Using milking robot data for genetic evaluation of behavioral traits in Holstein cattle

Hugo Bérat[1,2], Nicolas Gengler[1], Jacob M. Maskal[2], Jacquelyn P. Boerman[2], Luiz F. Brito[2]

(1) Gembloux Agro-Bio Tech, University of Liège, Gembloux, Belgium

(2) Department of Animal Sciences, Purdue University, West Lafayette, IN, USA

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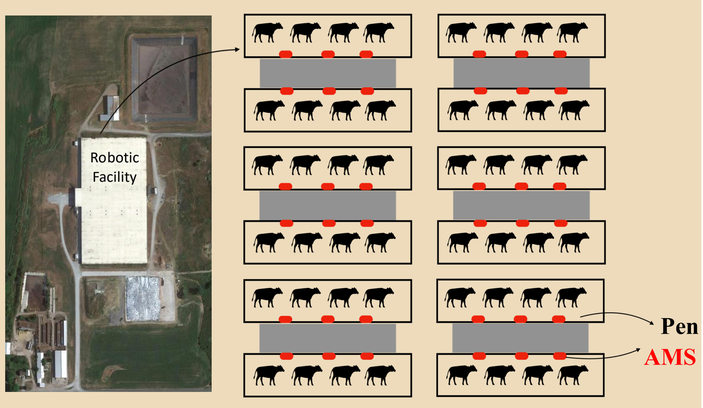
BACKGROUND

Used technology

Milking robot



AMS = Automated Milking System

OBJECTIVES

1. Derive behavioral traits based on AMS data and assess their phenotypic variability throughout lactation in North American Holstein cattle; and 2. Estimate variance components and genetic parameters for the derived AMS-based behavioral traits.

METHODOLOGY

Phenotypic data collected on 5,645 cows genotyped on 36 AMS between 2018 and 2021

Phenotypic Data

Editing steps	
Criterion	**Condition**
Missing data	Any
Days in milk (DIM)	> 350
Parity	= 0 or > 6
Age at first calving	≤ 650
Successful milking	No
Milk yield	≤ 0.44 lbs
Number of pens in 1 day	> 1

Genotypic Data

Item	Before QC	After QC
Total SNP	62,029	57,282
Mean Allele Frequency	0.733	0.713
Missing Genotype Rate	7.65%	0.00%

Models used

Single trait

$$y = Xb + Za + Wpe + e$$

Bivariate

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} W_1 & 0 \\ 0 & W_2 \end{bmatrix} \begin{bmatrix} pe_1 \\ pe_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}$$

Software used: R BLUPF90

List of traits

AMT: Average milking time
TMT: Total milking time
INT: Interval between milking
PCS: Preference consistency score
NoV: Number of visits
NSE: Number of successful entries
PSM: Perc. of successful milkings

