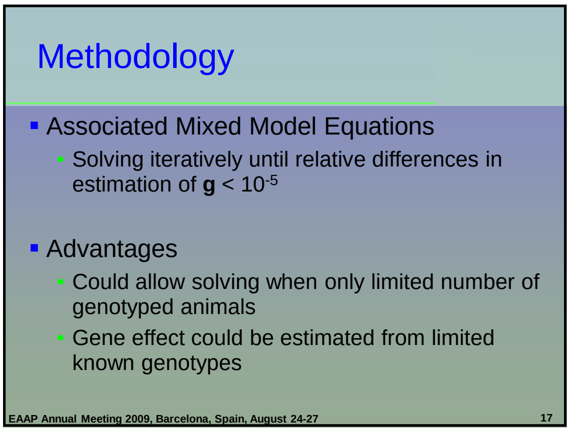
Methodology

- Associated Mixed Model Equations

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

  - Solving of whole system is equivalent of solving iteratively two systems of equations
    - ✓ 2nd, solving the system

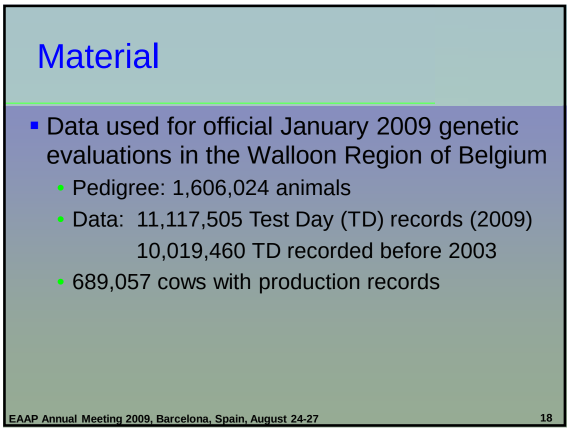
$$\begin{bmatrix}\mathbf{X'R^{-1}X} & \mathbf{X'R^{-1}Z}\\ \mathbf{Z'R^{-1}X} & \mathbf{Z'R^{-1}Z} + \mathbf{G^{-1}}\end{bmatrix}\begin{bmatrix}\hat{\boldsymbol\beta}\\ \hat{\mathbf{u}}^*\end{bmatrix} = \begin{bmatrix}\mathbf{X'R^{-1}y}\\ \mathbf{Z'R^{-1}y} + \mathbf{G^{-1}Q}\hat{\mathbf{g}}\end{bmatrix}$$



Methodology

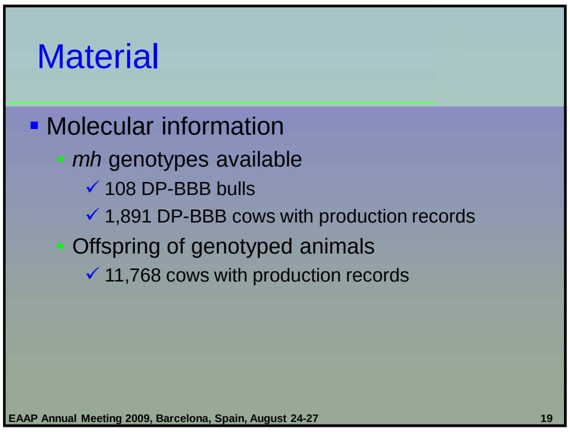
- Associated Mixed Model Equations
  - Solving iteratively until relative differences in estimation of **g** < 10^{-5}

- Advantages
  - Could allow solving when only limited number of genotyped animals
  - Gene effect could be estimated from limited known genotypes



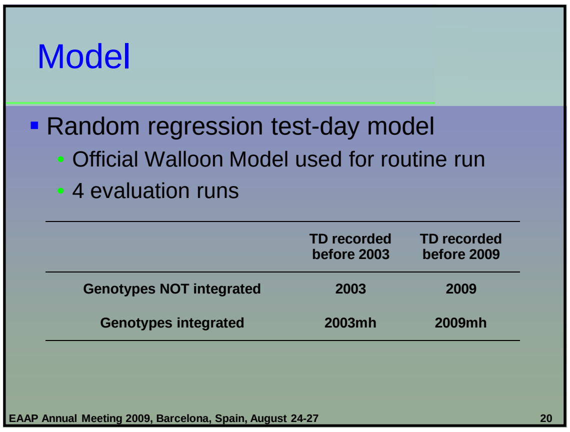
Material

- 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



Material

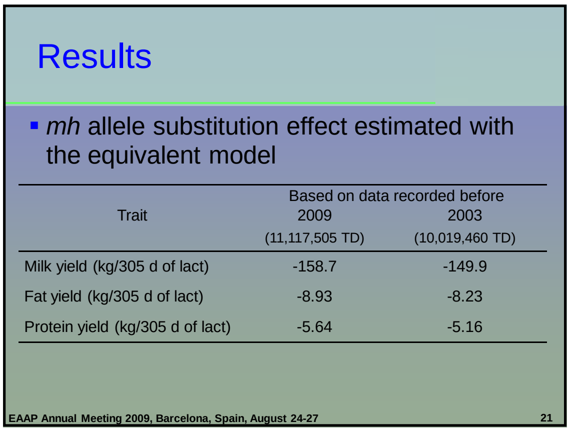
- Molecular information
  - *mh* genotypes available
    - ✓ 108 DP-BBB bulls
    - ✓ 1,891 DP-BBB cows with production records
  - Offspring of genotyped animals
    - ✓ 11,768 cows with production records



Model

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

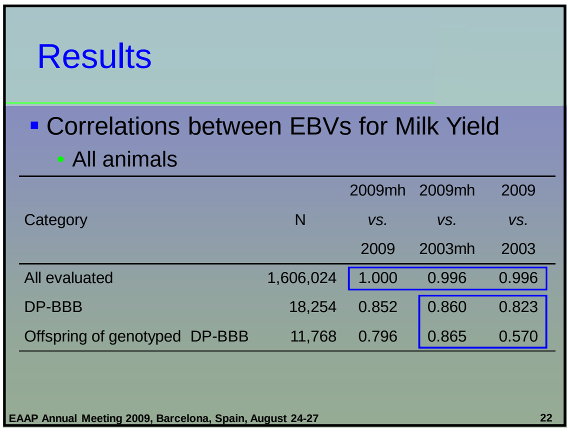
	TD recorded before 2003	TD recorded before 2009
Genotypes NOT integrated	**2003**	**2009**
Genotypes integrated	**2003mh**	**2009mh**



Results

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

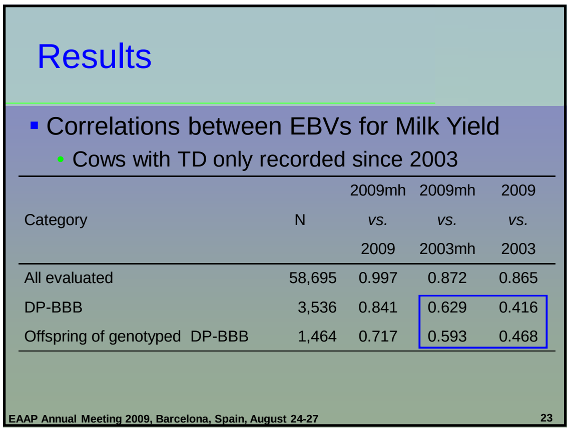
Trait	Based on data recorded before 2009 (11,117,505 TD)	2003 (10,019,460 TD)
Milk yield (kg/305 d of lact)	-158.7	-149.9
Fat yield (kg/305 d of lact)	-8.93	-8.23
Protein yield (kg/305 d of lact)	-5.64	-5.16



Results

- Correlations between EBVs for Milk Yield
  - All animals

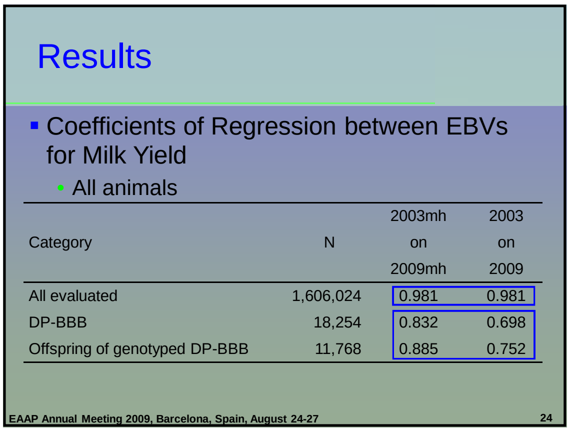
Category	N	2009mh *vs.* 2009	2009mh *vs.* 2003mh	2009 *vs.* 2003
All evaluated	1,606,024	1.000	0.996	0.996
DP-BBB	18,254	0.852	0.860	0.823
Offspring of genotyped DP-BBB	11,768	0.796	0.865	0.570



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	0.872	0.865
DP-BBB	3,536	0.841	0.629	0.416
Offspring of genotyped DP-BBB	1,464	0.717	0.593	0.468



Results

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

Category	N	2003mh on 2009mh	2003 on 2009
All evaluated	1,606,024	0.981	0.981
DP-BBB	18,254	0.832	0.698
Offspring of genotyped DP-BBB	11,768	0.885	0.752

Results

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

Category	N	2003mh on 2009mh	2003 on 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

Conclusion

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

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

Thank you for your attention

- Study related to two European projects
- Acknowledgments
  - European Commission
  - Walloon Regional Ministry of Agriculture
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  - Walloon Breeding Association (AWE)

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