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SOMATIC CELL COUNT AND MILK UREA NITROGEN LEVELS IN HOLSTEIN AND FLECKVIEH X HOLSTEIN COWS IN A TOTAL MIXED RATION FEEDING SYSTEM

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SUMMARY

Mastitis in dairy cows affects milk yield, welfare and production efficiency. In this paper the somatic cell count (SCC), milk urea nitrogen (MUN) and lactose percentage of 41 Holstein (H) and 30 Fleckvieh x Holstein (FxH) cows were compared using 1688 repeated test-day records. Production parameters did not differ between breeds except for fat and protein percentages being higher in FxH cows. Log transformed SCC did not differ between breeds. However, log transformed SCC was repeatable at 0.21 and should respond to current herd selection. Reducing SCC concentrations in milk would improve welfare of cows as cull rates for mastitis are reduced.

INTRODUCTION

Mastitis is defined as an inflammatory reaction of the udder tissue to bacterial infection. It is one of the most common diseases in dairy cows. The somatic cell count (SCC) of healthy milk is below 200,000 cells/ml of milk with an increase indicative of an infection (Robertson 2016). Mastitis is next to fertility one of the main reasons for cows being culled. Crossbreeding is gaining popularity worldwide as crossbred cows seem to be more robust (Weigel & Barlas, 2003). One aspect of robustness is the ability of cows to withstand developing mastitis under farming conditions. Heins *et al.* (2011) found that breeds differed for SCC showing that Montbéliarde x Holstein and Scandinavian Red x Holstein cows had lower ($P < 0.01$) SCCs than Holstein and Normande x Holstein cows. Milk yield between these breeds also differed ($P < 0.01$) with Holsteins producing the most milk. Somatic cell score (SCS) also increased from first to fifth lactation being 2.73 vs. 4.02 for Holsteins. Montbéliarde x Holstein cows were superior to the other breed groups across lactations for SCS. Prendeville *et al.* (2010) found that even though milk yield differed, udder health (SCS and the incidence of mastitis at least once per lactation) did not differ between Holstein-Friesian, Jersey and Holstein-Friesian x Jersey cows under grazing conditions. The total incidence of mastitis (accounting for repeated incidences) were higher for Jersey cows in comparison to Holstein-Friesian cows, being 1.54 vs. 1.24. Washburn *et al.* (2002) and Berry *et al.* (2007) found that the prevalence of mastitis was higher for Holstein and Holstein-Friesian (HF) cows in comparison to Jersey cows. In South Africa, dairy farmers in pasture-based systems, have attempted crossbreeding using the Fleckvieh breed, a Simmental derived dual-purpose breed from Germany. Muller *et al.* (2009) and Metaxas *et al.* (2014) have shown better fertility and higher fat and protein percentages in FxH cows in comparison to H cows. Farmers perceive a lower incidence of mastitis in Fleckvieh crossbred cows. These claims have not been tested in previous research. The aim of this study is thus to compare the SCC, mastitis incidence, MUN levels in milk of H and FxH cows in a total mixed ration feeding system.

MATERIALS AND METHODS

Data. The study was conducted at the Elsenburg Research Farm of the Western Cape Department of Agriculture. The area has a typical Mediterranean climate with short, cool, wet winters and long, warm, dry summers with an average annual rainfall of 650 mm. Milk production data of H and FxH

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cows in a zero-grazing system were collected over six years between 2008 and 2013. Cows from both breeds were kept together in a dry lot (open camp) with a fence-line feeding trough. Cows were fed a total mixed ration (TMR) providing 17% CP and 11 MJ ME/kg DM. Feeding was twice a day at *ad libitum* levels, i.e.orts not exceeding 5% of feed provided. Fresh drinking water was freely available. Cows were machine-milked twice a day in a milking parlour about 500m from the dry lot. The milk yield of cows at the evening and following morning's milking was recorded approximately every 35 days during the lactation period. Each cow had at least three and a maximum of nine milk recording events per lactation. At each milk production recording event, milk samples were collected at both evening and morning milking sessions. Samples were combined and analysed at the milk testing laboratory of the National Milk Recording Scheme for their fat, protein and lactose concentrations as well as SCC and milk urea nitrogen (MUN) of each sample.

