Validation of US genomic prediction for milk and fat yield for Holstein cattle in subtropical Taiwan

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Abstract

Taiwan is located in the subtropical zone, with high temperature and high humidity and small temperature difference between day and night. It is not an ideal place to raise Holstein dairy cows. It is worth wondering how efficacies for US genome-enhanced genetic predictions for actual milk and fat production traits of Holstein cows in subtropical Taiwan. The correlation between genomically-enhanced predicted milk and fat transmitting ability (gPTAM and gPTAF) and the first lactation milk and fat yield (305, 2X, ME) were conducted and 733 dairy cows from 19 farms were used as experimental animals. The correlation coefficient is 0.36 and 0.29 for milk and fat yield, respectively. The correlation coefficient for milk and fat yield of the 19 herds ranged from -0.02 to 0.70 and -0.01 to 0.90, respectively. gPTAM and gPTAF were used to rank and assign animals to quartiles (genetic groups: worst 25%, 26–50%, 51–75%, and best 25%). The average first milk yield performance of the above four herds was 8,410 (±1,499), 8,916 (±1,653), 9,324 (±1,539) and 9,993 (±1,679) kg, respectively. The average first fat yield performance of the above four herds was 370 (±72), 394 (±73), 402 (±77) and 428 (±83) kg, respectively. Significant differences were observed between quartiles for milk and fat production (P < 0.05). According to Taiwan average raw milk price ($1.17 dollar per kg), the profit differences between the top and bottom quartiles were $1,852 dollar per cow. It showed that the gPTA of genetic testing can be used as a breeding tool for selecting superior dairy cows. With proper management, it will help increase the profitability of the herd in subtropical zone.

Key words: Holstein cattle; Genetic testing; Genomically-enhanced predicted transmitting ability.

Introduction

A technology based on the detection of single nucleotide polymorphisms (SNP) is a major revolution in animal breeding, as a tool termed genomic selection (Meuwissen *et al.*, 2001), combined with phenotype and pedigree data to comprehensively detect the allelic variances that affect these phenotypes have the advantages of increasing accuracy of selection, selection intensity, and reducing generation interval to accelerate genetic gain (Seidel, 2010). Widespread use of DNA markers have significantly impacted breeding program strategies and reduce breeding costs. After Illumina launched the first genome-wide SNP chip (BovineSNP50 BeadChip) in 2007, it first published genomic estimated breeding value (GEBV) of American Holstein cattle in 2009. Since then, dairy-advanced countries have established genomic evaluation of Holstein cattle and other dairy cattle breeds on a routine basis (Cole, 2014; Lund *et al.*, 2011; De Haas *et al.*, 2012; Durr and Philipsson, 2012). Norman *et al.* (2014) reported that the implementation of genomic evaluation has changed the breeding program

in the United States. The number of genotyped US bulls and cows has increased steadily since 2007. Over 6.5 million dairy animals have been genetically evaluated. Genomically-enhanced predicted transmitting abilities (gPTA) and reliabilities was calculated for each trait to assess how well or bad it is.

The correlation assessment between genetic predictions and the observed performance of tested animals in externally validated populations or even foreign populations is helpful in evaluating the accuracy of any genetic evaluation or prediction algorithm. McNeel *et al.*, (2017) and Wijma *et al.*, (2022) have evaluated the validity of genetic prediction of wellness traits and abortion in commercial herds of American Holstein dairy cattle, respectively. The tested herds did not provide any phenotypic information and were not involved in genetic evaluation. Fessenden *et al.* (2020) also assessed that a specific selection index comprising gPTAs was able to predict successfully the observed lifetime profits in American Holstein animals. It is worth wondering how efficacies for such prediction apply to herds in other regions. Therefore, a validation study was performed to assess the efficacy of genome-enhanced genetic predictions for milk and fat production traits in Holstein cows located outside the United States, such as subtropical Taiwan.

