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BRIEF COMMUNICATION: Quantitative trait loci associated with variation in maximum milk flow rate in Friesian-Jersey cross bred cows

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Keywords: milking; milking speed; genetic improvement; crossbred cows

Introduction

On New Zealand dairy farms, the milking process consumes more than half of the available labour hours (Jago et al. 2010). While some recent research has shown some potential to improve labour efficiency of dairy farms during milking (Jago et al. 2010), the speed of milking is, in large part, dictated by the slowest milking cows in the herd.

The milking process for dairy cows includes a let-down lag phase of 30 to 60 seconds, a peak milk flow phase of maximum flow (Maxflo) of several minutes, a brief period of declining flow and an over-milking phase (Tancin et al. 2006). Variation in maximum flow is large, ranging from 0.5 to >5.0 kg/minute, and depends on contained milk volume, the pressure differential across the teat canal and teat canal length and diameter. The size of the teat orifice, at least in part, is under adrenergic control (Butler et al. 1992). Duration of milking for an individual cow can range from a few minutes up to 15 to 20 minutes for particularly slow milkers.

Slow milking is mostly associated with slow flow during the peak milking/maximum flow rate phase following milk let down. Variation in let-down time, or later phases of milk flow, usually adds little to overall variation in milking duration.

Milking speed is a heritable trait which has a high genetic correlation with milk yield and a high phenotypic correlation with milk yield at that milking (Miller et al. 1975). Hence, as milk yield has increased through genetic improvement and change in breed composition and feed management, there has been corresponding increase in average flow rate during a milking (Arave et al. 1987). However, the potential for increased incidence of mastitis in cows with a high Maxflo is significant (Grindal & Hillerton 1992).

Several studies have identified quantitative trait loci (QTLs) that relate to milking speed although the traits have been assessed by subjective scoring of speed rather than direct measure of flow rate (Boichard et al. 2003; Karacaoren et al. 2006; Sandor et al. 2006).

Materials and methods

Milking phenotypes were collected from a population of 561 F2 Friesian X Jersey cows, being the progeny of six F1 Friesian X Jersey sires and F1 Friesian X Jersey dams. These animals were produced for a quantitative trait locus (QTL) mapping

experiment (Spelman et al. 2001). The entire pedigree was genotyped using the Affymetrix Bovine 10K SNP GeneChip (Affymetrix, Santa Clara, USA). A total of 6,634 informative SNP markers were placed on the map and QTL analysis was undertaken as described by Berry et al. (2010).

The phenotypic data analysed here were collected during a once-a-day milking (OAD), whole-lactation study, over Lactation 4 in 2005-06 for Cohort 1 and in 2006-07 for Cohort 2. Cows were milked through a 60-bale rotary shed and data collected for Maxflo and milk yield via Westfalia, Metatron (now GEA Technologies, Cambridge, New Zealand) milk meters. Data were sampled during the period around peak lactation at a mean of 55 days in milk (DIM) and also in November at 90 DIM, in February at 190 DIM and in May at 280 DIM for Cohort 2 only, to examine repeatability of measurements. Phenotypes for QTL analysis were generated using the average of five consecutive days of Maxflo and milk yield data from early October for both cohorts at 55 DIM. QTL analysis with Maxflo as the phenotype, was undertaken using unadjusted data or data adjusted for milk yield and cohort using both line of descent and half-sib models described in Spelman et al. (2001).

Maxflo data were taken directly from the milk meter. In a separate study, Maxflo calculated from the rate of change in accumulated milk volume during milking was compared with the Maxflo data from the Metatron meter. While the correlation between the measures was high ($R^2 = 0.83$), the manual calculation of flow provided Maxflo estimates that were only 60% of the estimates provided by the meter. Maxflo data presented here have been multiplied by 0.6 to account for this difference.

Results and discussion

Maxflo in both cohorts in early October showed a normal distribution of 0.5 kg/min to >5 kg/min. Mean Maxflo \pm standard error of the mean was 2.11 ± 0.03 kg/min. Median flow was 1.97 kg/min with 50% of the animals being in the range of flow of 1.60 to 2.60 kg/min. Mean Maxflo in the lowest 10% was 1.2 kg/min.

