Proc. Assoc. Advmt. Anim. Breed. Genet. 20:199-202

GENETIC EVALUATION FOR RESISTANCE TO METABOLIC DISEASES IN CANADIAN HOLSTEINS

F. Miglior[1,2], A. Koeck[3], J. Jamrozik[3], D.F. Kelton[4], S. Loker,[3,5] K. Stachowicz,[3,6] and F.S. Schenkel[3]

[1]Guelph Food Research Centre, Agriculture and Agri-Food Canada, Guelph, ON, Canada, N1G 5C9
[2]Canadian Dairy Network, Guelph, ON, Canada, N1K 1E5
[3]Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, N1G 2W1
[4]Department of Population Medicine, Ontario Veterinary College, Guelph, ON, Canada, N1G 2W1
[5]Livestock Improvement Co, Newstead, Hamilton 3284, New Zealand
[6]AbacusBio Limited, PO Box 5585, Dunedin, New Zealand

SUMMARY

The overall objective of this study was to investigate if a genetic evaluation for resistance to metabolic diseases (**METAB**), which jointly includes cases for ketosis, displaced abomasum and milk fever, would be feasible in Canada. Health data recorded by producers were available from the national dairy cattle health recording system. Heritability estimates for METAB were 0.03 and 0.02 in first and later lactations, respectively. METAB in first lactation was a different trait than METAB in later lactations (genetic correlation = 0.76). Moderate genetic correlations were found between METAB and body condition score, fat to protein ratio and milk ß-hydroxybutyrate in first lactation cows. Pearson correlations between breeding values for METAB resistance and other routinely evaluated traits were computed, which revealed noticeable favorable relationships to direct herd life and fertility. The present study showed that a genetic evaluation for resistance to METAB based on producer-recorded health data would be feasible in Canada. Selection for METAB would also have a positive impact on cow's fertility and longevity.

INTRODUCTION

In Canada, a national dairy cattle health and disease data management system was started in 2007. The main objectives of this initiative are to provide information to dairy producers and their veterinarians for herd management and to establish a national genetic evaluation system for genetic selection for disease resistance. Eight diseases that are known to affect herd profitability are recorded by producers on a voluntary basis: mastitis, displaced abomasum, ketosis, milk fever, retained placenta, metritis, cystic ovaries and lameness. The feasibility of using producer recorded health data for genetic evaluations for disease resistance in Canada has been shown previously by Neuenschwander *et al.* (2012). In this study the first results of a genetic evaluation for resistance to metabolic diseases (**METAB**) in Canadian Holsteins are presented.

MATERIALS AND METHODS

Data. Health data recorded by dairy producers from April 2007 to August 2012, body condition score (**BCS**) records, as well as test-day records of milk, fat and protein yield between 5 and 55 DIM, were obtained from the Canadian Dairy Network (Guelph, Ontario). Data on milk ß-hydroxybutyrate (**BHBA**), which is only recorded in some herds in Quebec, was available from January 2011 onwards. In order to ensure that all cows were from herds with reliable recording of METAB, several editing criteria were applied. Only herds having at least two records of METAB were considered. The first and last record had to be at least 180 d apart to remove herds which had

done recording just for a short time period. In addition, a minimum disease frequency (reported cases per herd and year) of 1% was applied to ensure continuous data recording within individual herds. For genetic analyses, only records from first to fifth lactation Canadian Holstein cows were considered. The sire pedigree file was generated by tracing the pedigrees of sires and maternal grandsires back as far as possible.

Traits. The trait METAB was defined as a binary trait (0 = no disease case, 1 = at least one disease case) based on whether or not the cow had at least one case for ketosis, displaced abomasum or milk fever in the period from calving to 100 d after calving. Three traits that are indicators of energy balance and may subsequently be related to the metabolic status of an animal were included: BCS, fat to protein ratio (**F:P**) and milk BHBA. BCS was routinely recorded by professional type classifiers on a scale from 1 to 5 in increments of 0.25. Only first classifications within 365 DIM were analyzed. For BCS only information from first lactation cows was available. For F:P and milk BHBA the first-day record between 5 and 55 DIM was considered as almost all cases of METAB occur during this time period. For the traits METAB, F:P and milk BHBA first and later lactation records were considered as different traits. Summary statistics of the analyzed data is given in Table 1.

