# Genetic and genomic evaluations of quantitative milking speed phenotypes

*A.M. Miles[1], J.L. Hutchison[1], S. Toghiani[1], J.R. O'Connell[2], R.H. Fourdraine[3], P.M. Van Raden[1], K.L. Parker Gaddis[4], S. Sievert[5], S. Eaglen[6], J. Bewley[7] and J.W. Dürr[4]*

*[1]Animal Genomics and Improvement Laboratory, USDA-ARS, 10300 Baltimore Ave, Beltsville MD 20705, USA*
*[2]University of Maryland School of Medicine, 655 W. Baltimore St, Baltimore MD 21201, USA*
*[3]Dairy Records Management Systems, North Carolina State University, 313 Chapanoke Rd, 27603 Raleigh, USA*
*[4]Council on Dairy Cattle Breeding, 4201 Northview Dr, 20716 Bowie, USA*
*[5]National Dairy Herd Information Association, Quality Certification Services, 5940 Seminole Centre Ct, 53711 Fitchburg, USA*
*[6]National Association of Animal Breeders, 8413 Excelsior Dr Suite 140, 53717 Madison, USA*
*[7]Holstein Association USA, Inc., 1 Holstein Pl, 05301 Brattleboro, USA*
*Corresponding Author: asha.miles@usda.gov*

## Abstract

Many milking systems with inline milk meters can record the milk yield and duration of each milking for individual cows. The objective of this work was to determine the suitability of milking speed traits for genetic and genomic selection and the amount of phenotype data required to produce a reliable evaluation. Records from January 2021 to December 2022 were retrieved by Dairy Records Management Systems, comprising data from 305 herds, 9 different original equipment manufacturers and 23,201 complete lactations of 23,180 cows, including 4,246 genotyped cows.

Milking speed was defined as milk yield divided by milking duration for each individual milking. Four traits were compared:

1. Average of total lactation data for all parities.
2. Average of test days for all parities.
3. Average of total lactation data for first parity only.
4. Average of test days for parity 1.

Breed, milking frequency, parity, lactation length, and meter manufacturer were included in the genetic model along with genetic groups and permanent environment. The pedigree relationship matrix included 219,703 animals with records or descendants with records plus 96 million other animals. Variances were estimated by both Gibbs sampling and REML; estimates were very similar. Residual variance was 51% higher for test day traits compared to total lactation traits. Milking speed test day heritability was 28% vs. 37% for total lactation data; genetic correlation between them was 0.97, suggesting that even with a 99% reduction in amount of phenotypic data included they are describing the same trait. Milking speed was less stable in parity 1 compared to other parities, but high genetic correlations (> 0.92) suggest the same trait is being captured. Milking speed had a small favorable genetic correlation with milk yield but

unfavorable with somatic cell score based on 756 Holstein bulls with reliability > 50%. Genomic predictions for young animals born in the last 10 years averaged 37% reliability compared to ~70% reliability for several other traits. We conclude that evaluations for milking speed are not only feasible but would have significant economic impact for producers using various milking systems. Work on implementing an evaluation for milking speed is currently underway.

*Keywords: milking speed, heritability, genomic prediction, genetic selection.*
*Presented at the ICAR Anual Conference 2024 in Bled at the Session 9: Genomic's impact on Livestock Sustainability*

## Introduction

In October of 2021, the Council on Dairy Cattle Breeding (CDCB) appointed a task force to investigate the feasibility to implementing milking speed (MSPD) evaluations in the United States. The research efforts to standardize a phenotype definition for quantitative measures of MSPD derived from electronic in-line milk meters have been previously described in Miles *et al*., (2022) and Miles *et al*., (2023). The major conclusions of this work were that milking frequency, parity, breed, and milking meter manufacturer (OEM) all have substantial effects on quantitative MSPD phenotypes. Data sparsity remains a major challenge – as phenotypes are stratified by more factors, trends become harder to elucidate and there is a significant reduction in statistical power. Thus, the research presented in this paper was conducted using only Holstein phenotypes collected from conventional milking parlors (no robotic systems). The goals of this research were to determine the heritability of various MSPD traits and develop methods for genetic and genomic evaluations that can be feasibly implemented in the USA.

