Challenging Concept for Tropical Sire Summary

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Summary

Genetic evaluation beyond common economic traits are necessary in tropical sire summary. Thailand Tropical Holstein dairy cattle has been development for improvement of milk yield (MY), milk composition (Fat, Protein, SNF), SCC, days open under tropical environment for decades. Nowadays, there are several challenges in dairy genetic evaluation under climate change, especially in production under hot-humid environment. In tropical countries, most of dairy cattle are crossbred (*Taurine* x *Zebuine*) with different genetic fractions of *Bos tuarus*. Therefore, the development of suitable model for genetic evaluation to improve EBV accuracy is necessary. The genetic evaluation under heat stress has been researched. The critical temperature-humidity index (THI) for heat stress under hot-humid production was estimated. Effect of heat stress on Thai Holstein crossbreds increased greatly with parity and for cows with high *Taurus* genetics. It was found that the moderate and severe heat stress occur when THI > 74 and THI > 80, respectively. Nowadays, EBV under heat stress (heat tolerance index) could be estimated under THI-BLUP model (Boonkum et al., 2011). Milk fat to protein ratio was a convenient indicator for negative energy balance (NEB) and acidosis in dairy production. Our study showed that the optimum FPR was in the range of 0.9 to 2.1. Apply this critical range, the genetic evaluation for negative energy balance tolerance can be performed (Puangdee et al., 2017). Another challenging trait for sire evaluation under heat stress is conception rates (CR). Continuous improving milk yield has induced a decrease in reproductive performance. The effects of heat stress accelerate the severe effects. Data recording is one of the difficulty. Although the indirect trait such as days open is available, the conception rate was claimed to a direct fertility response trait. We developed random regression threshold models (RR-THM) with Legendre polynomials for genetic evaluation of conception rate in tropical sire summary (Buaban et al., 2016). According to low quality of tropical feed resources and low-technology input in production, the genetic potential could not be fulfilled. In addition, the culling parity has been decreased drastically. Therefore, genetic improvement for robust and endurable/longevity traits has been developed and aimed to be included in tropical sire summary (Saowaphak et al., 2017). EBV index combining production, milk quality, and fertility under heat stress should be developed under multi-trait analysis. In modern sire summary, genetic evaluation (EBV/GEBV) for NEB tolerance, longevity, genetic markers from candidate or GWAS approaches should be included.
Keywords: sire evaluation, heat tolerance, NEB tolerance, robust, Thailand Tropical Holsteins

Introduction

Genetic evaluation beyond common economic traits are necessary in tropical sire summary. Thailand Tropical Holstein dairy cattle has been development for improvement of milk yield (MY), milk composition (Fat, Protein, SNF), SCC, days open under tropical environment for

decades. Nowadays, there are several challenges in dairy genetic evaluation under climate change, especially in production under hot-humid environment. In tropical countries, most of dairy cattle are crossbred (*Taurine x Zebuine*) with different genetic fractions of *Bos tuarus*, Therefore, the development of suitable model for genetic evaluation to improve EBV accuracy is necessary. Heat stress is an important problem for dairy production in many parts of the world because of its negative effects on productivity and profitability. Ravagnolo and Misztal (2002) proposed a method for the study of genetic response under heat stress. After calving, in extreme states of negative energy balance (NEB). The milk fat to protein ratio (FPR) is used primarily as a diagnostic tool to determine NEB. The optimum FPR has been previously established to be between 1.2 and 1.4 for healthy cows. Dairy cows become metabolically stressed and develop increased incidences of disease and metabolic disorders. There are several scientific reported about NEB effects to length of productive life (LPL) and days open (DO). Therefore, these economic traits are necessary in tropical sire summary of Thailand. EBV index combining production, fertility, NEB tolerance and longevity and under heat stress has been challenged. In modern sire summary, genetic evaluation (EBV/GEBV) for, genetic markers from candidate or GWAS approaches should be included.

