Alternative Use of Somatic Cells Counts in Genetic Selection for Mastitis Resistance: A new Estimated Breeding Value for Italian Holstein Breed

Finocchiaro R.[1], G. Visentin[1], M. Penasa[2], J.B.C.H.M. van Kaam[1], M. Marusi[1], G. Civati[1] & M. Cassandro[2]

[1] Associazione Nazionale Allevatori Frisona Italiana (ANAFI), Via Bergamo 292, 26100, Cremona, Italy (raffaellafinocchiaro@anafi.it). [2] DAFNAE, Dipartimento di Agronomia Animali Alimenti Risorse Naturali e Ambiente, Università di Padova, Legnaro (PD), Viale dell'Università 16, 35020 Legnaro (PD), Italy

Abstract

A new breeding value estimation for mastitis resistance has been implemented in the Italian Holstein dairy genetic evaluation. This breeding value uses indicators derived from test-day somatic cell counts (SCC) in order to predict the breeding value for resistance to mastitis occurrence. The pattern of test-day SCC contains additional information on mastitis resistance beyond its mean value usually used. These breeding values are combined in an "udder health" index, using different weights based on (co)-variance structure among indicators and direct mastitis observations. This new index will be additional to the already used somatic cell score index. The correlation between the two indexes is estimated at 80% meaning that the two are in the same direction, but they differ in terms of ranking individuals. In order to set up the new index, several indicators, derived from test-day somatic cell counts, have been derived. Alternative SCC traits were: mean and standard deviation of somatic cell score within lactation (SCS_t and SD_SCS_t, respectively), between 5 and 150 DIM (SCS_{150} and SD_SCS_{150}, respectively), and between 151 and 305 DIM (SCS_{305} and SD_SCS_{305}, respectively); infection, a dichotomous trait indicating that at least one SCC test-day record was above 100,000 cells mL^{-1} within lactation; severity, the ratio between the number of test-days with SCC greater than 100,000 cells mL^{-1} and the total number of test-days; severity, the ratio between the number of test-days with SCC greater than 400,000 cells mL^{-1} and the total number of test-days; and cell's peak defined as the number of peaks during lactation (number of times when SCC shows a change from <100,000 to >400,000 mL^{-1} on three consecutive test-days). Once indicators traits have been defined, these have been validated on a sample data-set with direct mastitis information. Multiple trait animal model has been applied and genetic parameter for these traits including direct mastitis have been estimated. The highest genetic correlations between mastitis itself and indicators were with SCS_{150}, SD_SCS, severity and peak equal to 0.39, 0.44, 0.41 and 0.51 respectively. Selection index methodology was applied to estimate appropriate weights to combined these four traits in the aggregate udder health index. This index has been published for the first time during December 2017 evaluation with mean 100 and standard deviation 5. Initially this index will be published only for national and international bulls. Following steps are to set up the genomic evaluation and, also, to participate to the GMace evaluation.

Key words: mastitis, somatic cell count, udder health, breeding value estimation, Holstein

Introduction

Alternative traits derived from somatic cell count (SCC), different from lactation averages, have been recently explored in different studies. They include average test-day SCC in early or late lactation, distribution characteristics such as variation of SCC curve throughout the entire lactation period, and level of infection such as patterns of SCC peaks. Green *et al.* (2004) suggested that maximum SCC and standard deviation of SCC were better indicators of clinical mastitis than geometric mean SCC. Genetic correlations of clinical and subclinical mastitis with several alternative SCC traits were estimated by de Haas *et al.* (2008), who concluded that the use of a combination of different SCC traits may be more successful in improving udder health than the traditional SCC. Similarly, Urioste *et al.* (2010) investigated a number of alternative SCC traits to capture changes in SCC distribution, time and

level of infection, and time of recovery, in comparison to the traditional lactation-mean SCC, and the reported SCC standard deviation and presence of test-day SCC > 500,000 cells mL^{-1} were promising for breeding purposes. Koeck *et al.* (2012) demonstrated that mean somatic cell score (SCS) in early lactation, standard deviation of SCS and presence or absence of test-day SCC > 500,000 cells mL^{-1} were the best predictors of mastitis resistance.

