

Relationship of Endocrine Pathway SNP and Molecular Breeding Value with Milk Production in Heat Stressed Holstein Cows

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Abstract: Milk performance data were collected from lactating Holstein cows (n=660) in the Yaqui Valley, Sonora, Mexico where temperatures in summer average 32°C. Cows were genotyped for 179 SNP from 41 genes in the growth hormone signaling and prolactin pathways. Twenty-four SNP had significant association with milk production traits and used to calculate molecular breeding value (MBV; 4448.8 ± 33 L) in 551 cows. Two statistical models were used: full model with effects for age, lactation season, contemporary group (farm management) and MBV, and a reduced model with MBV. The coefficients of determination among the models were compared and we found 2.7% of the variation in adjusted 305 days milk production ($\sigma^2=598.9 \times 10^{-3}$) was attributed to MBV. Our findings support our hypothesis, MBV predicts milk performance traits in heat stressed Holstein cows in Sonora.

Key words:

SNP

PRL pathway

MBV

Introduction

One of the challenges of milk production in tropical climates is heat stress. With high temperatures and intense radiant energy, lactating dairy cows accumulate metabolic heat, increasing body temperature and subsequently decreasing feed intake and therefore milk production (West (2003)). Although management strategies to alleviate heat stress in dairy cattle have been implemented, production markedly decreases during summer (i.e milk yield decreases by 10-15%, Dunshea et al. (2013)). When heat stress persists, gene expression changes lead to altered physiological state referred to as “acclimation” a process largely controlled by endocrine systems. (Collier et al. (2008)).

Genotype data from dairy cattle, in particular genes associated with endocrine pathways involved in lactation, have the potential to be used as tools to improve milk production. Prolactin and growth hormone play crucial roles in the initiation and maintenance of lactation in mammals and it has been reported that there is a significant association between genotypes in these genes and the milk performance in Holsteins (Lü et al. (2010)). We hypothesized that

MBV predicts milk performance traits in heat stressed Holsteins cows in Sonora. The objective of this study was to determine if the MBV account for a portion of the variation in phenotypes.

Materials and Methods

Animals. Data were from Holstein cows (n = 666) of three commercial dairy farms located in Block 910 of the Yaqui Valley in Ciudad Obregon Sonora, Mexico (27°21' N, 109°54' W). Cows were progeny of 159 sires and 360 dams. Cows were housed in free stall barns, with free access to shade and water and were fed twice daily with a ration of 75% alfalfa hay and 25% corn silage, and a commercial vitamin and mineral premix. This mixed ration was provided according to the NRC (2001) requirements established for lactating Holstein cows weighing 650 kg, and producing ~30 kg/d of milk with average composition (i.e., 3.5% fat and 3.2% true protein).

Milk performance data was adjusted to 305 days of lactation and used to calculate total adjusted milk production and daily average adjusted milk production per cow. These data were also used to determine the peak day and milk produced at peak day.

SNP and MBV. Forty-one genes within the prolactin and growth hormone-insulin-like growth hormone pathways were previously re-sequenced and yielded a panel of 179 tag SNP. DNA was extracted from whole blood spotted on FTA cards and genotyped with the Sequenom MassArray platform (GeneSeek, Inc., Lincoln, NE). The MBV for 551 Holstein cows were calculated by summing the additive genotype effect at each locus (4448.8 ± 33.0 L) for 24 SNP that showed a significant (P<0.05) association with milk performance traits

Statistical analysis. Summary statistics for milk performance adjusted to 305 days were calculated with SAS. A regression-prediction analysis using Proc Mixed was used to estimate a full and reduced model with the effects of age, lactation season (lac.s), contemporary group (CG) as farm management and MBV respectively:

$$Y_{305} = \beta_{age} + \beta_{lac.s} + \beta_{MBV} + \beta_{CG}$$

$$Y_{305} = \beta_{MBV}$$

Lactation seasons were calculated by partitioning the year into three seasons: from January to March, April to June, and August to December and using the calving date as a reference. Pearson correlations of age, MBV and milk production adjusted to 305 days were also calculated.

Results and Discussion

Summary statistic and correlations.

Distribution of milk performance adjusted to 305 days of lactation measurements was normal and summary statistics are presented in **Table 1**. A low positive correlation was observed between MBV and milk production adjusted to 305 days, along with moderate positive correlation with the age of the cow (**Table 2**). The low correlation of MBV and milk production may be explained by heat stress.

Evaluation of the full vs. reduce model. The full model had a coefficient of determination of 42.7%, in comparison with the coefficient of determination of 2.7% for the reduce model with only the MBV. The difference between the models was 40.1% (**Table 3**). The small amount of variation due to MBV led us to postulate that the high ambient temperatures to which dairy cattle were be exposed may have negated a cow's positive MBV.

Parameter estimations. Within the full model, only season of lactation showed no significance (**Table 4**). This may be due to the steady high temperatures during the year in Sonora, Mexico. Parameters estimate for the remainder effects were significant ($P < 0.05$) in both models as expected (Pryce et al. (1998)). Further research is necessary to perform better genetic evaluations in dairy cattle under heat stress conditions.

Conclusions

The MBV estimated from SNP in prolactin and growth hormone signaling genes was weakly associated with milk production adjusted to 305 days in Holstein cows. This MBV accounted for 2.7% of the phenotypic variation in milk production adjusted to 305 days. Taking in account the moderate effect of the small number of SNP effects used to calculate MBV, our findings support our hypothesis, MBV predicts milk performance traits in heat stressed Holstein cows in Sonora.

References

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Table 1. Summary statistic for milk production adjusted to 305 days of lactation.

Trait	N	Mean ²	SD ²	Min ²	Max ²
Adj305 ¹	549	6,257.2	1,467.9	632.1	10,787.5

¹ Milk performance adjusted at 305 days of lactation
² mean, standard deviation (SD), minimum (Min) and maximum (Max) values are given in liters.

Table 2. Correlation between continuous effects and milk production adjusted to 305 days of lactation.

Fixed effects	305 days milk production
Age	0.43115
MBV ¹	0.16267

¹ Molecular breeding value

Table 3. Coefficients of determination for the two models.

Model	coefficient of determination
Full ¹	0.4273
Reduce ²	0.0265

¹ $Y_{305} = \beta_{age} + \beta_{lac.s} + \beta_{MBV} + \beta_{GG}$.

² $Y_{305} = \beta_{MBV}$

Table 4. P-values for fixed effects on the full model.

Fixed effect	p-values
CG ¹	< 0.0001
Age	< 0.0001
Lactation season	0.4641
MBV ²	< 0.0001

¹ CG: farm management

² Molecular breeding value