## Materials and methods

Records from January 2021 to December 2022 were retrieved by Dairy Records Management Systems, comprising data from 305 herds, 9 different original equipment manufacturers (OEM) and 23,201 complete lactations of 23,180 cows, including 4,246 genotyped cows. Milking speed was defined as milk yield divided by milking duration for each individual milking between 10 and 305 days in milk (DIM). Four possible traits were compared:

1. Avg_all: average of total lactation data for all parities,
    a. a hypothetical 3X cow would have 3 * 295 DIM = 885 records contributing to phenotype
2. Avg_TD: average of test days for all parities,
    a. a hypothetical 3X cow would have 3 * 10 test days = 30 records contributing to phenotype, and a ~34% reduction in data
3. Avg_all_P1: average of total lactation data for first parity only,
4. Avg_TD_P1: average of test days for first parity only.

Trait 1) represents the most complete phenotype it is possible to assemble; Trait 2) was evaluated to address the feasibility of collecting, transmitting, and storing the data required to compute Trait 1; Traits 3) and 4) were evaluated to address the potential that MSPD is a different trait for first parity animals.

Breed, milking frequency, parity, lactation length, and meter manufacturer were included in the genetic model along with genetic groups and permanent environment. The pedigree relationship matrix included 219,703 animals with records or descendants

with records plus 96 million other animals. Variances were estimated by both Gibbs sampling and REML; estimates were very similar and REML was used in evaluation models.

## Results and discussion

The higher residual variance observed in TD traits (Table 1) is expected because there are fewer data points. The higher heritability observed for Average_all_P1 was not expected, but there is greater standard error indicating heritabilities are less accurate with less data. Both P1 traits have higher residual variance suggesting MSPD is less stable in first parity, the very high $h^2$ SE for Average_TD_P1 (0.21± 0.18) may be related to the fewer number of animals but suggests this trait is less useful than others compared.

Avg_all and Avg_TD had high genetic correlation (0.97) suggesting they are describing the same trait even with a significant reduction in data (Table 2). Parity 1 traits were also highly correlated (>92%) to MSPD traits including all parities, suggesting that they can be evaluated together with other parities.

Approximately 23,000 cows had full lactations for phenotype assembly. Preliminary PTAs were generated with the fixed effects of breed, parity, and OEM. Below are descriptive stats on >50% REL HO bulls born since 2012 for each of the four MSPD traits (Trait 1 inTable 3; Trait 2 in Table 4; Trait 3 in Table 5, Trait 4 in Table 6), with comparison to SCS and NM$.

*Table 1. Heritabilities, standard error, and residual variance computed for each trait in AIMREMLF90 ver. 1.148.*

| Trait | N | $h^2$ (SE) | Residual Variance |
|---|---|---|---|
| Trait 1) Avg_all | 23,180 | 0.37 (± 0.02) | 1.10 |
| Trait 2) Avg_TD | 22,227 | 0.28 (± 0.02) | 1.66 |
| Trait 3) Avg_all_P1 | 9,569 | 0.38 (± 0.04) | 1.12 |
| Trait 4) Avg_TD_P1 | 9,208 | 0.21 (± 0.18) | 2.05 |

*Table 2. Genetic correlations (upper diagonal) and phenotypic correlations (lower diagonal) for traits compared*

| | Avg_all | Avg_TD | Avg_all_P1 | Avg_TD_P1 |
|---|---|---|---|---|
| Avg_all | | 0.968 | 0.916 | 0.976 |
| Avg_TD | 0.821 | | 0.944 | 0.991 |
| Avg_all_P1 | 1.000 | 0.819 | | 0.924 |
| Avg_TD_P1 | 0.820 | 1.000 | 0.819 | |

