

Abstract Submission Form

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Preferred presentation

Oral

Preferred session

Session 6: SC Dairy Cattle Milk Recording – Presentation and evaluation of new analytical parameters in herd management for dairy farms

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Title of your paper

Genetic and genomic evaluations of quantitative milking speed and duration phenotypes

Insert ABSTRACT text

Many milking systems with inline milk meters can record the milk yield and duration (DUR) of each milking for individual cows. The objective of this work was to determine the suitability of milking speed (MSPD) or DUR 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 (OEM), and 23,201 complete lactations of 23,180 cows, including 4,246 genotyped cows. Milking speed (MSPD) was defined as milk yield divided by milking duration for each individual milking. Eight traits were compared: 1) average of total lactation data for all parities, 2) average of DHI test days (TD) for all parities, 3) average of total lactation data for first parity (P1) only, 4) average of TD for P1, for each MSPD and DUR. Breed, milking frequency, parity, lactation length, and OEM 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. Concerning MSPD, residual variance was 51% higher for TD traits compared to total lactation traits. MSPD TD 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. MSPD was less stable in P1 compared to other parities, but high genetic correlations (> 0.92) suggest the same trait is being captured. MSPD had a small favorable genetic correlation with milk yield but unfavorable with somatic cell score based on 756 Holstein bulls with reliability (REL) for MSPD $> 50\%$. Heritability for DUR was higher than MSPD at 44% across all parities and 48% for P1. Genetic correlation of DUR with MSPD was -0.81 and phenotypic correlation was -0.52 . Genomic predictions for MSPD for young animals born in the last 10 years averaged 37% REL compared to $\sim 70\%$ REL for several other traits. We conclude that evaluations for MSPD or DUR are not only feasible but would have significant economic impact for producers using various milking systems. However, DUR is likely to be artificially impacted by milking management and parlor systems. Work on implementing an evaluation for MSPD is currently underway.

Enter keywords

milking speed, milking duration, heritability, genomic selection