Alternative strategies for genetic analyses of milk flow in dairy cattle

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ABSTRACT

Measurements for average milk flow (AMF) in kilograms of milk per minute of milking time from 629,161 Holstein cows from calving years 1990 to 2008 were used to estimate genetic covariance components using a variety of statistical models. For bivariate linear-threshold model applications, Gaussian-distributed AMF (linear sire model) was categorized into 2 distinct classes (threshold sire model) by setting arbitrary thresholds for extremely slow or extremely fast milking cows. In different bivariate runs with the 2 traits, Gaussian AMF and binary AMF, within a Bayesian framework, thresholds for the binary trait were 1.2, 1.6, 2.6, and 2.8 kg/min. Posterior heritabilities for AMF from the linear and the threshold models in all runs were in a narrow range and close to 0.26, and the posterior genetic correlation between AMF, defined as either a Gaussian or binary trait, was 0.99. A data subset was used to infer genetic and phenotypic relationships between AMF with test-day traits milk yield, fat percentage, protein percentage, somatic cell score (SCS), fat-to-protein ratio, and energy-corrected milk using recursive linear sire models, standard multiple trait linear sire models, and multiple trait linear sire models accounting for the effect of a trait 1 on a trait 2, and of trait 2 on trait 3, via linear regressions. The time-lagged 3-trait system focused on the first test-day trait after calving (trait 1), on AMF (trait 2), and on the test-day trait (trait 3) after the AMF measurement. Posterior means for heritabilities for AMF from linear and recursive linear models used for the reduced data set ranged between 0.29 and 0.38, and were slightly higher than heritabilities from the threshold models applied to the full data set. Genetic correlations from the recursive linear model and the linear model were similar for identical trait combinations including AMF and test-day traits 1 and 3. The largest difference was found for the genetic correlation between AMF and fat percentage from the first test day (i.e., −0.31 from the recursive linear model vs. −0.26 from the linear model). Genetic correlations from the linear model, including an additional regression coefficient, partly differed, especially when comparing correlations between AMF and SCS and between AMF and fat-to-protein ratio recorded after the AMF measurement data. Structural equation coefficients from the recursive linear model and corresponding regression coefficients from the linear model with additional regression, both depicting associations on the phenotypic scale, were quite similar. From a physiological perspective, all models confirmed the antagonistic relationship between SCS with AMF on genetic and phenotypic scales. A pronounced recursive relationship was also noted between productivity (milk yield and energy-corrected milk) and AMF, suggesting further research using physiological parameters as indicators for cow stress response (e.g., level of hormones) should be conducted.
Key words: milk flow, genetic parameters, recursive model, threshold model

INTRODUCTION

Functional traits reflecting dairy cow behavior are of increasing importance (König et al., 2007). The importance of behavior addresses an economic component, but also animal welfare issues from a consumer's perspective (Kramer et al., 2013). Nevertheless, dairy cattle behavior is a complex trait category that includes temperament, curiosity, aggressiveness, or cow-calf associations. Also, feeding behavior (Durunna et al., 2011) or voluntary entries into automatic milking systems (König et al., 2006) were traits of interest in quantitative-genetic studies, which mostly identified moderate heritabilities. Etiologists are interested in human-dairy cow relationships by using different stimuli or specific test procedures (Rousing and Waiblinger, 2004). In this context, preliminarily work has been done in beef cattle (e.g., by assigning temperament scores or visual flight-speed scores when the animal is jumping out of the crush; Hoppe et al., 2010). Handling of dairy cows (i.e., the effect of humans) in a positive or negative way

can either increase or decrease productivity and fertility (Hemsworth et al., 2000; Waiblinger et al., 2002). Jensen and Andersson (2005) discussed the importance of behavior with regard to adaptation of animals to their social and physical environments.