Material and methods

The hair follicles or blood sampling approach was similar to previous report by our group (Chao *et al.*, 2022). Briefly, samples were collected from 733 random cows in 19 herds (herds from Northern, Central, Southern, and Eastern Taiwan and Kinmen Islands, respectively). The animal use protocol was reviewed and approved by the Institutional Animal Care and Use Committee of the Taiwan Livestock Research Institute (LRI-IACUC108-1 and LRI-IACUC109-1). The data, including the date of birth, sire and dam of the tested cow and sample collection card were mailed to the Neogen Genomics Lab in Lincoln, NE, United States, and the GGP bovine 50K SNP chips that use Illumina Infinium technology (Illumina, 2017) were used for genotyping. The CDCB-certified laboratory at Neogen uses the Illumina Infinium XT genotyping assay platform (Illumina, 2017).

The milk production traits analyzed in this study include milk yield and fat yield. Taking the milk yield of the full lactation period as an example, it refers to the accumulated milk yield of a cow after adjusting the lactation days of the first parity to 305 days after parturition. The data editing procedure included the following steps: (1) Extracted the "Monthly Lactation Record Data" of the DHI database as the data source. (2) Screened more than 7 monthly milk sampling times with lactation days between 235 and 315 days, and added them to the data set. (3) For lactation records with less than 305 days of lactation, used the linear regression method to calculate the milk yield on the day without milk sampling records (Robert *et al.*, 1997).

Results and discussion

The aim of this study was to evaluate the associations between gPTAs of genomic evaluation and observed milk and fat performance in Taiwan cattle, and to dissect whether the accuracy of genomic prediction analysis is different due to environments. A total of 733 dairy cattle were verified the accuracy of genomic prediction. The correlation between the gPTAM, gPTAF and the first lactation milk, fat yield is 0.36 and 0.29, respectively (Figure 1 and 2). Further comparison of the data among 19 herds showed that the correlation of the gPTAM and the first lactation milk yield were different, and the value of the correlation ranged from -0.02 to 0.70 and -0.01 to 0.90, respectively. The higher correlation between gPTAM and the first lactation milk yield indicated that
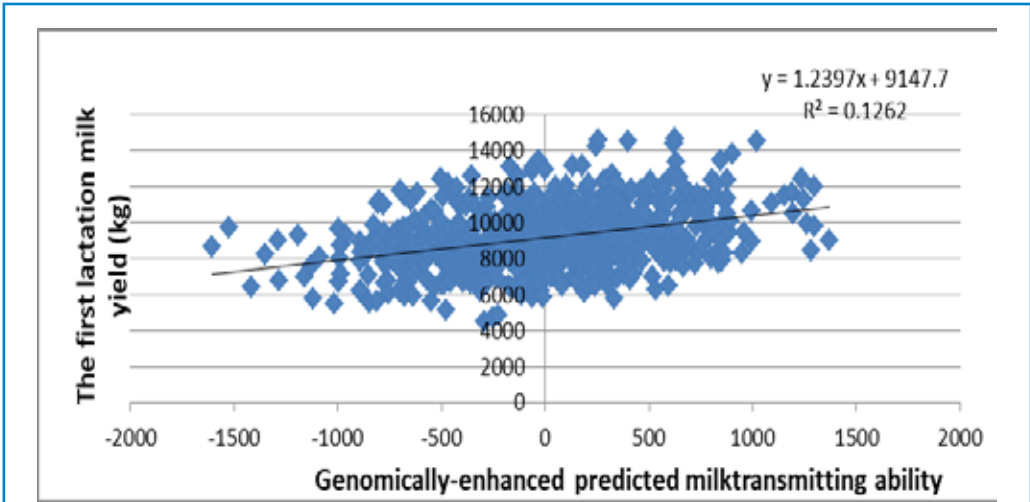
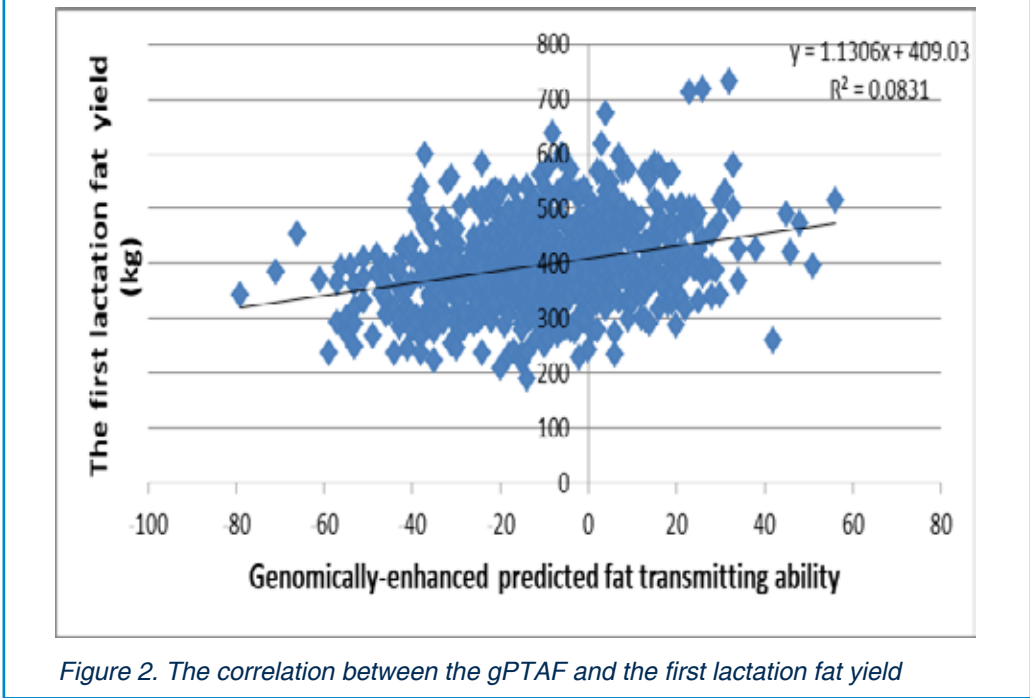Figure 1. The correlation between the gPTAM and the first lactation milk yield.