Based on the aforementioned findings, the aim of the present study was to set up a new udder health index for mastitis resistance in the Italian Holstein dairy population using indicators derived from test-day SCC.

Material and Methods

Traits

Single test-day SCC data of each animal were log-transformed to somatic cell score (SCS; Ali and Shook, 1980) as $SCS=\log_2(SCC/100{,}000)$. Novel traits were defined to capture different aspects of mastitis. Alternative SCC traits were: mean and standard deviation of SCS within lactation (SCS_t and SD_SCS_t, respectively), between 5 and 150 DIM (SCS_{150} and SD_SCS_{150}, respectively), and between 151 and 305 DIM (SCS_{305} and SD_SCS_{305}, respectively); infection, a dichotomous trait indicating that at least one test-day SCC record was above 100,000 cells mL^{-1} within lactation; $severity_1$, the ratio between the number of test-days with SCC greater than 100,000 cells mL^{-1} and the total number of test-days within lactation; $severity_2$, the ratio between the number of test-days with SCC greater than 400,000 cells mL^{-1} and the total number of test-days within lactation; and peak defined as the number of peaks during lactation (number of times when SCC shows a change from <100,000 to >400,000 mL^{-1} on three consecutive test-days). Once indicators traits have been defined, these have been validated on a sample data-set with direct mastitis information, and those with the strongest genetic correlation with the objective of selection (i.e., clinical mastitis) have been retained to develop the aggregate selection index and define index weights.

Statistical Model

Currently breeding values are available only for first parity cows. Cows with at least 3 test-days SCC records, first test-day within 60 days from calving and interval between test-days within 70 days are included in the analysis. Cows with 20 to 40 months of age at calving are considered in the analysis. Fixed effects are herd-year-season, age of the cow at calving, number of test-days within lactation, while animal is considered as random. Genealogical information traces back up to 5 generations. Genetic correlations between alternative SCS traits, and direct clinical mastitis have been estimated using a multiple trait animal model. Linear models were applied in this study as they were found to be robust for genetic analysis on such traits (Negussie *et al.*, 2008; Koeck *et al.*, 2010). The new udder health index was built following selection index methodology in order to estimate appropriate weights to combine the alternative traits in the aggregate udder health index. Variance components were estimated using the software VCE (ver. 6.0, Groeneveld *et al.*, 2010).

Results and Discussion

Descriptive statistics of the breeding objective (clinical mastitis) and selection criteria (SCS_{150}, SD_SCS_t, severity of infection, and peak pattern), are depicted in Table 1. Average clinical mastitis was 9%, whereas mean SCS from 5 to 150 DIM was 2.58. Mean SD_SCS_t, severity of infection, and peak pattern were 1.20, 0.11, and 0.10, respectively. Heritability estimates of the udder-health related traits suggested that 2-7% (peak pattern and severity of infection, respectively) of the total variation was due to differences in animal's genetic merit. The low heritability estimates of all traits reported in Table 1 were consistent with findings of de Haas *et al.* (2008) and Urioste *et al.* (2010). Heritability of the aggregate udder health index was 0.15. Considerable genetic variation existed for all the udder health related traits indicating that, despite the low heritability estimates, genetic gain for the reduction of mastitis events is indeed achievable. Genetic correlations between mastitis and alternative SCS traits are reported in Table 1, ranging from 0.39 (between clinical mastitis and SCS150) to

0.51 (clinical mastitis and peak pattern). Nevertheless, the genetic correlation between the breeding objective and SD_SCSt and severity of infection was 0.44 and 0.41, respectively. The correlation between the current SCS index and the new udder health index is 0.80 (Figure 1). This correlation shows that the two indices are in the same direction but they differ, therefore the new index gives an additional information about the cow's susceptibility to mastitis. Because of the less-than-unity correlation between the current SCS index and the new udder health index, bull rankings will differ.