However, a substantial lack of official recording schemes exist for behavior or temperament traits in dairy cattle. Traits used in official genetic evaluations partly included temperament of cows in the parlor during milking based on subjectively appraisals of producers, and to a large extent milking speed usually defined as average milk flow (**AMF**; Rensing and Ruten, 2005). Also, AMF reflects dairy cattle behavior because agonistic behavior of cows causes physiological changes (i.e., affecting the oxytocin hormone level and norepinephrine concentrations; Kondo and Hurnik, 1988), and in ongoing lactation reduced milk flow. The genetic correlation between temperament and AMF (Sewalem et al., 2011) also indicates that a cow entering the parlor voluntarily has a calm temperament and a better milk flow, whereas a more nervous cow has a longer milking time. Concentrations of cortisol and endogenous opioids in plasma were higher, and oxytocin concentrations were lower for cows milked in unfamiliar surroundings (Bruckmaier et al., 1993; Bruckmaier et al., 1997). In such cases where release of oxytocin is impaired, milk ejection is inhibited, thus causing a production loss and an increased risk for a mammary infection (Bruckmaier, 2005). Milk flow can be recorded on 2 different scales. The first one is a subjective scoring, mostly done by farmers on a scale from 1 to 5 or from 1 to 9. Subjectively scored milk flow is a trait with low to moderate heritability (Rupp and Boichard, 1999; Rensing and Ruten, 2005). The second scale is an objective measurement in kilograms per minute (during the complete milking event or only in the main milking phase). When objectively measured, AMF is a trait with moderate to high heritability (Lassen and Mark, 2008).

An increase in AMF is associated with a desired decrease in milking and labor time. However, AMF should be considered as a trait with an intermediate optimum, because extremely fast milking cows have higher incidences of clinical mastitis and an increased SCC (Zwald et al., 2005). Complex trait associations between AMF and other traits of dairy cattle breeding goals were inferred in numerous previous studies by applying standard linear mixed model theory (e.g., Sewalem et al., 2011; Berry et al., 2013). Linear mixed models are suitable for Gaussian-distributed traits, and they do not take into account recursive relationships among traits. Structural equation models (**STEM**), on the other hand, as originally developed for biology (Haldane and Priestley 1905), have the potential

to infer relationships and feedback situations among traits by reflecting a more physiological background. Structural equation models are models with recursive or with simultaneous effects, and were applied in previous studies to health and fertility traits (e.g., Sorensen and Varona, 2006; López de Maturana et al., 2007). When applying STEM, associations between traits are reflected by solutions for so-called structural equation coefficients. In a time-lagged 3-trait system, high milk yield (**MY**) may increase AMF, and AMF could affect levels of MY in the ongoing lactation. Karacaören et al. (2006) and Samoré et al. (2010) found a positive genetic correlation between MY and AMF, but they did not investigate the recursive relationship between the 2 traits. More obvious are causalities between udder health and AMF (Luttinen and Juga, 1997): clinical or subclinical mastitis (extremely high SCC) extends the milking process but, in turn, antagonistic relationships between AMF and SCC were identified.

The aim of the present study was to apply alternative statistical models to infer genetic (co)variance components of AMF. Alternative modeling was based on 2 different approaches. First, we used threshold methodology by treating AMF as a binary trait, based on previous findings that AMF was described by bimodal or multimodal curves (distributions of daughter records within sires). In a second step, extensions of statistical modeling considered the inclusion of production and functional traits, combined with the application of STEM theory. In this context, (co)variance components and structural equation coefficients were compared with results from standard mixed models and with results from standard mixed models accounting for the effect of the response trait by incorporating a linear regression.

MATERIALS AND METHODS

Threshold Models Versus Linear Models

Data and Trait Definitions. Measurements for AMF (in kg/min) recorded with a stopwatch were available for 629,161 first-parity Holstein cows located in the regions of the federal states of Hessian and Lower Saxony, Germany. Official measurements for AMF were from the early period of lactation and mostly recorded at the second official test date of a cow. Calvings spanned the period from January 1990 to December 2008 and included cows from 24,459 different herds. Cows were daughters of 26,475 sires with, on average, 24 daughters per sire (minimum = 1 daughter per sire; maximum = 35,632 daughters per sire). The pedigree file traced back to founder animals born in 1940 included 2,229,849 animals.