Figure 2. The correlation between the gPTAF and the first lactation fat yield

superior cattle could be exerted their genetic potential outstandingly in well-managed herds. On the other hand, even if poorly managed herds own superior cattle that could only be achieved moderate production performance, and moreover, even poor management makes the performance of superior cattle even worse. It can be seen that the genetic composition of cattle is the core for its production performance, and it needs to cooperate with management practice to achieve the genetic effect. These tests can also inform dairy producers on the genetic makeup and actual performance of the cattle on the farm to adjust management strategies.

Differences in milk and fat production were statistically significant between the genetic groups. gPTAM and gPTAF were used to rank and assign animals to quartiles (genetic groups: worst 25%, 26–50%, 51–75%, and best 25%). The average first

milk yield performance of the above four herds was 8,410 (±1,499), 8,916 (±1,653), 9,324 (±1,539) and 9,993 (±1,679) kg, respectively (Figure 3). The average first fat yield performance of the above four herds was 370 (±72), 394 (±73), 402 (±77) and 428 (±83) kg, respectively (Figure 4). Significant differences were observed between quartiles for milk and fat production ($P < 0.05$).

As shown in Figure 3 and 4, the differences between the top and bottom quartiles were 1,583 kg for milk production and 58 kg for fat production. According to Taiwan average raw milk price ($1.17 dollar per kg), the profit differences between the top and bottom quartiles were $ 1,852 dollar per cow. This indicated that animals with higher value
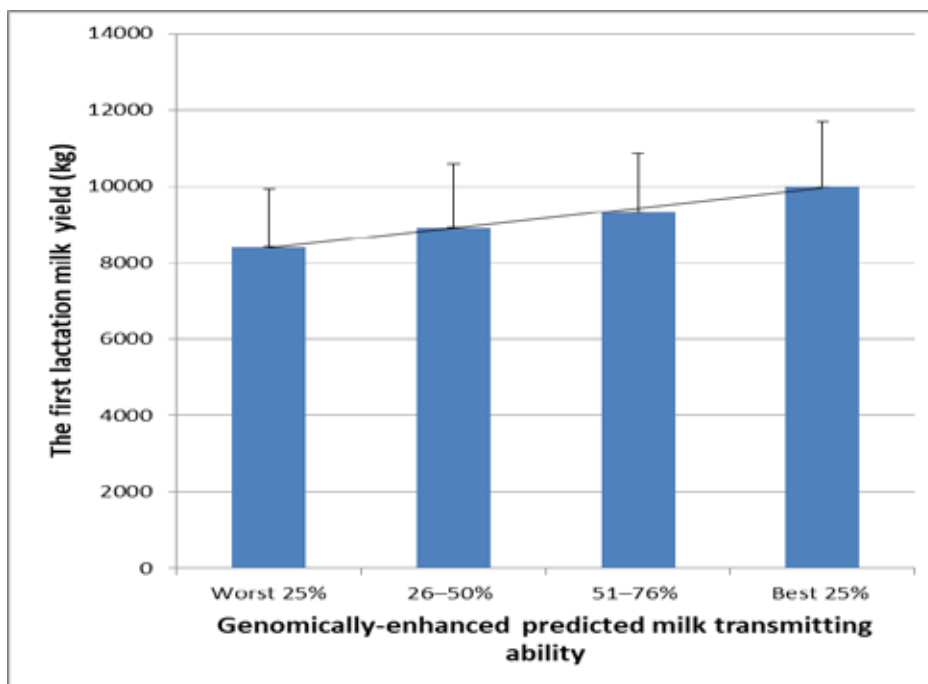

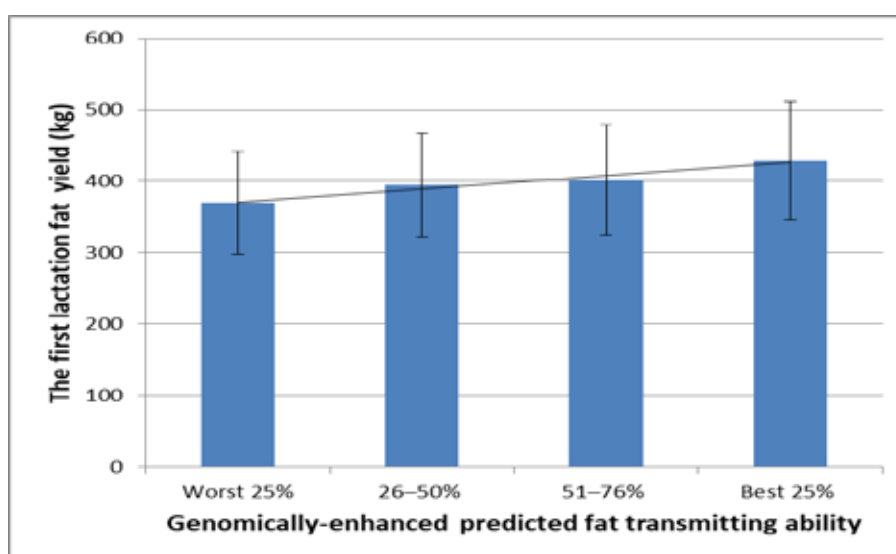Figure 3. Differences in milk production between the genetic groups.

Figure 4. Differences in fat production between the genetic groups.

predictions had higher observed profit than animals with lower value predictions. The observed results demonstrate the ability of production trait predictions to accurately predict production performance.

Our results showed that it is very suitable to use the gPTA values of tested heifers for making culling and breeding decisions. In the future, it can be expanded to milk protein, somatic cell counts and other traits for such association testing. It will move towards a balanced selection that takes into account all economic performances and use the gNM$ and productive life to select healthier, fertility and longevity cattle.

Acknowledgments

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