



## Genetic analyses of binary longitudinal health data in small low input dairy cattle herds using generalized linear mixed models



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### ABSTRACT

Genetic parameters were inferred for the health traits mastitis, metritis, retained placenta, ovarian cysts and acetonemia from 1247 Brown Swiss cows in first parity kept in 53 organic and low input farms in Switzerland. For genetic analyses, univariate animal and sire models, repeatability animal and sire models, and random regression sire models (RRM) in a “generalized linear mixed model (GLMM) context” were applied. The five health traits were defined as binary data, count data, and longitudinal binary data in the interval between  $-1$  and 120 d in milk (DIM). Firstly, binary data were analyzed by applying linear animal and sire models, and threshold animal and sire models with a probit link function. Secondly, data of total number of disease cases recorded within the defined time span were analyzed by using GLMM animal and sire models with a log link function for Poisson distributed count data. Thirdly, for longitudinal health data, linear repeatability animal and sire models, linear sire RRM, threshold animal and sire repeatability models, and threshold sire RRM with a probit link function were applied. Disease incidences of the five health disorders in organic farms were on a generally low level, with a highest incidence of 5.78% for mastitis within the time span of 120 d. With regard to mastitis, moderate heritabilities with an average value of 0.15 were realized from univariate models and binary data, and from GLMM with the log link function and count data. Heritabilities for mastitis were smaller ( $< 0.10$ ) when using the longitudinal data structure in combination with repeatability models and RRM. Repeatabilities and heritabilities for longitudinal data as realized from repeatability models were on a quite similar level. Only for longitudinal ovarian cysts, heritabilities substantially differed from repeatabilities. Heritability was 0.02 from the animal model and 0.01 from the sire model, but repeatabilities were 0.14, which indicates a substantial permanent environmental effect. Daily heritabilities for all health traits from linear and threshold RRM at the beginning of lactation and at the end of the defined interval were three times higher than corresponding heritabilities in the middle of lactation. Bayesian information criterion (BIC) and heritabilities themselves favored threshold models over linear models. However, linear models converged more easily than threshold models, and genetic parameter estimates had smaller standard errors. Similar BIC values were found when comparing

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animal with sire models, although generally higher heritabilities were realized from sire models. For RRM applications, BIC was smaller and heritabilities were higher for linear sire compared to threshold sire models.

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## 1. Introduction

Especially in the early period directly after calving and including the ‘peak phase’ of lactation, dairy cows are particularly susceptible for infections of udder quarters (e.g. Schwarz et al., 2011). Furthermore within the first 100 d in milk (DIM), metabolic diseases occur frequently, and reproduction disorders related to the puerperium are only relevant in the early stage of lactation. An overview of incidences for a variety of health disorders by DIM is given by Gernand et al. (2012). For all categories of health traits, i.e. reproduction, metabolism, claw disorders and mastitis, they found a substantial decrease of disease incidences with increasing DIM. König et al. (2005, 2008) used different statistical models to analyze the genetic background of claw disorders occurred in the first third of lactation. The above-mentioned studies used data from Holstein cows kept in large-scale contract herds located in East Germany, which are characterized by a high production level, especially at the first test-days directly after calving. Consequently, energy intake does not match energy requirement, and the negative energy balance is associated with an increasing risk of occurrence of health disorders in the ongoing lactation (Collard et al., 2000).

Test-day milk yield in the early period of lactation of Brown Swiss cows kept in organic or low input dairy cattle farms in Switzerland is substantially lower compared to the production level of Holstein cows from East German contract herds (Yin et al., 2012). Nevertheless, health disorders, mainly including reproduction and metabolism, play an important role in organic production systems in Switzerland (Rehbein et al., 2013). The economical losses per cow and year due to clinical mastitis in low input as well as in high input production systems ranged from 100\$ to 295\$ in several studies (Schepers and Dijkhuizen, 1991). Of economic relevance are also health disorders including female reproduction and metabolism. Both categories contribute to the increase of involuntary dairy cow cullings (Dubuc et al., 2011; Kesler and Garverick, 1982; Østergaard and Grohn, 1999). Due to the high priority of functional health traits especially in organic dairy cattle farming systems, Rozzi et al. (2007) developed overall organic breeding goals and organic selection indices.

Pre-requisites for traits to be included in an overall breeding goal are their economic importance, the availability of a suitable recording system (data quality), the size of additive genetic variance or of heritability, and genetic correlations with other traits of interest. The latter three arguments address statistical methodology for data preparation and genetic analyses. For test-day production data, official and identical recording systems across country borders exist, but for functional health traits, the variety of possible data definitions and completeness of data may cause differences in estimated genetic parameters. When

analyzing large datasets with different statistical models, only minor differences in genetic parameter estimates were found. An example is given by Shook et al. (2002), who used 4,531,536 reproduction records for genetic analyses based on different data definitions. In contrast, organic and low input populations are characterized by comparatively small population and herd sizes. The small number of animals within contemporary groups in organic herds was a substantial problem for genetic evaluations of production traits when applying over-parameterized statistical models (Yin et al., 2012). Basically, health data preparation in the early period of lactation includes three definitions. The easiest way is to focus on a specific interval, and to assign a score of 1 for diseased cows, irrespective the number of disease cases (e.g. König et al., 2005). Secondly, using the code=1 for diseased cows, and considering all disease cases within a defined interval, generates a longitudinal data structure (e.g. Carlén et al., 2009; Gernand et al., 2012). A third option is to count the total number of disease cases within a defined interval, resulting in a broader range of scores compared to the binary scores. This strategy was applied by König et al. (2007) for female reproduction traits. The latter two definitions make it difficult to distinguish between a new case of a disease, or an ongoing treatment. Hinrichs et al. (2005) suggested a 5 day interval to separate a new from a pre-existing disease.

With respect to statistical modeling for genetic evaluation of binary data, main questions addressed comparisons of sire versus animal models, and applications of the threshold concept instead of assuming a Gaussian data distribution. In the early 1980s, threshold models were developed and theoretically evaluated by Gianola and Foulley (1983) or by Harville and Mee (1984) for animal breeding objectives. In the following years, this concept was applied to real data in a multitude of scientific studies or in official genetic evaluations (e.g. Koeck et al., 2010b). Theoretically, threshold models which study the trait of interest on an underlying liability scale are more appropriate for depicting the physiological background compared to linear models. However, problems may occur for data with extreme incidences, such that some sub-cells of effects are underrepresented for certain scores (Hoeschele and Tier, 1995). Several genetic analyses for binary traits utilized threshold methodology within a Bayesian framework (e.g. Gernand et al., 2012; Sorensen et al., 2009). An alternative to Bayesian procedures is the application of REML to generalized linear mixed models (GLMM). Using GLMM, different link functions can be invoked to analyze data with different distributions, e.g. an identity link function for Gaussian traits, a probit or logit link function for binary data, or a log link function for Poisson distributed ‘count data’ (McCullagh and Nelder, 1989). An overview of methodologies in the context of GLMM applications for analyses of categorical health traits is given in Table 1. As a further

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