Statistical analyses. Repeated test-day records ($n=1688$) of cross-bred (50% Fleckvieh) cows ($n=30$) were grouped together and compared to H cows ($n=41$). Fixed effects fitted in ASReml included parity (1 to 5), genetic group (FxFI or H), year (2008-2013) and the genetic group x year interaction. Days in milk were fitted as a fixed linear component as well as random cubic spline components to model deviations from linearity following a smooth trend (Gilmour *et al.* 2006). Random animal models were included to account for the repeated sampling of individual cows.

RESULTS AND DISCUSSION

Until recently, breeding programmes have put more emphasis on milk production performance without considering functional traits (Walsh *et al.*, 2009). The effect of breed (genotype) on udder health has been mostly comparing Holstein, Jersey and Jersey x Holstein cows. Although the Fleckvieh breed is the second largest dairy breed in the world, dairy farmers are not familiar with the breed, probably because of the breed's more pronounced dual-purpose characteristics. For this reason, crossbreeding studies in the USA and Ireland have used the Montbéliarde breed, a Simmental derived breed from France which shows more explicit dairy characteristics. Descriptive statistics of milk production parameters for both H and FxH cows are presented in Table 1. The coefficients of variation (CV) for production traits were in accordance with similar data. As expected, SCCs varied greatly, the appropriate CV being 213%. This is because of cows with mastitis showing extremely high SCCs. The repeatability of traits ranged from 0.02 for MUN to 0.25 for lactose percentage. All traits, except MUN, seem likely to respond to selective breeding in the current herd. Considering the relatively small sample size, it is pleasing to see that most repeatability estimates were significant ($P<0.05$), i.e. above twice the appropriate standard error.

Table 1. Descriptive statistics for the traits analysed on test day records ($n=1688$) for milk production traits, somatic cell count (SCC) and milk urea nitrogen (MUN), as well as the repeatability of the respective traits

Trait	Mean \pm s.d.	Range	Repeatability \pm s.e.
Milk yield (kg)	21.3 \pm 6.4	2.7 - 59.7	0.19 \pm 0.03
Fat (%)	4.17 \pm 0.56	2.61 - 6.53	0.16 \pm 0.03
Protein (%)	3.33 \pm 0.38	2.37 - 4.87	0.23 \pm 0.04
Lactose (%)	4.78 \pm 0.23	3.25 - 5.45	0.25 \pm 0.04
Untransformed SCC	372 \pm 795	3 - 9,233	0.21 \pm 0.04
MUN	15.5 \pm 4.8	5.9 - 34.4	0.02 \pm 0.01

Breed differences were observed, with fat and protein percentages being higher ($P<0.01$) for FxH vs. H cows (Table 2). Other traits did not differ between breed combinations. These results are in accordance with those of Metaxas *et al.* (2014). The distribution of SCCs did not differ ($P>0.05$)

for H and FxH cows over all lactation periods and lactation stages (Figure 1). Most, 63 and 67% of all H and FxH SCC records, respectively, had less than 200,000 cell/ml of milk. High SCC (>600,000 cells/ml milk) was recorded in 20 and 18% of all H and FxH records, respectively.