*Table 3. Predicted Transmitting Ability (PTA) and Reliability (REL) for Avg_all (n = 772 bulls, genetic correlation with somatic cell score (SCS) = 0.38, Net Merit (NM$) = 0.07).*

| | PTA | | | | REL | | | |
|---|---|---|---|---|---|---|---|---|
| Trait | Min | Mean | SD | Max | Min | Mean | SD | Max |
| MSPD | -0.80 | 0.12 | 0.30 | 1.00 | 50.10 | 67.05 | 11.84 | 97.80 |
| SCS | -0.72 | -0.17 | 0.18 | 0.67 | 50.00 | 92.95 | 10.50 | 99.90 |

*Table 4. Predicted Transmitting Ability (PTA) and Reliability (REL) for Avg_TD (n = 603 bulls, genetic correlation with somatic cell score (SCS) = 0.43, Net Merit (NM$) = 0.06).*

| | PTA | | | | REL | | | |
|---|---|---|---|---|---|---|---|---|
| Trait | Min | Mean | SD | Max | Min | Mean | SD | Max |
| MSPD | -0.84 | 0.09 | 0.30 | 1.02 | 50.10 | 65.31 | 11.25 | 97.10 |
| SCS | -0.72 | -0.17 | 0.18 | 0.67 | 50.00 | 93.28 | 10.55 | 99.90 |

*Table 5. Predicted Transmitting Ability (PTA) and Reliability (REL) for Avg_all_P1 (n = 344 bulls, genetic correlation with somatic cell score (SCS) = 0.42, Net Merit (NM$) = 0.09).*

| | PTA | | | | REL | | | |
|---|---|---|---|---|---|---|---|---|
| Trait | Min | Mean | SD | Max | Min | Mean | SD | Max |
| MSPD | -0.76 | 0.17 | 0.30 | 1.03 | 50.10 | 67.10 | 11.81 | 94.60 |
| SCS | -0.72 | -0.18 | 0.19 | 0.67 | 50.00 | 89.10 | 13.68 | 99.90 |

*Table 6. Predicted Transmitting Ability (PTA) and Reliability (REL) for Avg_TD_P1 (n = 198 bulls, genetic correlation with somatic cell score (SCS) = 0.51, Net Merit (NM$) = -0.01).*

| | PTA | | | | REL | | | |
|---|---|---|---|---|---|---|---|---|
| Trait | Min | Mean | SD | Max | Min | Mean | SD | Max |
| MSPD | -0.46 | 0.15 | 0.28 | 0.82 | 50.20 | 64.00 | 10.09 | 91.20 |
| SCS | -0.58 | -0.17 | 0.18 | 0.31 | 50.00 | 89.56 | 13.71 | 99.90 |

## Conclusions

The above data suggest that producing a reliable evaluation for MSPD using quantitative inline meter data is possible. While using a significantly reduced dataset (e.g., the TD traits) appears adequate, the task force recommends adopting Trait 1) Avg_all with the highest heritability with lowest standard error and residual variance in the model. Ensuring data flow will be critical to the successful implementation of this trait, and a new data transfer Format 8 has been developed to provide the required data for delivery of a MSPD evaluation. Collection, transfer, and storage of high-resolution sensor-based data like that used in this study requires significant investment in infrastructure by both CDCB and USA data providers. Work is ongoing in this area and represents an opportunity to develop pipelines and precedent for other high-throughput phenotypes besides MSPD.

## List of references

**Miles A.M., R Fourdraine, S. Sievert, K. Gaddis, J. Bewley, S. Eaglen, J. Weiker, and J. Durr.** 2022. Considerations in using quantitative measurements of milking speed for geneti.c evaluation in the USA. Proceedings of the 2022 Interbull Meeting 57:48-53.

**Miles A.M., R. Fourdraine, J.L. Hutchison, S. Sievert, K. Gaddis, J. Bewley, S. Eaglen, J. Weiker, and J. Durr.** 2023. System and biological effects on quantitative milking speed phenotypes from inline milk meters. Proceedings of the 2023 ICAR Meeting, ICAR Technical Series No. 27:175-180. https://www.icar.org/Documents/ITS-27-Toledo-2nd-draft.pdf