Conclusion

This index has been published for the first time following the December 2017 evaluation with mean 100 and standard deviation 5. Initially this index will be published only for proven national and international bulls. Following steps are to set up the genomic evaluation and, also, to supply data for GMACE evaluation. Moreover, the breeding values will be extended also to pluriparous cows.

Table 1. Mean, standard deviation (SD), heritability (h^2), and genetic correlation (r_g) between clinical mastitis and predictive traits.

Trait	Mean	SD	h^2	r_g
Clinical mastitis	0.09	0.28	0.03	
SCS_{150}	2.58	1.37	0.06	0.39
SD_SCS_t	1.20	0.62	0.02	0.44
Severity of infection	0.11	0.19	0.07	0.41
Peak pattern	0.10	0.31	0.02	0.51

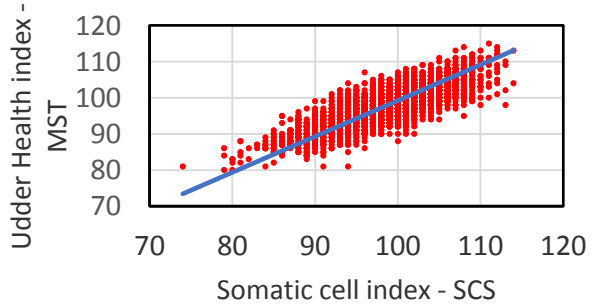

Figure 1. Udder health index (MST) plotted against somatic cell index (SCS).

Acknowledgments

This study was supported by Latteco project "Fondo europeo agricolo per lo sviluppo rurale: Autorità di gestione: Ministero delle politiche Agricole Alimentari e Forestali (MIPAAF)"., sottomisura 10.2 of the PSRN-Biodiversity 2014-2020.

List of References

Ali, A.K.A. & Shook, G.E. 1980. An optimum transformation for somatic cell concentration in milk. *J. Dairy Sci. 63*, 487–490.

Green, M.J., Green, L.E., Schukken, Y.H., Bradley, A.J., Peeler, E.J., Barkema, H.W., de Haas, Y., Collis, V.J. & Medley, G.F. 2004. Somatic cell count distributions during lactation predict clinical mastitis. *J. Dairy Sci. 87*, 1256–1264.

de Haas, Y., Ouweltjes, W., ten Napel, J., Windig, J.J. & de Jong, G. 2008. Alternative somatic cell count traits as mastitis indicators for genetic selection. *J. Dairy Sci. 91*, 2501–2511.

Koeck, A., Heringstad, B., Egger-Danner, C., Fuerst, C. & Fuerst-Waltl, B. 2010. Comparison of different models for genetic analysis of clinical mastitis in Austrian Fleckvieh dual-purpose cows. *J. Dairy Sci. 93*, 4351–4358.

Koeck, A., Miglior, F., Kelton, D.F. & Schenkel, F.S. 2012. Alternative somatic cell count traits to improve mastitis resistance in Canadian Holsteins. *J. Dairy Sci. 95*, 432–439.

Groeneveld, E., Kovač, M. & Mielenz, N. 2010. VCE User's Guide and Reference Manual, version 6.0. Institute of Farm Animal Genetics, Neustadt, Germany.

Negussie, E., Strandén, I. & Mäntysaari, E.A. 2008. Genetic analysis of liability to clinical mastitis, with somatic cell score and production traits using bivariate threshold-linear and linear-linear models. *Livest. Sci. 117*, 52–59.

Urioste, J.I., Franzén, J. & Strandberg, E. 2010. Phenotypic and genetic characterization of novel somatic cell count traits from weekly or monthly observations. *J. Dairy Sci. 93*, 5930–5941.