

Implementing a national routine genetic evaluation for milk fat compositions as first step towards genomic predictions

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Context

Walloon Region of Belgium:

- collecting fatty acid composition since March 2005
- first experimental on 25 farms
- **currently nearly all cows under milk recording**



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864 835 test-days with fatty acid (all-lactation)

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INTERBULL Report 2010:

development of a genetic evaluation system

Context

This report:

- Status of the data collection
 - Status of the model and needed (co)variances
 - Expressing results
 - Nutritional Quality Index (NQI)
 - First computations and results
 - Some examples of evaluated sires
 - Towards genomic predictions
 - Using MACE for correlated traits
 - A proposal !
 - Other traits
- 

Status of Data Collection

➤ **Reminder:**

- ❑ **fatty acids (FA)** predicted from MIR spectral data
- ❑ use of latest equation (Soyeurt et al., 2011)

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March 2012:

2 150 404 test-day MIR spectra records (all-lactation)

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**We are adding approximately
55 000 FA records / month**

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Status of Model and (Co)variances

- Previous research done has shown for milk fat composition traits (e.g., Soyeurt et al., 2008):
 - ❑ **genetic variation** and
 - ❑ **medium to high heritabilities**
 - **Some modelling** issues however:
 - ❑ repeated records
 - ❑ longitudinal traits
 - ❑ highly correlated traits
 - ❑ with traditional traits (milk, fat, protein)
 - ❑ among different fatty acids and fatty acid groups
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Use of historical test-day data



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Large number of relevant traits



Status of Model and (Co)variances

- Selection of traditional traits
 - ❑ based on **INTERBULL traits**
 - ❑ milk, fat, and protein yield
- Selection of milk fat composition traits
 - ❑ based on potential place in breeding goal
 - ❑ milk pricing
 - ❑ **saturated fatty acid content** (SFA) in milk (g/100g)
 - ❑ potentially health related
 - ❑ **monounsaturated fatty acid content** (MUFA) in milk (g/100g)

⇒ **ML – MT – TD – RRM**

Status of Model and (Co)variances

- Heritabilities (**diagonal**) and used genetic correlations (above) expressed on a lactation base
-

Trait	Trait				
	MILK	FAT	PROT	SFA	MUFA
MILK (kg)	0.37	0.91	0.97	-0.28	-0.38
FAT (kg)		0.43	0.93	0.00	0.01
PROT (kg)			0.41	-0.22	-0.23
SFA (%)				0.71	0.40
MUFA (%)					0.56

Status of Model and (Co)variances

Banded

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Expressing Results?

- Should be based on breeding goal !
 - Two potential components could contribute to breeding goal (even if there is no consensus)
 - ❑ **trends In milk pricing:** SFA
 - ❑ **potentially human health related:** MUFA
 - To avoid: risk of deleterious effects on other important traits especially milk and fat
 - Solution: **restricted selection index**
 - ❑ Std. relative “a values”: **-1 SFA and +1 MUFA**
 - ❑ **Restricting changes** in milk and fat yields to 0 !!!
 - ❑ Computation of “b values”
- 

Expressing Results

- Computation of **Nutritional Quality Index (NQI)**
- **Standardized b values:**
 - ❑ Milk yield : + 0.478
 - ❑ Fat yield : - 0.425
 - ❑ Protien yield : 0.000
 - ❑ SFA: - 0.934
 - ❑ MUFA: + 0.934
- Some parameters for **Nutritional Quality Index (NQI)**

- ❑ Heritability: **0.54**

- ❑ Correlation with

MILK	FAT	PROT	SFA	MUFA
0.00	0.00	0.05	-0.69	0.38

First Computations and Results

➤ Data from 1st, 2nd and 3rd lactation

Trait*	N	Mean	SD
MILK (kg)	16 029 574	18.80	8.10
FAT (kg)	16 024 529	0.75	0.34
PROT (kg)	15 992 387	0.62	0.25
PFAT (%)	16 024 529	4.03	0.74
PPROT (%)	15 992 387	3.37	0.41
SFA (%)	1 168 692	2.85	0.57
MUFA (%)	1 169 520	1.15	0.27

