



Potential use of milk based biomarkers to assess and to select for heat tolerance in dairy cattle

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Background

- Heat stress (HS) impacts
 - Animal performances
 - Well-being and welfare
- Growing interest in **adapting** animals to HS
- Direct measures of HS
 - Difficult & complex
 - Not available routinely
- Unlike **high-throughput technics**
 - E.g., milk mid-infrared (MIR) analyses

Material & Methods

Data

- 202,733 test-day records (2007-2010)
 - Milk, fat, protein & somatic cell score
 - 7 groups and 10 individual milk fatty acid (FA) predicted by MIR
- 34,468 primiparous Holstein cows from 862 herds
- 12,045 daily weather records from 4 national meteorological stations (2000-2010)
- Daily temperature humidity records (THI)

$$THI = (1.8 \times T_{db} + 32) - [(0.55 - 0.0055 \times RH) \times (1.8 \times T_{db} - 26)]$$

where T_{db} = Dry bulb temperature & RH = Relative humidity

Model

- 23 univariate reaction norm models
 - 6 conventional production traits
 - 10 individual & 7 groups of milk FA

$$y = Xb + Q_{HS} (Wt + Z_1p + Z_2a) + e$$

where y = Vector of observations

b = Vector of fixed effects

→ Herd x test-day

→ Minor lactation stage

→ Gestation stage

→ Lactation stage x calving age x calving season

t = Vector of fixed regression coefficients on THI scale

p = Vector of permanent environmental random effects

a = Vector of additive genetic random effects

Q_{HS} = Covariate matrix for 1st order Legendre polynomials for standardized THI [-1;1]

X, W, Z_1 & Z_2 = Incidence matrices

e = Vector of residuals

Objectives

- ✓ Estimation of HS impacts on milk production, health & milk fine composition traits
- ✓ Assessing the potential use of milk biomarkers as indicator of HS

Conclusions

cis-9 C18:1 : - most sensitive to hot conditions
 - reflects body reserve mobilisation
 → Suitable milk biomarker as indicator of HS

Results

- Ratios & correlations (r) between level (0) and slope (HS) for additive genetic effects and heritability (h^2) of traits

Trait	$\sigma^2_{aHS}/\sigma^2_{a0}$	$r_{a0,aHS}$	h^2	Trait	$\sigma^2_{aHS}/\sigma^2_{a0}$	$r_{a0,aHS}$	h^2
Milk (kg)	<u>0.06</u>	-0.28	0.19	C16:0	0.03	-0.43	0.44
Fat (kg)	<u>0.09</u>	-0.19	0.16	C17:0	0.02	-0.35	0.41
Protein (kg)	<u>0.07</u>	-0.16	0.15	C18:0	0.04	0.13	0.23
Fat (%)	0.02	-0.27	0.39	<i>cis-9 C18:1</i>	<u>0.09</u>	0.05	0.16
Protein (%)	0.04	-0.15	0.39	UFA	0.05	0.13	0.21
SCS	<u>0.11</u>	0.25	0.08	SFA	0.02	-0.29	0.47
C4:0	0.04	0.18	0.37	MUFA	<u>0.06</u>	0.06	0.20
C6:0	0.03	0.09	0.44	PUFA	0.04	0.38	0.30
C8:0	0.03	-0.01	0.44	SCFA	0.03	0.02	0.42
C10:0	0.03	-0.13	0.42	MCFA	0.02	-0.39	0.47
C12:0	0.03	-0.25	0.42	LCFA	<u>0.06</u>	0.15	0.19
C14:0	0.03	-0.20	0.45				

SFA = Saturated FA ; MUFA = Monounsaturated FA ; PUFA = Polyunsaturated FA ; UFA = Unsaturated FA ; SCFA = Short chain FA ; MCFA = Medium chain FA ; LCFA = Long chain FA

- Genetic correlations between a THI of 25 (cold) and the rest of THI scale