Table 1. Summary statistics of the data set used [metabolic diseases (METAB), body condition score (BCS), first test-day fat to protein ratio (F:P) and milk ß-hydroxybutyrate (BHBA)]

Trait[1]	Number of records	Mean	SD
$METAB_1$, %	141,297	3.82	0.19
$METAB_{2+}$, %	266,677	7.99	0.27
BCS, points	124,259	2.82	0.36
$F:P_1$	134,100	1.32	0.27
$F:P_{2+}$	251,835	1.33	0.28
$BHBA_1$, mmol/l	7,701	0.15	0.08
$BHBA_{2+}$, mmol/l	14,894	0.16	0.09

[1]1 = first lactation cows; 2+ = second and higher lactation cows

Model. Linear sire models were fitted using the AI-REML procedure in the DMU package (Madsen and Jensen, 2008).

The model used for $METAB_1$, $F:P_1$ and milk $BHBA_1$ was: $\mathbf{y = X\beta + Z_h h + Z_s s + e}$
where **y** is a vector of observations; **β** is a vector of systematic effects, including fixed effects of age at calving for all traits, year-season of calving for all traits and days in milk for $F:P_1$ and milk $BHBA_1$; **h** is a vector of random herd-year of calving effects for all traits; **s** is a vector of random additive genetic sire effects; **e** is a vector of random residuals; and **X**, $\mathbf{Z_h}$, and $\mathbf{Z_s}$ are the corresponding incidence matrices.

The model for BCS was: $\mathbf{y = X\beta + Z_s s + e}$
where **y** is a vector of observations; **β** is a vector of systematic effects, including fixed effects of herd-round-classifier and age at calving-stage of lactation; **s** and **e** are as defined above; and **X**, and $\mathbf{Z_s}$ are the corresponding incidence matrices.

The model for $METAB_{2+}$, $F:P_{2+}$ and milk $BHBA_{2+}$ was: $\mathbf{y = X\beta + Z_h h + Z_s s + Z_p p + e}$
where **y** is a vector of observations; **β** is a vector of systematic effects, including fixed effects of parity, year-season of calving and days in milk; **p** is a vector of random permanent environmental effects; **h**, **s** and **e** are as defined above; and **X**, $\mathbf{Z_h}$, $\mathbf{Z_s}$, and $\mathbf{Z_p}$ are the corresponding incidence matrices. Bivariate models were carried out for each combination of 2 traits considered in the present study. Assumptions were that:

[**h**' **s**' **p**' **e**']' ~ N[**0**, **V**] with $\mathbf{V} = \sum_{i=1}^{4} \mathbf{V}_i$, where

$\mathbf{V}_1 = \mathbf{I} \otimes \mathbf{H}$, **I** is an identity matrix, **H** is a covariance matrix for HY effects;
$\mathbf{V}_2 = \mathbf{A} \otimes \mathbf{G}$, **A** is an additive relationship matrix, **G** is a genetic covariance matrix;
$\mathbf{V}_3 = \mathbf{I} \otimes \mathbf{P}$, **P** is a covariance matrix for permanent environmental effect;
$\mathbf{V}_4 = \sum_{i=1}^{N} \mathbf{E}_i$, $\mathbf{E}_i$ is a residual covariance matrix. Residuals for all traits were assumed to be correlated.

Breeding value estimation. Breeding values of sires with at least 30 daughters for METAB in first and later lactations were obtained from a bivariate analysis. Estimated breeding values were reversed in sign. Thus, higher breeding values indicate sires with daughters more resistant to METAB.