* FAT = fat yield, PROT = protein yield, PFAT = fat content, PPROT = protein content, SFA = saturated fatty acid content in milk and MUFA = monounsaturated fatty acid content in milk

First Computations and Results

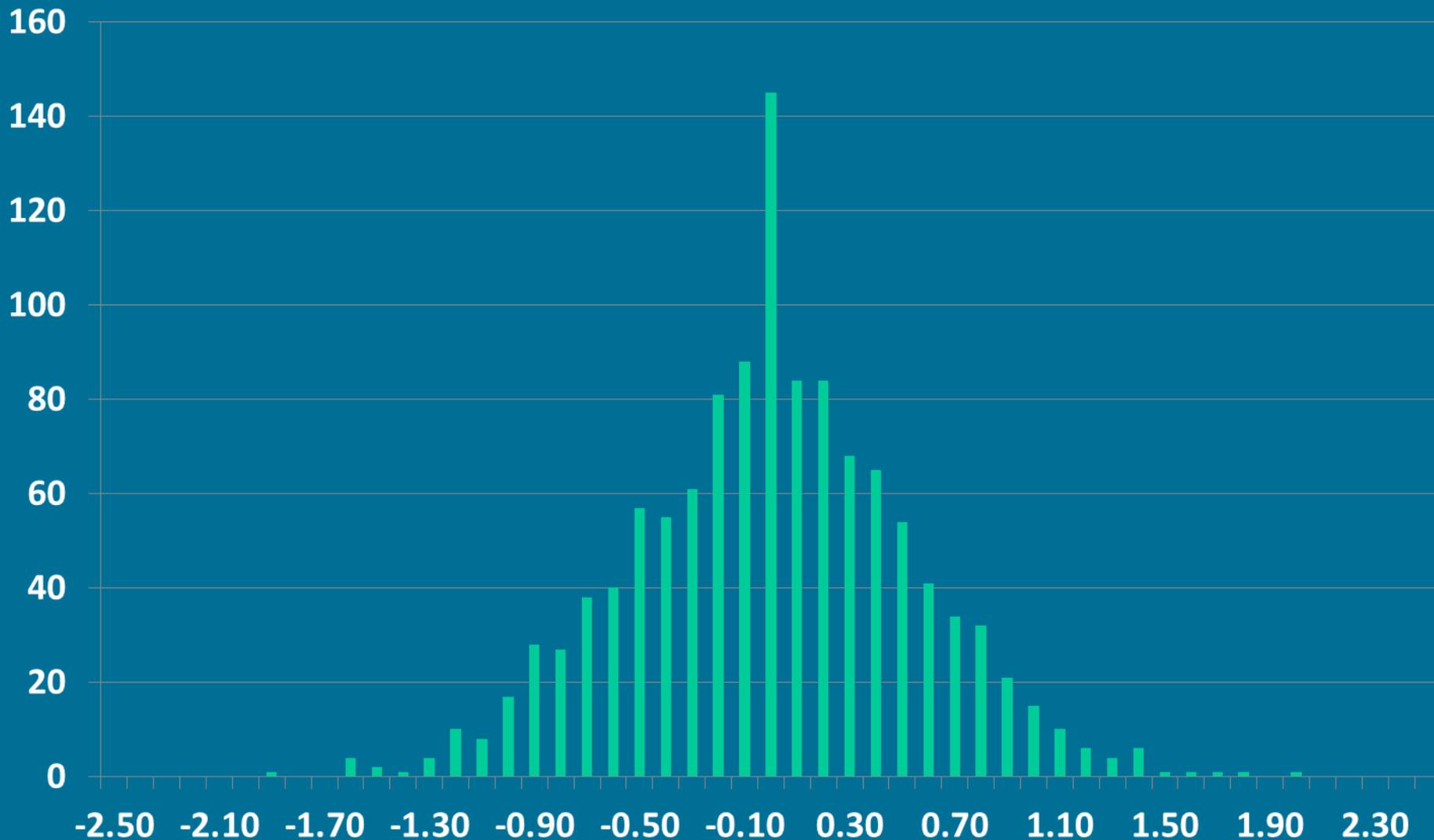
- **EBV** for SFA and MUFA and **NQI**
genetic base put to cow with FA records born 2005
(1196 sires $REL \geq 0.50$ and at least one daugh. with SFA/MUFA record)
-

Trait	EBV		REL	
	Mean	SD	Mean	SD
SFA (%)	0.022	0.252	0.77	0.13
MUFA (%)	-0.008	0.053	0.71	0.14
NQI (standardized)	-0.10	0.69	0.75	0.13



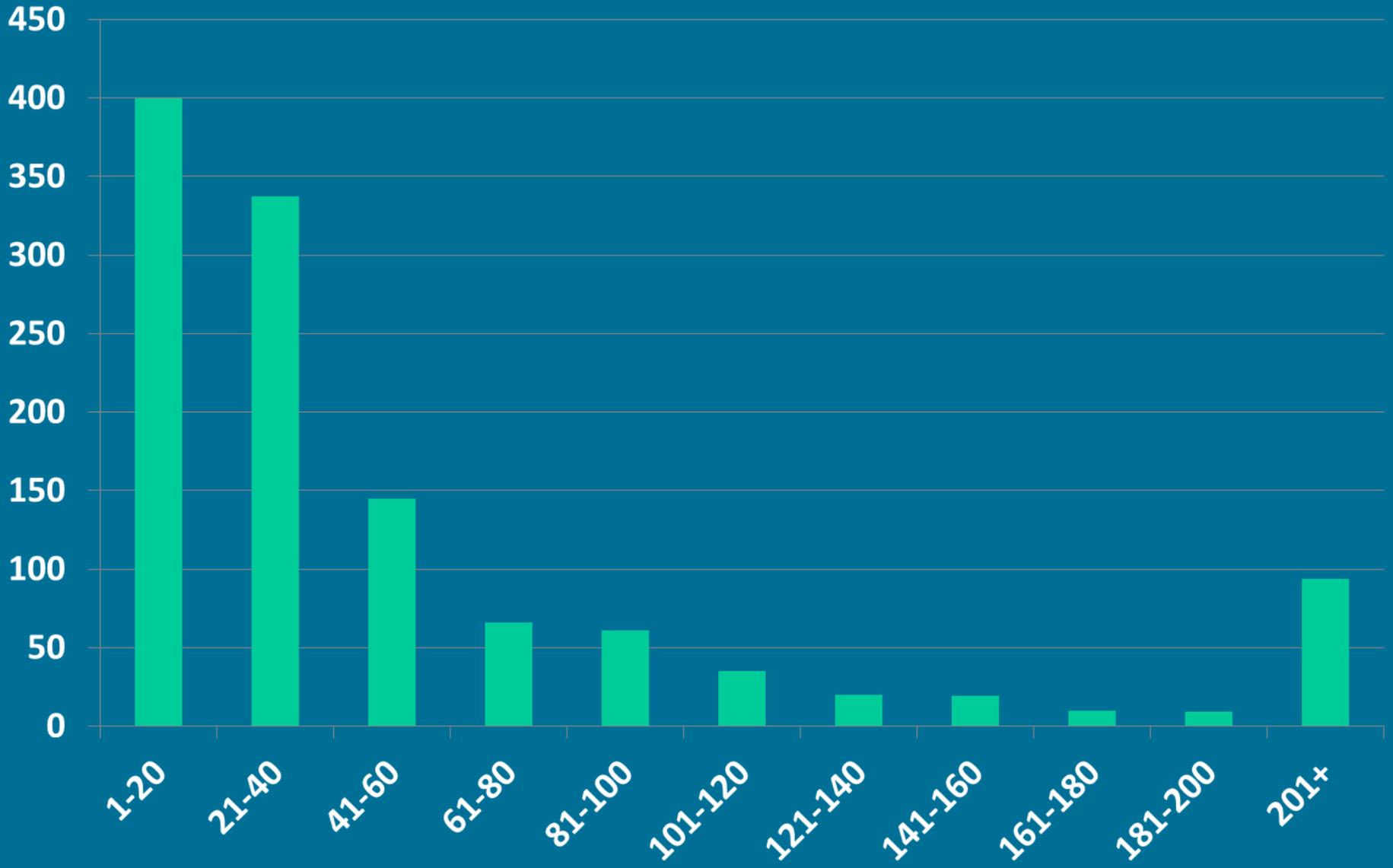
Distribution of NQI

(1196 sires REL ≥ 0.50 and daugh. with SFA/MUFA)



Distribution of Daughters

(1196 sires $REL \geq 0.50$ and daugh. with SFA/MUFA)



Some Bulls (Nearly Random)

Number of Herds and Daughters with FA Records

Name	Herds	Daughters
ALZI JUROR FORD	229	719
BRAEDALE GOLDWYN	166	593
CAROL PRELUDE MTOTO-ET	109	231
COMESTAR LEE	240	528
ETAZON LORD LILY	65	108
FABER ET	191	594
JOCKO BESN	439	1658
LADINO PARK TALENT-IMP-ET	330	1175
LADYS-MANOR WILDMAN-ET	149	509
LONARD	459	1454
MANAT	330	1142
O-BEE MANFRED JUSTICE-ET	26	101
PICSTON SHOTTLE	49	106
RAMOS	159	519
RICECREST MARSHALL-ET	51	120
ROYLANE JORDAN-ET	218	624

Perspectives

➤ Adding more data:

- ❑ currently > 500,000 records added every year
- ❑ If international sires used ⇒ get reliable proofs

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- ❑ ongoing development **to integrate MACE EBV for MILK, FAT and PROT** (e.g., Vandenplas and Gengler, 2012)

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⇒ Towards Genomic Predictions

Remark on International Collaboration

- Phenotypes (the “**King**” in the World of Genomics):
 - ❑ Other countries getting FA records (potentially limited subpopulations)
 - ❑ Pooling phenotypes for FA makes sense!
 - ❑ Directly (**single evaluation**)
 - ❑ Indirectly (including **external EBV for FA**)
 - ❑ But also for **other traits** based on MIR:
 - ❑ **Collaboration and exchange**



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⇒ **Opportunity for partners to join forces**

More on International Collaboration

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combining all available phenotypes with genotypes
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- Until now **no genotype / phenotype collaboration for FA** on a genetic / genomic evaluation level

Towards Genomic Predictions

- Following under hypothesis local development



Towards Genomic Predictions

- Following under hypothesis local development
 - Single step method:
 - ❑ specific situation (ML-MT-TD-RRM) **well suited to use one step approach** (Aguilar et al., 2010)
 - ❑ integration of external MACE EBV straight forward as for normal BLUP only **A ⇒ H**
 - ❑ therefore information of all animals contributes (e.g. MACE EBV of ungenotyped ancestors)
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- ## ➤ Given arrangements (e.g., providing genotypes)
- base for service to provide **genomically enhanced NQI**

Conclusions

- Implementation of **genetic evaluation system for milk fat composition** in the Walloon Region of Belgium: Expected in **June 2012**
 - First step **towards genomic prediction** for novel traits
 - Not only FA trait, but all you can predict from MIR data
 - Example of another novel trait: **methane emissions**
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⇒ **Opportunity for collaborations**



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