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Genetic and phenotypic parameters for individual cow somatic cell counts in Zimbabwean Holstein-Friesian cattle

Dedicated to Professor Dr. Erhard Kallweit on the occasion of his 65th birthday

Summary

Genetic and phenotypic parameters for lactation average individual cow SCC in Holstein cattle were estimated. Records from the Zimbabwe Dairy Services Association included a total of 7912 lactation records, from which were 1453 first lactation, 2211 second lactation and 4248 third and later lactation records for the period 1994 to 1998. SCC were transformed through a base 2 logarithm. Genetic parameters were estimated with the AIREML programme. A univariate mixed animal model was used to estimate heritabilities and repeatabilities. The heritability estimates for $\log_2$SCC were 0.10, 0.12 and 0.14 for the respective first, second, third and subsequent lactations. Estimate of repeatability for $\log_2$SCC was 0.17. Genetic and phenotypic correlations were estimated with a multivariate mixed animal model. Genetic correlation estimates between $\log_2$SCC and the production traits were low to medium and negative (-0.05 to -0.55) whilst the phenotypic correlation estimates were low and negative (-0.04 to -0.22). As individual cow SCC data collection continues in Zimbabwe, there are opportunities for genetic re-evaluation of this trait with a larger data set. This could possibly include udder type traits, most of which have been reported to be associated with SCC.

Key Words: Zimbabwe, Holstein-Friesian, somatic cell counts (SCC), milk yield, fat corrected milk (FCM), fat kg, protein kg

Zusammenfassung

Titel der Arbeit: **Genetische und phänotypische Parameter für individuelle somatische Zellzahlen bei Holstein-Friesen Kühen in Simbabwe**

Die genetischen und phänotypischen Parameter für individuelle somatische Zellzahlen (SCC) in Holstein-Friesen wurden geschätzt. Die Datensätze des simbabwischen Milchkontrollverbandes umfassten insgesamt 7912 Laktationen, darunter 1453 Erstlaktationen, 2211 Zweitlaktationen und 4248 Dritt- und höhere Laktationen für den Zeitraum 1994 bis 1998. SCC wurde logarithmisch zu Basis 2 umgeformt. Genetische Parameter wurden mit AIREML geschätzt. Ein univariates gemischtes Tiermodell wurde zur Schätzung von Heritabilitäten und Wiederholbarkeiten benutzt. Die Heritabilitätsschätzungen für $\log_2$SCC betrugen 0,10, 0,12 und 0,14 für die erste, zweite und dritte und höhere Laktation. Die geschätzte Wiederholbarkeit betrug 0,17 für den Parameter $\log_2$SCC. Genetische und phänotypische Korrelationen wurden mit einem multivariaten Tiermodell geschätzt. Die genetischen Korrelationen zwischen $\log_2$SCC und den Milchleistungsmerkmalen waren niedrig bis mittel und negativ (-0,05 bis –0,55) während die phänotypischen Korrelationen im niedrigen und negativen Bereich (-0,04 bis –0,22) lagen. Da die individuelle Erfassung des somatischen Zellgehaltes in Simbabwe fortgesetzt wird, ergeben sich Möglichkeiten für eine erneute genetische Analyse mit einem umfangreicheren Datensatz. Eutermerkmale, die einen Zusammenhang mit dem somatischen Zellgehalt zeigen, sollten möglichst dabei berücksichtigt werden.

Schlüsselwörter: Simbabwe, Holstein-Friesen, somatische Zellzahl, Milchleistung, fettkorrigierter Milchertrag, Fett kg, Eiweiß kg