Material and methods
In heat stress model, a temperature humidity index (THI) based upon the formula utilized by the National Oceanic and Atmospheric Administration (1976). THI = (1.8 x temp + 32) - (0.55 - 0.0055 x RH) x (1.8 x temp - 26). A repeatability test day model (REP) proposed by Ravagnolo and Misztal (2000) was utilized. Firstly, univariate analyses by parity were performed using the REMLF90 program (Misztal, 1999). The model was as follows:

$$y_{ijklmn} = hmy_{ij} + dim_k(bg_{jl}) + age_{jm} + a_{jn} + \alpha_{jn} \times f(THI) + p_{jn} + \pi_{jn} \times f(THI) + e_{ijklmn}$$

$f(THI)$ is a function of THI and was defined as:

$$f(THI) = \begin{cases} 0 & THI \leq THI_{threshold} \quad (\text{no heat stress}), \\ THI - THI_{threshold} & THI > THI_{threshold} \quad (\text{heat stress}) \end{cases}$$

In our study, the outcome of an insemination event (referred to as the conception rate, or CR) is defined as a binary trait when estimating parameters using RR-THM. The basic underlying idea consists of modeling the additive genetics and other random effects in the model as a function of an observed dependent variable (DIM) through a set of random coefficients. The equation for analyzing conception rate was written as such:

$$l = X\beta + Z_h h + Z_\alpha \alpha + Z_p p + Z_s s + e$$

where l is a vector of unobserved liabilities for service records from a binary outcome of insemination events (1 = success or 0 = failure) and the other notation was described in Buaban et al. (2016)

Results and Discussions
Evaluation of milk yield under heat stress
Figure 1 shows declining of test-day milk yield across all crossbreds and parities was found at two points, THI of 74 and 80 for moderate and severe heat stress, respectively. The threshold for effect of heat stress on test-day milk yield was set to a THI of 80. The effect of heat stress on Thai Holstein crossbreds increased greatly with parity and was especially large after a THI of 80 for cows with a high percentage of Holstein genes ($\geq 93.7\%$). The THI threshold of 80 is higher than the thresholds of 72 to 76 reported for US Holsteins (Ravagnolo et al., 2000). Effect of heat stress on Thai Holstein crossbreds increased greatly with parity and for cows with high *Taurus* genetics. Correlations between additive effects (EBV) and heat stress effects (α) was range -0.21 to -0.31 for all parities. The result showed that the increasing of genetics
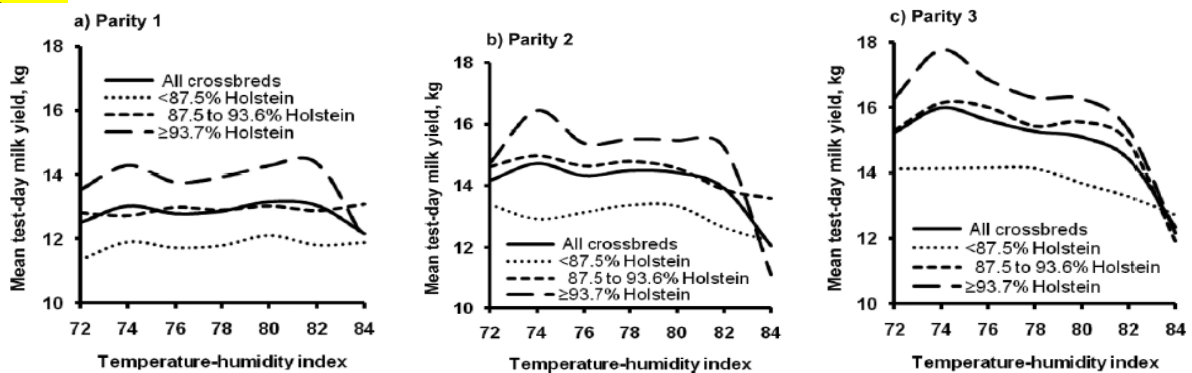
Figure 1. Mean test-day milk yield for Thai Holstein crossbreds across a temperature-humidity index by breed group based on percentage of Holstein genetics for a) parity 1, b) parity 2, and c) parity 3 (Boonkum et al., 2011).

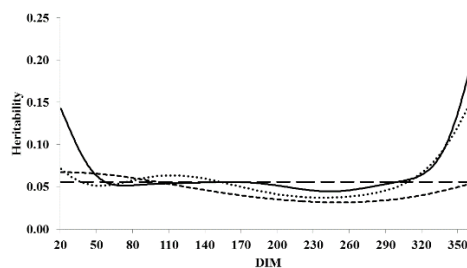**Evaluation of Conception rate**

Figure 2 Heritability of conception rate using RR-THM as a function of time with the second- (------), third- (.…....) and fourth- (——) order of Legendre polynomials. (Buaban et al., 2016)

Determination of optimum FPR at genetic level

The estimated heritability of MY along the FPR ranged from 0.19 to 0.27. The heritability of MY in this study was in the range of previous reports for tropical Holsteins (Boonkum and Duangjinda 2014). In addition, the oscillated of the heritability curve of MY revealed an imbalance of energy utilization leading to different individual genetic expressions of FPR effects outside the range of 0.9–2.1. The high heritability for MY reflected the genetic difference in cow sensitivity to NEB influence upon FPR, resulting in accuracy of genetic evaluation. Therefore, the results suggest that the threshold for optimum FPR corresponding to genetics-controlled energy balance for MY was 0.9–2.1. This appears acceptable with regard to high FPR corresponding to NEB, whereas the low FPR corresponded to ruminal acidosis (Toni et al. 2011).