Using the Cohort 2 data set, it was possible to address correlation of the Maxflo estimates through time. Correlations of Maxflo in November, February and May with Maxflo in October were 0.74, 0.67 and 0.43. All of these were higher than the corresponding

Figure 1 Variation in least square mean \pm standard error of the mean of maximum milk flow rate for six sires measured in their daughters in the Friesian-Jersey crossbred trial. The number of daughters per sire ranged from 78 to 109.

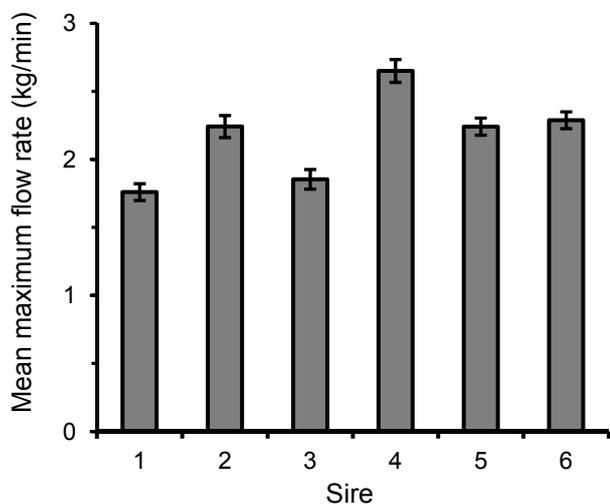
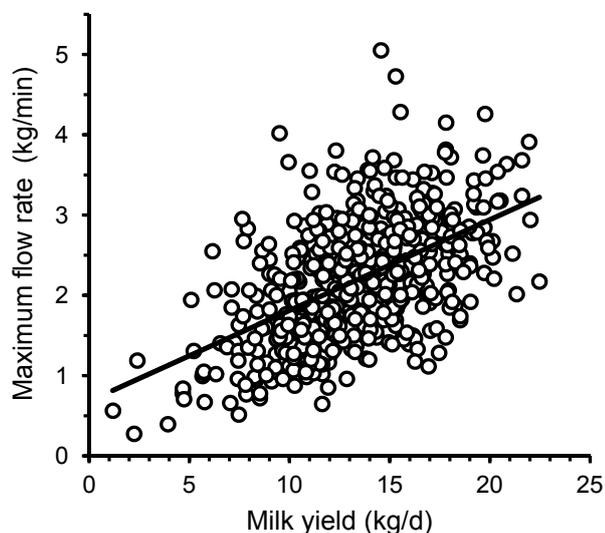


Figure 2 Association of maximum milk flow rate with milk yield in 4th lactation cows close to peak lactation. (N = 561, $r = 0.54$, $P < 0.01$). Data are means of five days of data collected in early-October, 2005 and 2006 while cows were being milked once-daily.



correlations of milk weight of 0.60, 0.54 and 0.20 in 218 cows.

There was a significant effect of sire on milk flow rate (Figure 1). Among the 6 sires used in the trial, mean Maxflo varied from 1.75 kg min for sire 1 to 2.65 kg/min in sire 4. Milk production among sires ranged from 12.7 to 13.9 kg/min with the highest yielding sire also showing the highest average Maxflo. Milk weight was correlated with Maxflo ($r = 0.54$) at the same milking (Figure 2).

QTL were identified on several chromosomes, notably, BTA2, BTA13, BTA 26 and BTA29. Others have identified milk flow QTL, based on subjective

assessments, on a range of chromosomes but there has been little agreement across studies (Schrooten et al. 2000; Boichard et al. 2003; Karacaoren et al. 2006).

Currently, milking speed is a trait included indirectly in New Zealand breeding worth as part of the survivability breeding value calculation (New Zealand Animal Evaluation Ltd., 2013). The trait is based on a subjective scoring system around milking duration. QTL analysis of this trait assessed in the same Friesian-Jersey crossbred animals did not reveal any genomic regions of interest, probably because of the relative imprecision of trait assessment.

Given the high heritability and repeatability of milking speed and the identification of several genomic regions relevant for Maxflo, it should be possible to provide more objective methods for genetic improvement in milking speed. Faster milking and more uniformity in milking times will help reduce labour requirements for milking.

Acknowledgements

The authors gratefully acknowledge the contribution of Brian Walsh and the farm team at the Fonterra Farm, Whareroa; Janine Melis and Suzanne Young for some of the data collation and analysis and Jenny Jago at DairyNZ for helpful discussions.

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