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

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Context

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- collecting fatty acid composition since March 2005
- first experimental on 25 farms
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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)

April 2010:

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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 hertitabilities
- 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

- Heritabilies (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

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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

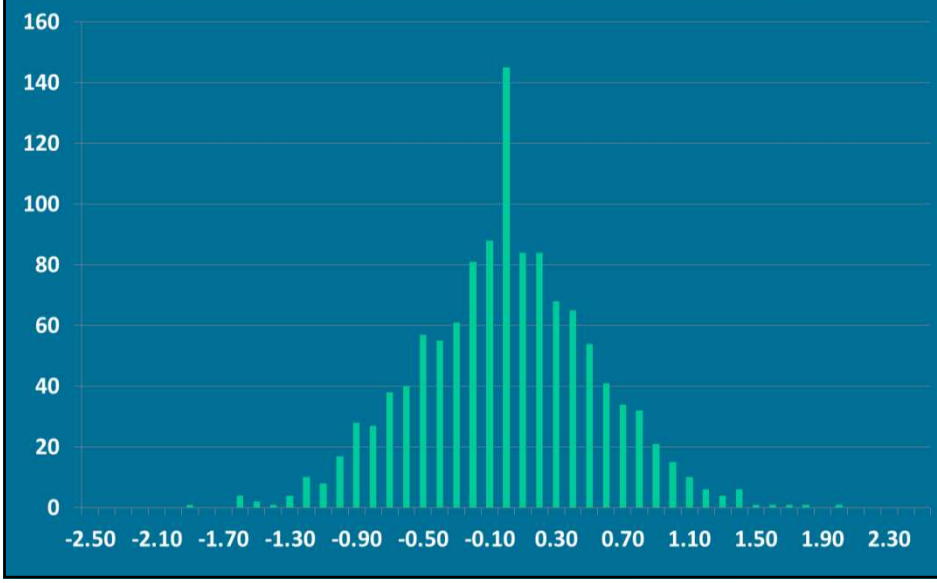
First Computations and Results

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

	EBV		REL	
Trait	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

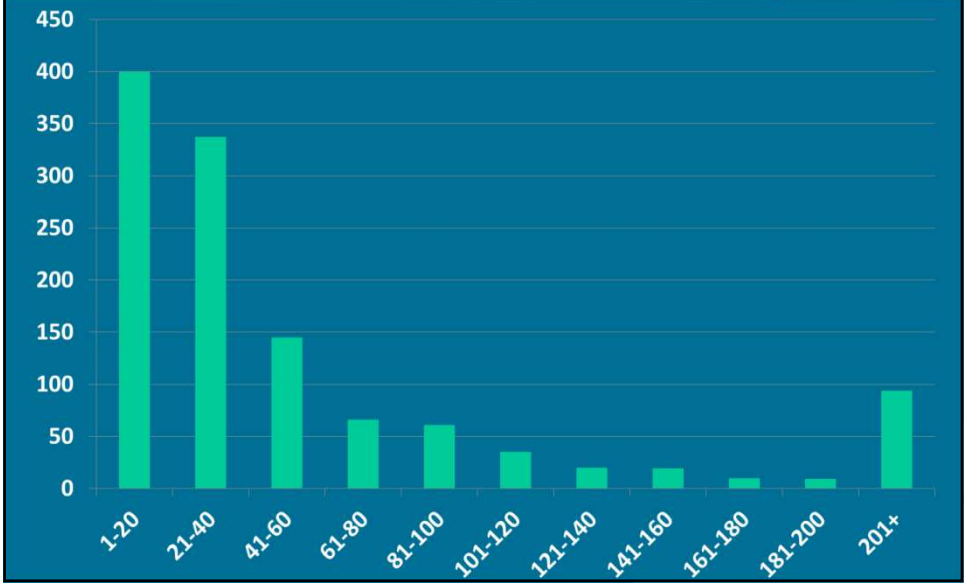
Distribution of NQI

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



Distribution of Daughters

(1196 sires REL ≥ 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:
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  - If international sires used ⇒ get reliable proofs

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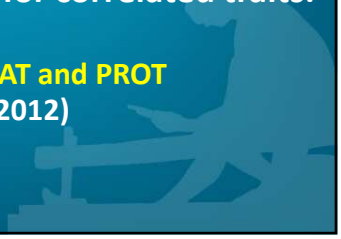

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⇒ Towards Genomic Predictions

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:
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⇒ Opportunity for partners to join forces

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- Until now no genotype / phenotype collaboration for FA on a genetic / genomic evaluation level

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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
  - first results indicate R^2_{cv} in the direction of 0.80 (Dehareng et al., 2012)
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