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Estimation of *Myostatin* gene effects on production traits and fatty acid contents in bovine milk

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Context

- High interest in the milk fat composition
 - Nutritional quality
 - Technical properties of dairy products
- Improvement of milk fat quality
 - Genetic variability of milk fatty acids (FA)
 (Soyeurt et al., 2008; Stoop et al., 2008)
 - Calibration equations to predict FA composition of milk
 - From mid-infrared (MIR) spectra (Soyeurt et al., 2011)
 - Desirable gene variants

Context

- Mutations in Myostatin gene: `mh' allele
 - Responsible for double-muscling phenotype in all cattle breeds (Bellinge et al., 2005)
 - Influence on FA composition of meat (Raes et al., 2001)
 - Deletion in Dual-Purpose Belgian Blue (DP-BBB)
 - Influence on milk performance traits (Buske *et al.*, 2010 & 2011)
 - → Influence of `mh' allele on milk fat composition?

Objectives

- **→ Estimation of genetic parameters** in DP-BBB of:
 - Milk, fat, and protein yields
 - Saturated (SFA) and monounsaturated FA (MUFA) contents in milk
- → Estimation of `mh' allele effects on these traits

- Data used for the official routine genetic evaluation for Walloon Region of Belgium
- 3,098 DP-BBB cows
 - 1,082 genotyped DP-BBB cows
 - 2,016 non-genotyped DP-BBB cows
 - With known sire
 - From 38 herds

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- 3,098 DP-BBB cows
- 51,613 test-day records
 - 24,124; 16,144; and 11,345 records for 1st, 2nd, and 3rd lactations, respectively
 - Milk, fat, and protein yields (kg/day)
 - SFA and MUFA contents (g/dL of milk)
 - Predicted from MIR spectral data
 - Calibration equations (Soyeurt et al., 2011)

- Data structure & genotypes
 - Pedigree file: 5,796 animals
 - 1,250 genotyped DP-BBB animals
 - Few genotyped animals
- Gene content estimation
 - For non-genotyped animals
 - Estimation of gene content (Gengler et al., 2007)

- Statistical model to estimate variance components
 - Based on routine genetic evaluation model for milk production traits (Auvray & Gengler, 2002; Croquet et al., 2006)
 - Multi-lactation, multi-trait random regression model
 - 3 datasets
- Statistical model to estimate 'mh' effects
 - Same model
 - + Fixed regression on observed or estimated gene content

- Statistical model to estimate 'mh' effect
 - 3-lactations 5-traits model

$$y = X\beta + \begin{bmatrix} q \\ \hat{q} \end{bmatrix} g_s + Q(Wh + Zp + Za) + e$$

- $-g_s$ = Fixed regression coefficient
 - q = observed gene content
 - $\hat{\mathbf{q}}$ = estimated gene content

- Genotype frequencies of the Myostatin gene
 - For genotyped animals (n=1,250)

Genotype	Frequency (%)
+/+	9.84
mh/+	25.12
mh/mh	65.04

High frequency for genotype mh/mh

Genetic parameters of studied traits

Averaged daily heritabilities across lactations

Trait	Milk (kg/day)	Fat (kg/day)	Protein (kg/day)	SFA (g/dL of milk)	MUFA (g/dL of milk)
Milk	0.14	0.69	0.86	-0.10	0.17
Fat	0.66	0.11	0.81	0.52	0.65
Protein	0.76	0.66	0.12	0.15	0.39
SFA	0.06	0.21	0.11	0.34	0.73
MUFA	-0.05	0.05	-0.02	0.28	0.15

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- Allele substitution effects of the 'mh' allele
 - Milk, fat, and protein yields (kg per lactation) for each lactation & averaged through all lactations (n=51,613)

kg per lactation	All lactations	Lactation 1	Lactation 2	Lactation 3
Milk yield	-209.39	-211.06	-154.97	-262.13
Fat yield	-8.18	-7.97	-6.61	-9.96
Protein yield	-7.17	-6.86	-5.92	-8.72

- √ 1 copy of the 'mh' allele
 - Decrease in milk, fat, and protein yields

Similar to Buske et al. (2010; 2011) and Colinet et al. (2010)

- Allele substitution effects of the 'mh' allele
 - On SFA & MUFA contents (g/dL of milk) (n=6,296)

g/dL of milk	All lactations	Lactation 1	Lactation 2	Lactation 3
SFA	-0.021	-0.014	-0.039	-0.009
MUFA	0.024	0.024	0.008	0.038

- √ 1 copy of the 'mh' allele
 - Decrease in SFA content in milk
 - Increase in MUFA content in milk

Similar to Buske et al. (2011)

Conclusions

- High averaged daily heritability for SFA in DP-BBB
- Estimation of the 'mh' allele effects
 - Negative effect
 - Milk, fat, and protein yield
 - SFA content in milk
 - Positive effect
 - MUFA content in milk

















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