RESULTS AND DISCUSSION

The frequency of METAB was 3.8 and 8.0% in first and later lactations, respectively. Heritability estimates and genetic correlations for all traits are given in Table 2. Heritability estimates for METAB were 0.03 and 0.02 in first and later lactations, respectively. In agreement with previous studies, a heritability of 0.23 was obtained for BCS. Heritabilities for F:P were 0.15 and 0.12 in first and later lactations, respectively. For milk BHBA a heritability of 0.12 was obtained in first and later lactations. METAB in first lactation was a different trait than METAB in older cows (genetic correlation = 0.76). In first lactation cows, METAB was moderately correlated with BCS (-0.44). Moderate correlations of 0.29 and 0.32 were also found between METAB and F:P and METAB and milk BHBA, respectively, in first lactation cows. Genetic correlations between METAB in later lactation cows and F:P and milk BHBA were lower.

Table 2. Heritabilities (on the diagonal) and genetic correlations (above the diagonal) for metabolic diseases (METAB), body condition score (BCS), first test-day fat to protein ratio (F:P) and milk ß-hydroxybutyrate (BHBA)

Traits	$METAB_1$	$METAB_{2+}$	BCS	$F:P_1$	$F:P_{2+}$	$BHBA_1$	$BHBA_{2+}$
$METAB_1$	**0.03**	0.76	-0.44	0.29	-0.05	0.32	-0.08
$METAB_{2+}$		**0.02**	-0.13	0.01	0.12	0.25	0.11
BCS			**0.23**	-0.33	-0.03	-0.36	-0.02
$F:P_1$				**0.15**	0.75	0.32	0.02
$F:P_{2+}$					**0.12**	0.12	0.19
$BHBA_1$						**0.12**	0.68
$BHBA_{2+}$							**0.12**

(1 = first lactation cows; 2+ = second and higher lactation cows)

Correlations of sire breeding values for resistance to METAB with other routinely evaluated traits are shown in Table 3. Routinely evaluated traits in Canada, with the exception of SCS, are scored so that a higher breeding value is favorable. Higher angularity was genetically linked with more cases of METAB. Favorable associations were found with fertility and longevity, which indicate that selection for resistance to METAB would lead to selection for cattle with improved fertility and longer herd life. Also, a higher resistance to METAB in later lactations was associated with a better Lifetime Profit Index (**LPI**) and the LPI-Production component.

Table 3. Pearson correlations between breeding values of sires with at least 30 daughters for resistance to metabolic diseases in first ($METAB_1$) and later lactations ($METAB_{2+}$) and other routinely evaluated traits (n=number of sires)

Trait[1]	$METAB_1$ (n=525)	$METAB_{2+}$ (n=1,084)
LPI (Lifetime Profit Index)	0.04	0.21***
LPI – Production	-0.03	0.23***
LPI – Durability	0.10*	-0.02
LPI – Health & Fertility	0.08	0.06*
Milk yield	-0.02	0.09**
Direct herd life	0.31***	0.18***
Somatic cell score	0.02	-0.04
Calving to first service	0.20***	0.09**
First service to conception (cows)	0.09*	0.03
Days open	0.15***	0.06
Angularity	-0.32***	-0.14***

[1]$METAB_1$, $METAB_{2+}$ and routinely evaluated traits, with the exception of SCS, are scored so that a higher breeding value is favorable. Significant effects: *P<0.05, **P<0.01, ***P<0.001.

CONCLUSIONS

The present study showed that a genetic evaluation for resistance to METAB based on producer-recorded health data would be feasible in Canada. Selection for METAB would also have a positive impact on cow's fertility and longevity.

ACKNOWLEDGMENTS

All dairy producers recording health data are acknowledged. This study was funded by the DairyGen council of CDN (Guelph, ON, Canada) and the NSERC of Canada (Ottawa, ON, Canada).

REFERENCES

Madsen P. and Jensen J. (2008) Danish Institute of Agricultural Sciences, Tjele, Denmark.

Neuenschwander T.F.-O, Miglior F., Jamrozik J., Berke O., Kelton D.F. and Schaeffer L.R. (2012) *Animal* **6**:571.