Implementing a genetic evaluation for milk fat composition in the Walloon Region of Belgium

Gengler, N.*[,1], Troch, T.[1], Bastin, C.[1], Vanderick, S.[1], Vandenplas, J.[1,2] and Soyeurt, H.[1,2]

[1] ULg - GxABT, Passage des Déportés, 2, 5030 Gembloux, Belgium

[2] FNRS, Rue d'Egmont, 5, 1000 Brussels, Belgium

nicolas.gengler@ulg.ac.be

- ✓ Genetic evaluation: key element in the improvement of traits of interest in dairy cattle
- ✓ Can provide practical breeding tools for milk fat composition to dairy farmers
- ✓ Milk fat composition defined by composition in fatty acids (FA)
- ✓ Data available based on mid-infrared (MIR) spectra routinely recorded through milk recording
- ✓ Genetic variation in FA already confirmed

- ✓ Multi-lactation (1-3 lactation)
- ✓ Multi-trait (milk, fat, protein yields)
  ⇒ extended to five traits
- ✓ Test-day random regression model
- ✓ Integrated correction of outliers based on residuals
- ✓ PCG solver ⇦ restart from old solutions
- ✓ Three computations / year (linked to INTERBULL runs)

Table 1. Yield and FA data available evaluation July 2012

Trait	First lactation			Second lactation			Third lactation		
	N	Mean	SD	N	Mean	SD	N	Mean	SD
Milk (kg)	7,086,538	17.2	6.99	5,302,270	19.6	8.71	3,791,717	20.9	9.26
Fat (kg)	7,084,217	0.69	0.29	5,300,728	0.79	0.36	3,790,564	0.84	0.39
Protein (kg)	7,064,771	0.57	0.22	5,293,333	0.66	0.28	3,785,262	0.69	0.29
Fat content (%)	7,084,217	4.02	0.88	5,300,728	4.04	0.82	3,790,564	4.04	1.37
Protein content (%)	7,064,771	3.33	0.49	5,293,333	3.41	0.49	3,785,262	3.39	0.91
Saturated FA (%)	559,935	2.78	0.55	436,787	2.89	0.59	309,321	2.90	0.59
Monounsaturated FA (%)	560,304	1.16	0.28	437,135	1.14	0.26	309,558	1.15	0.28

Table 2. Genetic parameters used

	Heritabilities and genetic correlations					
Trait	Milk	Fat	Protein	SFA	MUFA	NQI*
Milk (kg)	0.37	0.91	0.97	-0.28	-0.38	0.00
Fat (kg)		0.43	0.93	0.00	-0.01	0.00
Protein (kg)			0.41	-0.22	-0.23	0.05
Saturated FA (%)				0.71	0.40	-0.69
Monounsaturated FA (%)					0.64	0.38
NQI*						0.56

* Nutritional quality selection index (NQI) based on SFA (-) and MUFA (+), restricting changes in milk and fat to 0

Routine genetic evaluation for milk, fat and protein yields

FA data, genetic parameters

Genetic evaluation for milk fat composition

Already available

EBV for sires
based on many daughters, some examples

International sire	Herds	Daughters with FA
ALZI JUROR FORD	239	770
BRAEDALE GOLDWYN	168	650
CAROL PRELUDE MTOTO-	109	232
COMESTAR LEE	242	538
ETAZON LORD LILY	65	108
FABER ET AA	194	607
JOCKO BESN	442	1693
LADINO PARK TALENT-IMP-ET	340	1277
LADYS-MANOR WILDMAN-ET	170	618
LONARD	463	1495
MANAT	331	1145
O-BEE MANFRED JUSTICE-ET	27	113
PICSTON SHOTTLE	73	199
RAMOS	168	557
RICECREST MARSHALL-ET	51	120
ROYLANE JORDAN-ET	219	634



Some very important sire of sons are present!

EBV for Walloon cows and many (foreign) sires

Table 3. Mean and SD of EBV for SFA; MUFA and relative values for NQI with their associated REL for 1292 sires with REL ≥ 0.50 for FA traits and min 1 daughters with FA records in 1 herd

	EBV		REL	
Trait	Mean	SD	Mean	SD
Saturated FA (%)	-0.026	0.253	0.77	0.13
Monounsaturated FA (%)	-0.007	0.066	0.71	0.14
NQI* (in genetic SD)	0.043	0.570	0.75	0.13

* Nutritional quality selection index (NQI) based on SFA (-) and MUFA (+), restricting changes in milk and fat to 0; standardized weights used were: NQI = 0.479 MILK - 0.425 FAT - 0.934 SFA + 0.934 MUFA.

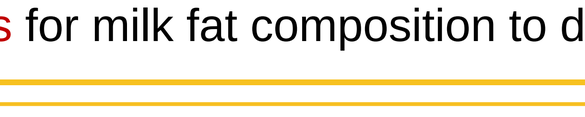

Figure 1. Distribution of 1292 sires among classes of NQI index values

Breeding tools for dairy farmers

Near future

Genomic prediction

International collaboration ?

- ✓ Phenotypes (“King” in the World of Genomics):
  - Other countries getting FA records (potentially limited subpopulations)
  - Pooling phenotypes for FA makes sense!
  - But also MIR database available to predict other traits (methane, ...)
- ✓ Genotypes:
  - Optimum combining all available phenotypes with genotypes
  - However more interaction between owners of both needed, e.g. owners providing their genotypes to phenotype owners to get predictions for their animals for novel traits: win-win situation

- ✓ Next step: Integrating external EBV for traditional traits in model ⇦ INTERBULL evaluations
  - Bayesian integration of external values for correlated traits
  - Increased reliabilities
- ✓ Also: Implementing Genomic evaluation
  - Reference population ⇦ collaboration?
  - Advanced single-step methods
  - Prediction of GEBV for important sires ⇦ collaboration of bull owners
- ✓ Deploying practical breeding tools for milk fat composition to dairy farmers ⇦ Industry collaboration

This research receives a financial support from the European Commission, Directorate-General for Agriculture and Rural Development, under Grand Agreement 211708 (Robustmilk project) and form the Commission of the European Communities, FP7, KBBE-2007-1. This poster does not necessarily reflect the view of these institutions and in no way anticipates the Commission’s future policy in this area.
This study was also supported by the Public Service of Wallonia and the Walloon Breeders Association (AWE).

Gembloux Agro-Bio Tech