Short communication: Implementation of a breeding value for heat tolerance in Australian dairy cattle

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ABSTRACT

Excessive ambient temperature and humidity can impair milk production and fertility of dairy cows. Selection for heat-tolerant animals is one possible option to mitigate the effects of heat stress. To enable selection for this trait, we describe the development of a heat tolerance breeding value for Australian dairy cattle. We estimated the direct genomic values of decline in milk, fat, and protein yield per unit increase of temperature-humidity index (THI) using 46,726 single nucleotide polymorphisms and a reference population of 2,236 sires and 11,853 cows for Holsteins and 506 sires and 4,268 cows for Jerseys. This new direct genomic value is the Australian genomic breeding value for heat tolerance (HT ABVg). The components of the HT ABVg are the decline in milk, fat, and protein per unit increase in THI when THI increases above the threshold of 60. These components are weighted by their respective economic values, assumed to be equivalent to the weights applied to milk, fat, and protein yield in the Australian selection indices. Within each breed, the HT ABVg is then standardized to have a mean of 100 and standard deviation (SD) of 5, which is consistent with the presentation of breeding values for many other traits in Australia. The HT ABVg ranged from −4 to +3 SD in Holsteins and −3 to +4 SD in Jerseys. The mean reliabilities of HT ABVg among validation sires, calculated from the prediction error variance and additive genetic variance, were 38% in both breeds. The range in ABVg and their reliability suggests that HT can be improved using genomic selection. There has been a deterioration in the genetic trend of HT, and to moderate the decline it is suggested that the HT ABVg should be included in a multitrait economic index with other traits that contribute to farm profit.
Key words: heat tolerance, genomic selection, milk production

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Heat stress is an issue of growing concern for many livestock production systems worldwide, including the dairy industry in some regions of Australia. Heat stress affects not only animal welfare but also economic returns (Kadzere et al., 2002; St-Pierre et al., 2003). When exposed to heat stress conditions, such as high temperature and humidity, cows produce less milk due to reduced feed intake and secretory function of the udder (Silanikove, 1992). Heat stress is also known to reduce conception rates (Hansen and Aréchiga, 1999) and increase the incidence of health problems and mortality rates in dairy cows (Kadzere et al., 2002; Dikmen and Hansen, 2009).

Mitigation of heat stress can be multifaceted and includes physical protection, nutritional management, and genetic improvement (Beede and Collier, 1986). Although efforts have been made at a herd management level to provide a suitable environment for cows (i.e., shade and cooling devices) and extensive research has been conducted in nutritional management for lactating cows in hot climates (Beede and Collier, 1986; West, 1998), genetic improvement for heat tolerance (**HT**) has not been practiced in the dairy industry. It is, however, widely recognized that genetic variation is associated with the performance of dairy cows under heat stress conditions, making the selection for this trait possible (Bohmanova et al., 2008).

In Australia, genomic selection for HT can take advantage of the genotypes from thousands of cows and bulls already available. Nguyen et al. (2016a) used herd test-day and weather records over an 11-yr period to

estimate tolerance to heat stress. They determined the extent of the decline in milk, fat, and protein yield as temperature-humidity index (**THI**) increased for Holsteins and Jerseys. Genomic EBV for HT were determined using high-density SNP data. These HT genomic EBV were also empirically validated through a heat challenge experiment in which genomically predicted heat-tolerant cows showed significantly less milk yield losses as well as lower rectal and intravaginal temperatures than the predicted heat-susceptible animals when challenged with a mild simulated heat wave (Garner et al., 2016).

Here, we describe an implementation plan of the Australian genomic breeding values for HT (**HT ABVg**) for Holstein and Jersey dairy cattle. Definition, expression, and methods of how breeding values for HT could be derived and implemented are presented and discussed.

Breeding values for HT can be expressed in several ways (Nguyen et al., 2016b). Following consultation with Australian dairy industry representatives, HT is expressed as the decline in milk, fat, and protein yield per unit increase in THI when THI increases above the threshold of 60, weighted by their respective economic weights. It is then standardized to have a mean of 100 and standard deviation of 5 for each breed. This method of expressing the breeding value is typical of many breeding values evaluated for Australian dairy cattle. To calculate HT ABVg, first, SNP effects for the decline in milk, fat, and protein yield with increasing heat stress were calculated using the following steps.

(1) **Calculation of phenotypes for HT for cows**
    The data set used to calculate phenotypes for HT for cows was similar to that used by Nguyen et al. (2016a), with several improvements: (1) climate data (i.e., hourly temperature and relative humidity) were extended to include recent data (i.e., to August 2016); (2) the distance between herds and weather stations was measured using the GPS coordinates of each herd instead of its postcode centroid, where possible; and (3)

herds that did not have a weather station within a 60-km radius were excluded from analyses. A summary of the final data set is given in Table 1. The rates of decline (slope) in milk, fat, and protein yield after a heat stress event were estimated using a reaction norm model (Nguyen et al., 2016a). In this model, data on milk, fat, or protein yield were fitted with fixed effects of herd test day, year season of calving, parity, a third-degree polynomial on age at calving, parity × an eighth-degree polynomial on DIM, and stage of lactation × a linear polynomial on THI. Random effects included a random regression on a linear orthogonal polynomial of THI and a residual term. In the model, the threshold of THI was set to 60 following Hayes et al. (2003). The analyses were conducted using ASReml (Gilmour et al., 2009) and were done separately for Holsteins and Jerseys.

(2) **Calculation of pseudophenotypes for HT for sires**
    Using the cow slope solutions obtained in step 1, sire slopes or daughter trait deviations (equivalent to daughter yield deviations) for decline in milk, fat, and protein yield as THI increases were estimated.

(3) **Calculation of SNP effects**
    The SNP effects were calculated separately for the decline in milk, fat, and protein yield with increasing THI. The number of animals in the reference populations was 11,853 cows and 2,236 sires for Holsteins and 4,268 cows and 506 sires for Jerseys. The sires needed to have at least 5 daughters with phenotypes to be included in the reference sets. Genotypes for 46,726 SNP were obtained from DataGene (Melbourne, Australia) in September 2016. A genomic best linear unbiased prediction model was used to fit the daughter trait deviations obtained from step 2 (Nguyen et al., 2016a) and then back solved to obtain SNP effects. The HT ABVg were then calculated using the following steps.

Table 1. Characteristics of the data sets used in the calculation of heat tolerance phenotypes for cows

Item (no.)	Holstein			Jersey		
	1st parity	2nd parity	3rd parity	1st parity	2nd parity	3rd parity
Records	2,798,669	2,057,838	1,319,742	591,434	446,438	309,217
Herds	1,927	1,841	1,650	554	537	498
Cows	424,540	325,026	214,787	84,702	67,451	47,520
Sires	10,230	9,476	8,222	3,175	2,950	2,577