Introduction

Lying within the tropics south of the equator, Zimbabwe is characterised by a sub-tropical Savanna type of climate. It is divided into five agro-ecological regions according to altitude, climate and agriculture. The majority of the dairy farms are in agro-ecological region II. This region is characterised by two distinct seasons, the dry season from May to October, and the wet season from November to April. The dry season comprises of the cold dry period from May to July and the hot dry period from August to October. Climate for this region is characterised by an average annual range of maximum temperatures of 19°C in the cold dry period to 32°C in the hot dry and wet season. Maximum temperatures of up to 24°C have been recorded within this cold dry season. The range of relative humidity is from 55% during the dry season to 90% in the wet season. Average annual rainfall for this region is slightly above 900 mm with a maximum of 1200 mm recorded in some stations. Such conditions are conducive for the incorporation of cultivated pastures that are essential for cattle farming but can have negative effects, either directly or indirectly, on the health of dairy cattle. Besides increasing the numbers of pathogens to which the cows are exposed, these high temperatures and high humidity, especially in the summer period, also increase the susceptibility of the cows to infection by mastitis pathogens. As such, mastitis remains probably the major health threat to the productivity of dairy cattle in both commercial herds and the smallholder dairy development programmes in Zimbabwe. Of all the cows registered with the Zimbabwe Dairy Services Association (ZDSA) that were deliberately removed from the dairy herds for various production related reasons, 22% and 24% were culled because of clinical mastitis in 1997 and 1998 respectively (ZDSA, 1998). A lot more cows could have been culled in the unregistered herds but were not included in this statistic just as were those cows that had mastitis but were cured. Cows affected by sub-clinical mastitis were also not included in this statistic. This high culling rate has been observed despite the use of mastitis control measures, the main of which involve teat dipping, dry cow drug therapy, milking infected animals last and drying off of chronic clinical cases. Because of this, other methods of mastitis control have to be used. One probable method is to include the lactation average individual cow SCC in selection strategies for the local Holstein population.

The use of SCC, expressed as a logarithmic transformation, as an indicator trait for mastitis has been proposed (VECHT et al., 1985; SCHUTZ et al., 1994), since high genetic correlations have been reported between these two traits (EMMANUELSON et al., 1988). Whilst the measurement of mastitis is subjective, SCC measures are objective. The relatively lower variability and heritability estimates for mastitis (SIMIANER et al., 1991; MRODE and SWANSON, 1996) makes SCC a suitable trait on which to select against mastitis. There is therefore a need to determine the genetic properties of this trait for possible inclusion in the breeding strategies of dairy cattle. This has not been done in Zimbabwe although the recording and use of milk SCC to monitor both the cow and herd levels of mastitis was started in 1994 for all ZDSA registered herds. The objectives of this study were thus to estimate the heritability and repeatability values for log transformed lactation average individual cow SCC. The study also aimed at estimating the genetic and phenotypic correlation estimates between log transformed SCC and the yield of milk, 3.5% fat corrected milk (FCM), fat kg and protein kg in Zimbabwean Holstein-Friesian population.

Materials and methods

Analysis included unadjusted 305-day lactation records of the Zimbabwean Holstein population for the period 1994 to 1998 with a full complement of 10 individual cow SCC sample days for the entire lactation period. During this lactation period, milk from the individual cows under the milk recording system is sampled once every thirty days. Milk samples are taken to the ZDSA laboratory for analysis. After staining with a dye, milk samples are passed through a Bentley Somacounter. Vibrations of the stained DNA molecules are read from the counter with each vibration representing 1000 somatic cells per millilitre. In this study, the arithmetic mean of the 10 test-day SCC records for each cow within a lactation were used as the lactation average individual cow SCC. First lactation was restricted to cows calving for the first time at an age of not less than 20 months and not more than 44 months. Second lactation had cows calving for the second time at an age of not less than 33 months and not more than 55 months of age. Cows in the third and subsequent lactations were required to have calved at not less than 45 months and not more than 125 months of age.

Since the number of utilisable records was small, data edits with the Statistical Analysis System (SAS, 1994) imposed a restriction of at least four daughters per sire, to improve the accuracy of the estimated heritability. The restriction also ensured connectedness in the data and reduced bias due to preferential treatment of daughters of a particular sire in a group (JAIRATH et al., 1994). All herds with contemporary groups of less than ten cows were deleted since these would increase the prediction error variances, the magnitude of which is an indicator of the accuracy of prediction of animal breeding values. The data set with all lactation records was required to have only those records of cows with at least two consecutive lactations to improve the accuracy of estimation of the repeatabilities. Observations were assigned to herd-year-season subclasses with month of calving as the season.