Table 2. Least-squares means (\pm s.e.) depicting differences between Holsteins (H) and Fleckvieh x Holsteins (FxH) cows for test-day milk yield (MY), fat percentage (BF), protein percentage (PP), lactose percentage (LP), the log of somatic cell count (SCC) and milk urea nitrogen (MUN) recorded either in the autumn or spring

Effect and level	Trait					
	MY (kg)	BF (%)	PP (%)	LP (%)	SCC	MUN (mg/dL)
Breed	0.54	**	**	0.97	0.54	*
FxH	21.6 \pm 0.6	4.26 \pm 0.06	3.35 \pm 0.04	4.71 \pm 0.03	5.08 \pm 0.15 (161)	16.1 \pm 0.03
H	22.1 \pm 0.6	4.08 \pm 0.06	3.22 \pm 0.04	4.71 \pm 0.03	5.17 \pm 0.15 (175)	15.5 \pm 0.03

* P<0.01; ** P<0.01; Actual significance for P>0.05. Geometric means for SCC are in brackets

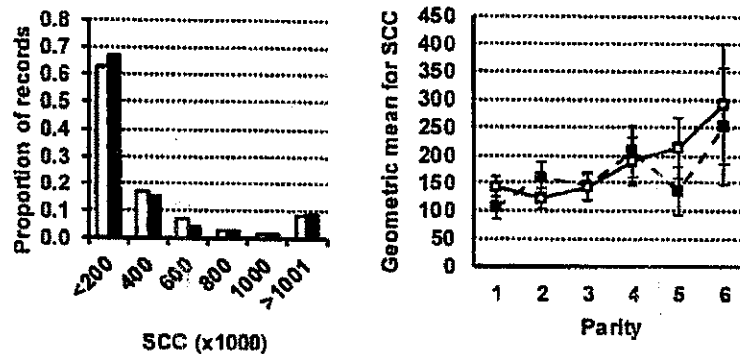


Figure 1. The distribution of somatic cell count (SCC) records within categories (a) and geometric means (\pm s.e.) for SCC or Holstein (c) and Fleckvieh x Holstein cows (m) across parities (b)

Walsh *et al.* (2007) noted that the production of cows within a feeding system is a function of their genetic merit and environmental effects. According to Mrode & Swanson (1996) milk yield is positively correlated with SCC. Significant differences between breeds for SCC are thus expected for breeds differing in milk yield. In the present study, the milk yield of H and FxH cows did not differ (P>0.05) reflecting small differences in the average SCC and, theoretically, the number of mastitis cases. The correlation between animal effects for milk yield and for SCC was accordingly small and not significant at 0.01 \pm 0.16 in the present study. Washburn *et al.* (2002) found that high-producing HF cows had higher SCCs than Jerseys.

The MUN levels in milk can be used to assess the protein and energy status of cows. High levels (greater than 18 mg/dl of milk) indicate a diet containing high levels of easily degradable protein sources (pasture containing high levels of CP), low fermentable energy levels in the diet, high milk yield levels as well as breed. Jersey cows seem to have lower MUN levels in comparison to Holstein

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cows (Johnson & Young, 2003). Contrary to these results, Wattiaux *et al.* (2005) found higher test-day MUN concentrations for Jersey and Brown Swiss cows in comparison to Holstein cows on the same diet. Miglior *et al.* (2006) found that the MUN concentration in Ayrshire milk was higher than in Holstein milk.

Kgoke (2013) found that non-genetic factors affecting MUN in Holstein cows were herd-test-day, lactation stage and year of calving. Herd-test-day contributed most to the observed variation in the latter study, namely 58.6 and 63.2% in parity 1 and 3, respectively. The heritability estimate for MUN was 0.09 ± 0.01 in first parity and 0.11 ± 0.01 in 2nd and 3rd parities. Between-animal variation in the present study was accordingly low, indicating that factors other than the animal contribute substantially to variation in MUN. Genetic correlations between MUN and milk production traits were positive, albeit low, ranging from 0.01 ± 0.00 to 0.10 ± 0.004 across parities (Kgoke 2013). This positive association is undesirable, indicating that high-producing cows are less efficient in utilizing dietary protein.

CONCLUSION

FxH cows outperformed H cows for fat and protein percentages with no observed difference in milk yield. Significant between-animal variation suggests that current herd gains are feasible for SCC in the cows studied. With repeatability being the theoretical upper limit of heritability, these results may suggest underlying genetic variation among cows which may be exploited by selection, thus benefiting the welfare of lactating cows.

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