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Genetic analysis of heat stress effects on yield traits, udder health, and fatty acids of Walloon Holstein cows

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ABSTRACT

Genetic parameters that considered tolerance for heat stress were estimated for production, udder health, and milk composition traits. Data included 202,733 test-day records for milk, fat, and protein yields, fat and protein percentages, somatic cell score (SCS), 10 individual milk fatty acids (FA) predicted by mid-infrared spectrometry, and 7 FA groups. Data were from 34,468 first-lactation Holstein cows in 862 herds in the Walloon region of Belgium and were collected between 2007 and 2010. Test-day records were merged with daily temperature-humidity index (THI) values based on meteorological records from public weather stations. The maximum distance between each farm and its corresponding weather station was 21 km. Linear reaction norm models were used to estimate the intercept and slope responses of 23 traits to increasing THI values. Most yield and FA traits had phenotypic and genetic declines as THI increased, whereas SCS, C18:0, C18:1 *cis*-9, and 4 FA groups (unsaturated FA, monounsaturated FA, polyunsaturated FA, and long-chain FA) increased with THI. Moreover, the latter traits had the largest slope-to-intercept genetic variance ratios, which indicate that they are more affected by heat stress at high THI levels. Estimates of genetic correlations within trait between cold and hot environments were generally high (>0.80). However, lower estimates (< = 0.67) were found for SCS, fat yield, and C18:1 *cis*-9, indicating that animals with the highest genetic merit for those traits in cold environments do not necessarily have the highest genetic merit for the same traits in hot environments. Among all traits, C18:1 *cis*-9 was the most sensitive to heat stress. As this trait is known to reflect body reserve mobilization, using its variations under hot conditions could be a very affordable milk biomarker of heat stress for dairy cattle expressing the equilibrium between intake and mobilization under warm conditions.

Key words: temperature-humidity index, heat stress, fatty acid, udder health, genetic variation

INTRODUCTION

Production losses, morbidity, and mortality due to heat stress are increasing concerns in tropical and subtropical regions, but recently also in temperate areas (Renaudeau et al., 2012). Feeding modifications (e.g., increasing feed intake), environmental conditioning (e.g., cooling and shading), and genetic selection for heat tolerance remain the 3 best strategies to alleviate the effects of heat stress on dairy cattle (Renaudeau et al., 2012). Environmental and feeding modifications are specific to each production system and mainly depend on their additional value for improving animal performances, fitness, and well-being compared with their costs. However, genetic improvement of livestock is cost effective by producing permanent and cumulative change (Wall et al., 2010). Selecting purebred or crossbred heat-tolerant animals is an effective management method for heat stress only if high production efficiency can be associated with a capacity to cope with hot and humid conditions.

Knowledge still is lacking about genetic variation for heat tolerance. Genetic selection for regulation of core body temperature is one potential strategy to mitigate effects of heat stress on dairy cows (Dikmen et al., 2012). However, the inheritance of physiological traits (e.g., rectal temperature and pulse) is still not understood well, primarily because of the difficulty and cost of routine accurate measurement of those traits. In contrast, large amounts of data are available on animal performance and weather parameters. Direct measures of an animal's capacity to produce, reproduce, and live under heat stress have been shown to be potentially useful for selecting animals for heat tolerance in tropical and subtropical conditions [e.g., dairy cattle (Ravagnolo and Misztal., 2000; Aguilar et al., 2009; Sánchez

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et al.., 2009; Boonkum et al., 2011), pigs (Zumbach et al., 2008), and dairy sheep (Finocchiaro et al., 2005)].

Genetic studies of heat stress effects in dairy cattle were based originally on (1) determining a tipping point for thermal index after which a linear decline of production occurred and (2) regressing phenotypic performance on remaining points after this threshold to model the additive genetic variance of heat tolerance. Such a modeling approach assumed that all cows had the same threshold and rate of decline in every region and over time. To overcome those limitations, Sánchez et al. (2009) proposed a more realistic approach based on a hierarchical Bayes model in which the threshold and decline rate were assumed to be different and variable for individual cows. However, those assumptions required more complicated and highly parameterized models that could make estimation procedures inefficient.