The edited lactation records were divided into four data sets. Data set 1 (all lactation records) had 7912 records from 266 sires and 2490 dams in 1 310 herd-year-seasons. Data set 2 (first lactation cows) had 1453 records from 113 sires and 1409 dams in 689 herd-year-seasons. Data set 3 (second lactation cows) had 2211 records from 139 sires and 2120 dams in 893 herd-year-seasons. Data set 4 (third and later lactation records) had 4248 records from 218 sires and 2955 dams in 1154 herd-year-seasons. Because lactation average individual cow SCC ('000/ml) are positively skewed with a median smaller than the mean but greater than the mode, they were transformed through a base 2 logarithm to $\log_2$SCC, to achieve a normal distribution and uniform variance, as suggested by ALI and SHOOK (1980). The descriptive statistics for the lactation average SCC for the respective lactations are shown in Table 1.

Table 1
Minima, maxima and means of lactation average individual cow SCC by parity (Minima, Maxima und Mittelwerte für individuelle Laktationsmittel der SCC in Abhängigkeit von der Laktationsnummer)

Parity	Minimum (per ml)	Mean (per ml)	Maximum (per ml)
All	5 000	614 258	9 999 000
1	6 000	448 420	9 999 000
2	17 000	526 570	9 999 000
3+	84 000	714 717	3 274 000

Estimation of genetic parameters

The genetic parameters were estimated with the Average Information Restricted Maximum Likelihood (AIREML) iterative algorithm (GILMOUR, 1995), with an equal design matrix. Although the inverse of the numerator (additive genetic) relationship matrix was included to account for relationships among all the animals, sire-sire relationships were not considered since an incomplete pedigree with no grandparents was used in this analysis.

A univariate repeatability mixed animal model was used to estimate the variance components for heritability, repeatability and the permanent environmental effects for all lactations (data set 1) and third and later lactation records (data set 4). The model included the fixed effects of herd-year-season, calving interval, linear and quadratic partial regression coefficients on age at calving and the random animal and permanent environmental effects. Analysis of second lactation (data set 3) records used an individual mixed animal model with the same fixed effects but excluding the random permanent environmental effects. A reduced individual mixed animal model used for the analysis of first lactation records (data set 2) had the fixed effects of herd-year-season and the linear and quadratic regressions on age at calving and the random animal effects.

Multivariate mixed animal models, with all traits fitted simultaneously, excluding the random permanent environmental effects, were used to estimate the genetic and phenotypic correlation estimates between the traits.

Results and discussion

The mean values for the individual cow SCC in Table 1 demonstrated an increase in SCC with lactation. This was consistent with published trends (MARCHAND et al., 1995; LABOHM et al., 1998). The mean SCC levels above 500 000 cells/ml of milk in lactations beyond the first indicate a general problem of SCC and mastitis in the analysed Zimbabwean Holsteins-Friesian herds.

Relatively small number of records was used in this study because of the limited availability of comprehensive full lactation somatic cell records. Since the records were for the period 1994 to 1998, the majority of records weré of cows with an average of two repeated records per cow. Few animals had more than three records per cow. Heritability estimates for lactation average $\log_2$SCC by parity are shown in Table 2.

Table 2
Genetic parameters and their standard errors for lactation average $\log_2$SCC (Genetische Parameter und Standardfehler für Laktationsmittelwerte)

Parity	h^2	Permanent environment	Repeatability
All	0.09 (0.03)	0.08 (0.03)	0.17 (0.03)
1	0.10 (0.09)		
2	0.12 (0.07)		
3+	0.14 (0.04)	0.14 (0.04)	0.28 (0.04)

The estimates of the heritabilities for lactation average $\log_2$SCC found in this study were low and consistent with those in literature (BOETTCHER et al., 1998; MRODE et al., 1998). The low estimates were mainly due to the relatively high residual variance and low additive genetic variance for $\log_2$SCC. The high residual variance was probably caused by the presence of factors, other than herd-year-season, age at calving and the random animal effects, that have a significant effect on individual cow SCC but were not fully accounted for by the fitted model. Such factors have been reported in literature to include the duration of milking of individual cows, milking speed (BOETTCHER et al., 1998), over-milking and stray voltage (RENEAU, 1986). Furthermore, there probably were different milking management groups within the different herds in which high yielding and healthy cows were subjected to milking management procedures different from those of the low and mastitic cows. These could include milking high yielding healthy cows for longer duration of time than mastitic cows as well as milking the latter with relatively lower pressure and speed. It, therefore, becomes necessary to adjust for these different fixed management groups within the different herds before estimating the genetic parameters for individual cow SCC.

Although the average individual cow SCC across lactations in this study is high (Table 1), this cannot be a contributing factor to their low individual estimates of heritability in the Zimbabwean Holstein-Friesian cattle. Research has established that the heritability estimates are similar for populations with low or high average log transformed SCC (BANOS and SHOOK, 1990). Despite the fact that heritability estimates tend to be high in low log transformed SCC herds, these differences have been reported to be statistically non-significant.

The heritability estimates for $\log_2$SCC increased, albeit non-significantly, with lactation number. This was caused by a relative decrease in the residual variance for $\log_2$SCC in later lactations. Similar increases in heritability estimates with lactation number have been reported elsewhere for log transformed SCC (BOETTCHER et al., 1998; PRYCE et al., 1998), but with different breeds of cattle. POSO and MANTYSAARI (1996) found heritability estimates of 0.15 and 0.16 in the first and second lactation of Finnish cattle respectively whilst MRODE et al. (1998) published estimates of 0.12 and 0.14 in the first and second lactation respectively. However, research has also established decreasing trends in heritability estimates for log transformed SCC with increasing lactation number (MONARDES et al., 1983; BANOS and SHOOK, 1990). This was attributed to a decrease in sire variance and an increase in the residual variance in higher lactations.

The repeatability estimate of $\log_2$SCC at 0.17 was lower than published estimates: 0.33 for the first three lactations in Holsteins (MRODE et al., 1998) and 0.35 (GROSSMAN et al., 1992; RUPP and HOICHARD, 1997) but consistent with those of MONARDES and HAYES (1985). The heritability estimates for $\log_2$SCC remains low and cannot be any greater than 17% across lactations since estimates of repeatability set the maximum limit of the estimates of heritability. With such a low repeatability estimate for $\log_2$SCC, it is difficult to select animals on the basis of the first lactation performance only since repeatability determines the accuracy of predicting the performance of an animal in later lactations based on its first lactation performance.

The genetic and phenotypic correlation estimates between milk production traits and $\log_2$SCC within and across lactations are in Table 3. Genetic correlation estimates between the production traits and log$_2$SCC were negative, more so within the first and second lactation. Apparently, most of the selection done by the farmers on the basis of individual cow performance is carried out within these first two lactations. As such, there is scope for including individual cow SCC in the overall selection indices for dairy cattle to achieve the maximum economic value of the cows. Direct selection for reduced SCC is not feasible because the individual cow SCC is a secondary trait with low relative economic importance as compared to the production traits.

Table 3
Genetic (below diagonal) and phenotypic (above diagonal) correlations and their standard errors between log$_2$SCC and yield traits across and within parity (Genetische – unterhalb der Diagonalen – und phänotypische – oberhalb der Diagonalen – Korrelationen und Standardfehler zwischen log$_2$SCC und Leistungsmerkmalen für innerhalb und über alle Laktationen)

Parity	Trait	FCM (kg)	Milk (kg)	Fat (kg)	Protein (kg)	Log$_2$SCC
All	FCM (kg)		0.95 (0.00)	0.97 (0.00)	0.96 (0.00)	-0.08 (0.02)
	Milk (kg)	0.93 (0.00)		0.86 (0.00)	0.96 (0.00)	-0.08 (0.02)
	Fat (kg)	0.96 (0.00)	0.81 (0.01)		0.88 (0.01)	-0.08 (0.02)
	Protein (kg)	0.95 (0.00)	0.95 (0.00)	0.88 (0.01)		-0.07 (0.02)
	Log$_2$SCC	-0.07 (0.05)	-0.05 (0.05)	-0.07 (0.05)	-0.05 (0.05)	
1	FCM (kg)		0.95 (0.01)	0.97 (0.00)	0.95 (0.00)	-0.05 (0.04)
	Milk (kg)	0.95 (0.02)		0.83 (0.01)	0.95 (0.00)	-0.06 (0.04)
	Fat (kg)	0.96 (0.01)	0.83 (0.07)		0.88 (0.01)	-0.04 (0.04)
	Protein (kg)	0.96 (0.01)	0.95 (0.02)	0.89 (0.04)		-0.04 (0.04)
	Log$_2$SCC	-0.46 (0.31)	-0.36 (0.32)	-0.50 (0.30)	-0.39 (0.32)	
2	FCM (kg)		0.95 (0.00)	0.97 (0.00)	0.96 (0.00)	-0.22 (0.03)
	Milk (kg)	0.94 (0.02)		0.84 (0.01)	0.95 (0.00)	-0.22 (0.03)
	Fat (kg)	0.96 (0.01)	0.81 (0.05)		0.89 (0.01)	-0.21(0.03)
	Protein (kg)	0.95 (0.01)	0.94 (0.01)	0.88 (0.02)		-0.20(0.03)
	Log$_2$SCC	-0.55 (0.10)	-0.49 (0.14)	-0.54 (0.11)	-0.54 (0.09)	
3+	FCM (kg)		0.95 (0.00)	0.98 (0.00)	0.96 (0.00)	-0.10 (0.02)
	Milk (kg)	0.92 (0.01)		0.86 (0.01)	0.96 (0.00)	-0.09 (0.02)
	Fat (kg)	0.96 (0.00)	0.78 (0.02)		0.90 (0.00)	-0.10 (0.02)
	Protein (kg)	0.95 (0.00)	0.93 (0.00)	0.87 (0.01)		-0.07 (0.02)
	Log$_2$SCC	-0.17 (0.03)	-0.15 (0.03)	-0.18 (0.04)	-0.13 (0.03)	

The negative genetic correlation estimates found in this study also tends to suggest that rapid improvements in individual cow SCC can be achieved through a correlated response to selection for increased yield of either of the production traits. In the multiple lactations, genetic correlations between the $\log_2$SCC and production traits were weak and almost non-significantly different from zero, especially for milk and protein yield. Similar results as well as the absence of genetic correlation between $\log_2$SCC and yield traits have also been reported in literature (POSO and MANTYSAARI, 1994; BEDO et al., 1996). However, research elsewhere has established low but positive correlation estimates (RUPP and HOICHARD, 1997; MRODE et al., 1998; PRYCE et al., 1998) between log transformed SCC and production traits, implying that selection for increased production would result in a correlated increase in milk SCC indicating an antagonistic relationship.

Phenotypic correlations between the production traits and the lactation average $\log_2$SCC were negative particularly in lactations higher than the first, indicating that environmental factors that favour elevated milk somatic cell counts tend to lower the yield of the production traits and vice versa. In this regard, high environmental temperatures and relative humidity increase the number of infecting pathogens and subsequent udder infections. This results in damage to the milk secreting parenchyma in the mammary gland due to the infection and the subsequent increases in the individual cow SCC levels in milk and corresponding reduction in the yield of milk and composition traits. Reduction of the individual cow SCC levels should thus result in an increase in the yield of production traits. Phenotypic correlation estimates between $\log_2$SCC and the yield of FCM and milk were weak whilst those with the yield of fat and protein in the first lactation were non-significantly different from zero and were relatively lower than those in the second lactation. This was as expected because the number of environmental factors, an important determinant of the phenotypic correlation estimates, influencing the milk SCC and production traits are few during the first lactation and increase with lactation number. In the multiple lactations, weak phenotypic correlation estimates were observed between the $\log_2$SCC and the production traits. MRODE et al. (1998) observed negative phenotypic correlations between the yield of protein and fat and log transformed SCC as did PRYCE et al. (1998).

Conclusion

The heritability estimates for log transformed SCC were low, indicating a strong contribution of the environment on the variation of the trait. As a secondary trait, direct selection on $\log_2$SCC is thus not recommended since the response to selection will be low and not economically beneficial to the farmer in the short term. Low individual cow SCC and hence effective mastitis control are better achieved with good herd management of the cows' health environment. Because of the low estimates of repeatability for $\log_2$SCC, the use of a repeatability model in any selection strategy for SCC is not recommended as of now.

The negative estimates of genetic correlation between log transformed SCC and production traits were low to medium within lactations. This study also emphasised the need to include the disease traits in the breeding objectives of dairy cattle in order to accurately estimate the total economic value of dairy cows. Dairy herd management intervention strategies should aim at lowering the milk SCC levels and thus increase the yield of the production traits. As individual cow SCC data collection continues in Zimbabwe, there are opportunities for genetic re-evaluation of this trait with a larger data set. This could possibly include udder type traits, most of which have been reported to be associated with SCC.

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Gesunde Klauen sind nicht nur, aber besonders für Hochleistungskühe eine wichtige Voraussetzung für Gesundheit, Wohlbefinden und eine dauerhafte Leistung. Das trifft um so mehr für Tiere zu, die überwiegend in Stallungen ohne ausreichende Bewegung oder auf Spaltenböden gehalten werden. Die ständige Überwachung der Klauen und die Erhaltung oder Wiederherstellung der natürlichen Funktionen durch sachgemäße Klauenpflege, sind daher für eine erfolgreiche Rinderhaltung unabdingbar. Eine fachgerechte Durchführung ist von einer guten Ausbildung und einem fundiertem Wissen abhängig. Mit diesem Buch dabei zu helfen, ist die Absicht der Autoren. Gleichzeitig soll es den Tierhalter besser befähigen Probleme und Krankheiten an den Klauen zu erkennen und die Zusammenarbeit mit dem Klauenpfleger oder dem Tierarzt effektiver zu gestalten.

Von der Tatsache ausgehend, dass das Wissen um den Bau und die Funktion der Rinderklaue eine Grundvoraussetzung funktioneller Klauenpflege bildet, werden in den ersten Buchteilen in mehreren Abschnitten die funktionelle Anatomie der Zehen des Rindes und die biochemischen Grundlagen ausführlich und anschaulich bebildert, dargelegt. Die folgenden Kapitel sind einer ausführlichen Beschreibung der einzelnen Schritte dieser in Holland erfolgreich entwickelten funktionellen Klauenpflege und den gebräuchlichen Hilfsmitteln, bis zum Anlegen von Klauenbinden, Klauenbädern oder dem Herdenmanagement gewidmet. Im nachfolgenden umfangreichsten Buchteil werden die häufigsten Krankheiten an den Klauen und ihrer Umgebung vorgestellt, die oft als Folgen mangelhafter Pflege auftreten. Übersichtlich und durch die sehr guten farbigen Abbildungen optisch anschaulich unterstützt, werden mittels gut verständlicher Texte zu jeder Krankheit u.a. Aussehen, Ursachen, Entstehen, Behandlung und Vorbeugemaßnahmen beschrieben.

Dieses sehr praxisrelevante, in allen Abschnitten wirkungsvoll durch farbige Abbildungen unterstützte Buch, eignet sich gut als Nachschlagewerk und ist durch die gewählte Spiralbindung auch gut handhabbar. Als wertvolles Sach- und Fachbuch hilft es vor allem Klauenerkrankungen vorzubeugen und diese besser zu erkennen. Es kann die Zusammenarbeit des Praktikers mit dem Klauenpfleger oder Tierarzt verbessern. Daher empfiehlt es sich vor allem praktischen Landwirten, Auszubildenden, Tierärzten aber auch weiteren Interessenten.

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