Investigation of QTL using GWAS

The GWAS results for all traits in this study, with variances explained for 10-SNP windows to identify the putative QTL regions. The QTL regions was performing by a high proportion of variances (higher than 2.3E-04, which is an expected proportion of variance accounted for

by one window). The diffuse peak spread mainly on chromosome 1, 4, 5, 8, 15, 26 and X. The result showing a total of 23 QTL regions were associated with all three traits, and gene that are within the QTL regions. We detected ten SNPs located in QTL regions were associated with LPL, which mostly located on BTA5 and BTAX. There are 4 genes within the regions on BTA5 (SYT1 gene) and BTAX (DOCK11, KLHL13 and IL13RA1 genes). Eight QTLs were associated with DO on BTA1, BTA4 and BTA26, which has only one gene within the region on BTA26 (*PRKG1* gene). Five QTLs were associated with FM305, which found within 2 genes on BTA8 (*GNA14* gene) and BTA15 (*LRRC4C* gene). In this study, not have overlapping regions between LPL, DO, and FM305 traits. Previous study reported QTL for trait in this study containing 867 QTL for length of productive life found on every chromosome, 10 QTL for day open found on BTA2, 4, and 18. 305-days milk yield found 26 QTL on BTA3, 4, 5, 6, 7, 12, 13, 14, 16, 18, 19, 23 and 29. (http://www.animalgenome.org/cgi-bin/QTLdb/BT/index).
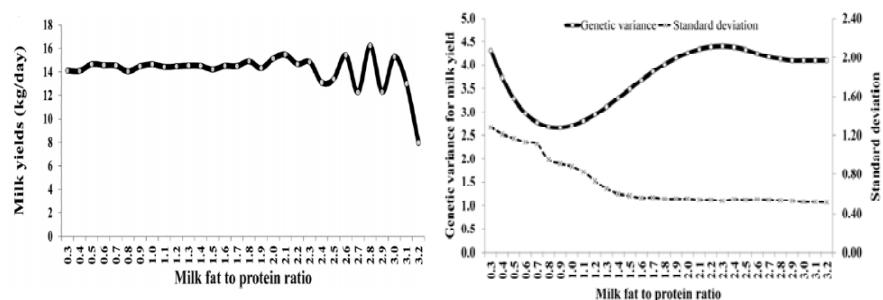

Figure 2 Average milk yield (a) genetic variance for milk yields at different milk fat to protein ratio (FPR) (Puangdee et al., 2017)

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References

Boonkum, W., I. Misztal, M. Duangjinda, V. Pattarajinda, S. Tumwasorn, and J. Sanpote. 2011. Genetic effects of heat stress on milk yield of Thai Holstein crossbreds. J. Dairy Sci. 94:487–492.

Buaban, S., K. Kuchida, M. Suzuki, Y. Masuda, W. Boonkum and M. Duangjinda. 2016. Genetic analysis of the rates of conception using a longitudinal threshold model with random regression in dairy crossbreeding within a tropical environment. Animal Science Journal (2016) 87, 961–971.

Puangdee, S., M. Duangjinda, W. Boonkum, S. Buaban, and S. Katawatin. 2016. Effect of milk fat to protein ratio on genetic variance for milk yield in Thai tropical Holstein cattle. Can. J. Anim. Sci. 96: 410–415.

Ravagnolo, O., and I. Misztal. 2002. Effect of heat stress on nonreturn rate in Holsteins: Fixed-model analyses. J. Dairy Sci. 85:3101–3106.

Saowaphak, P., M. Duangjinda, S. Plaengkaeo, R. Suwannasing and W. Boonkum. 2017. Genetic correlation and genome-wide association study (GWAS) of the length of productive life, days open, and 305-days milk yield in crossbred Holstein dairy cattle. Genetics and Molecular Research 16 (2): gmr16029091.