Few genetic studies on heat stress under temperate climate and production systems currently are available for dairy cattle. Brügemann et al. (2011) and Hammami et al. (2013) reported low thresholds for a temperature-humidity index (**THI**) for production traits compared with those reported under tropical and subtropical conditions (Bohmanova et al., 2008; Aguilar et al., 2009; Boonkum et al., 2011). Differences in cow response to changes in the prevailing environment require more consideration of genotype by environment interactions. Environments may be described as discrete units, such as country or region, or measured on a continuous scale using a range of environmental descriptors, such as climate variables (Hammami et al., 2009). Thermal indices, such as a THI, quantify climatic and seasonal effects on animals on a continuous scale. Individual response to each gradient of THI should be better quantified by using reaction norm models, which allow greater flexibility to model genetic variation of heat tolerance across the range of the THI scale without fixing a threshold level. By modeling cow performance as a function of a continuous THI, highly productive individuals with low sensitivity to THI potentially could be identified and selected.

Heat stress conditions have been associated with decreased milk, fat, and protein yields in addition to delayed conception and altered pregnancy rates (Thatcher and Collier, 1986). Nearly all comprehensive studies on genetics of heat tolerance in dairy cattle were conducted in the United States using productive and reproductive data from tropical and subtropical Holstein populations (Ravagnolo and Misztal, 2000; Bohmanova et al., 2008; Aguilar et al., 2009; Boonkum et al., 2011). Heritability estimates for both production and fertility traits were found to increase as a function of THI after a threshold of 72, which implies that selective improvement of heat tolerance is possible for milk traits (Ravagnolo and Misztal, 2000).

Recently, great interest has been shown in milk fat and its FA profile because of their effects on technological, sensorial, and nutritional properties of milk and dairy products. Most of the C4:0 to C14:0 and almost half of the C16:0 FA in milk are synthesized de novo, whereas the rest of the C16:0 and approximately all long-chain FA originate from blood lipids (Chilliard et al., 2000). Milk FA vary phenotypically and genetically across the lactation and have moderate to high heritabilities, which indicates that they could be changed by genetic selection (Bastin et al., 2013). Milk FA profile was also found to be a potential indicator of cow energy balance (Bastin et al., 2012) and methane emission (Chilliard et al., 2009). Although studies based on controlled experiments or a limited number of animals under a few commercial conditions reported that milk fat composition differed between seasons and weather conditions (Renna et al., 2010), no studies have evaluated genetic, phenotypic, and inheritance variation of FA over a continuous range of climate conditions (e.g., a THI scale). Such studies could provide added knowledge on the individual response to weather parameters (climate change) for milk FA profile and investigate the potential use of those milk biomarkers as indicators of heat stress. The objectives of the current genetic analysis were (1) to evaluate heat stress effects on yield traits (milk, fat, and protein yields and fat and protein percentages), udder health (SCS), and milk quality (FA profile) and (2) to assess the potential of milk FA as biomarkers for dairy cattle resilience to climate change.

MATERIALS AND METHODS

Data

The data included 202,733 test-day (**TD**) records of yield, milk content, and FA traits that had been collected between 2007 and 2010 from 34,468 primiparous Holstein cows in 862 herds. Records for daily milk, fat, and protein yields, fat and protein percentages, and SCS were collected by the Walloon Breeding Association (AWE, Ciney, Belgium). Additionally, 10 individual milk FA (C4:0, C6:0, C8:0, C10:0, C12:0, C14:0, C16:0, C17:0, C18:0, and C18:1 *cis*-9) and 7 FA groups [SFA, MUFA, PUFA, unsaturated FA (**UFA**), short-chain FA (**SCFA**), medium-chain FA (**MCFA**), and long-chain FA (**LCFA**)] were considered as performance traits. The groups of FA were defined similar to Bastin et al. (2013). Saturated FA includes C4:0, C6:0, C8:0, C10:0, C12:0, C12:0 *iso*, C12:0 *anteiso*, C13:0 *iso*, C14:0, C14:0 *iso*, C14:0 *anteiso*, C15:0, C15:0 *iso*, C16:0, C16:0 *iso*, C16:0 *anteiso*, C17:0, C17:0 *iso*,