RESULTS

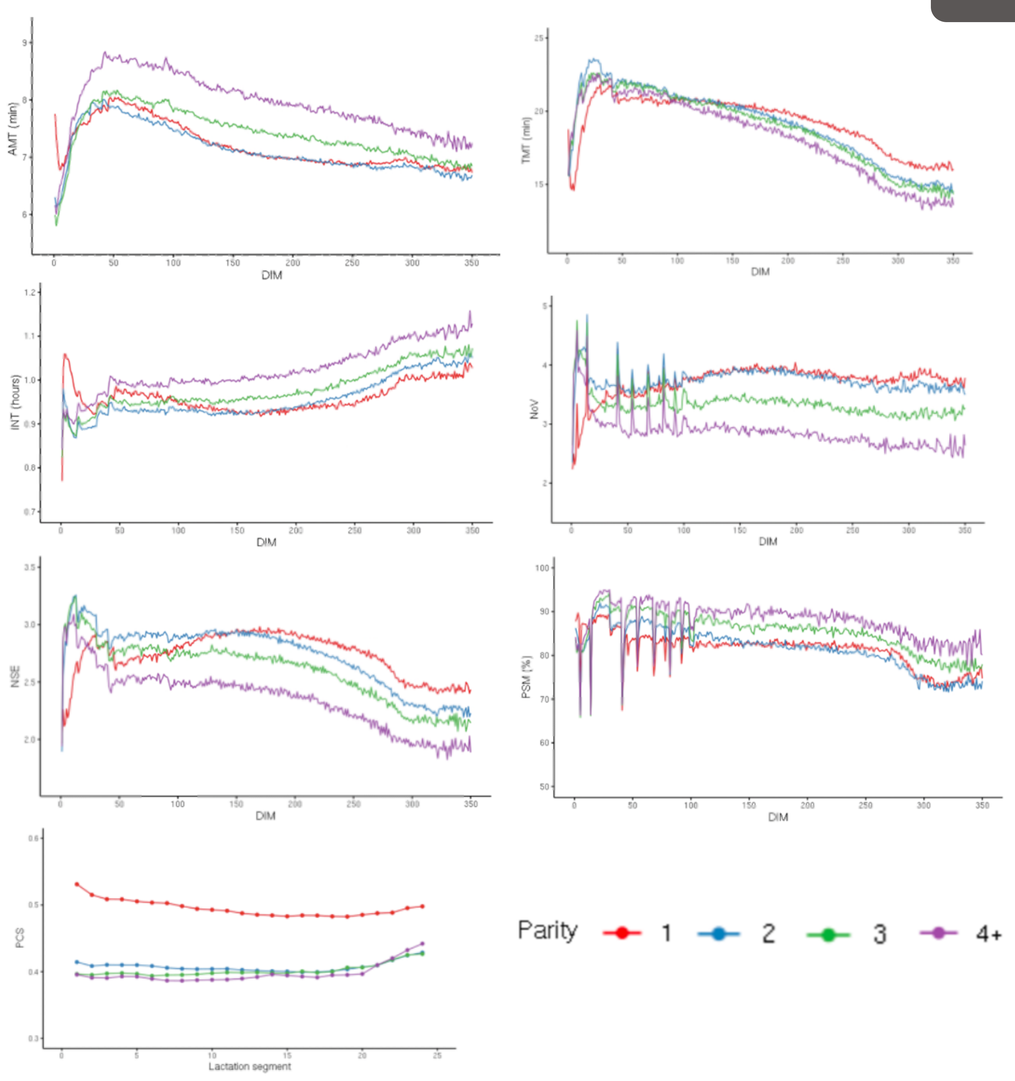


Figure 1. Phenotypic averages for behavioral traits in North American Holstein cows of 1st, 2nd, 3rd, and 4+th parity.

Table 1: Additive genetic variance (σ_a^2), permanent environmental variance between parities (σ_{pe}^2), permanent environmental variance within parities (σ_{pe2}^2), residual variance (σ_e^2), heritability ($h^2 \pm$ SE), repeatability ($t \pm$ SE) of cow behavioral traits in North American Holstein cattle.

Traits*	Parity	σ_a^2	σ_{pe}^2	σ_{pe2}^2	σ_e^2	h^2	t
AMT	1 - 6	1.75	0.72	0.34	1.02	0.46 ± 0.02	0.74 ± 0.01
TMT	1 - 6	11.25	5.67	5.17	20.24	0.27 ± 0.01	0.52 ± 0.01
INT	1 - 6	0.002	0.002	0.005	0.02	0.08 ± 0.01	0.34 ± 0.01
NoV	1 - 6	0.33	0.31	0.37	2.42	0.10 ± 0.01	0.29 ± 0.01
NSE	1 - 6	0.070	0.074	0.12	0.47	0.10 ± 0.01	0.29 ± 0.01
PSM	1 - 6	26.83	33.21	41.38	402.47	0.05 ± 0.01	0.20 ± 0.004
PCS	1 - 6	0.004	0.008	0.015	0.022	0.09 ± 0.01	0.55 ± 0.01

Table 2: Genetic correlations (± SE) table for derived traits from data obtained by the automated milking system for North American Holstein cattle with permanent environment effect within and between parities.

Traits*	TMT	INT	NoV	NSE	PSM	PCS
AMT	0.84 ± 0.02	0.24 ± 0.05	-0.36 ± 0.01	-0.34 ± 0.05	0.38 ± 0.05	-0.045 ± 0.06
TMT	-	-0.26 ± 0.05	0.12 ± 0.05	0.22 ± 0.05	0.012 ± 0.06	-0.20 ± 0.07
INT	-	-	-0.90 ± 0.02	-0.98 ± 0.05	0.71 ± 0.04	0.50 ± 0.06
NoV	-	-	-	0.92 ± 0.01	-0.94 ± 0.01	-0.44 ± 0.06
NSE	-	-	-	-	-0.72 ± 0.04	-0.35 ± 0.07
PSM	-	-	-	-	-	0.37 ± 0.07

CONCLUSIONS

All behavioral traits derived from AMS (AMT, TMT, INT, NoV, NSE, PSM, PCS) are heritable and show substantial additive genetic variance. Several positive and interesting genetic correlations were observed, particularly between AMT–PSM, INT–PSM, INT–PCS, and PSM–PCS, suggesting potential for genetic selection for improved robotic milking efficiency.

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PURDUE UNIVERSITY
LIÈGE université Gembloux Agro-Bio Tech

CONTACT INFORMATION

LinkedIn: