J. Dairy Sci. 97:1436–1445
http://dx.doi.org/10.3168/jds.2013-7205

Residual feed intake of lactating Holstein-Friesian cows predicted from high-density genotypes and phenotyping of growing heifers

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ABSTRACT

A genomic prediction for residual feed intake (RFI) developed in growing dairy heifers (RFI_{gro}) was used to predict and test breeding values for RFI in lactating cows (RFI_{lac}) from an independent, industry population. A selection of 3,359 cows, in their third or fourth lactation during the study, of above average genetic merit for milk production, and identified as at least 15/16ths Holstein-Friesian breed, were selected for genotyping from commercial dairy herds. Genotyping was carried out using the bovine SNP50 BeadChip (Illumina Inc., San Diego, CA) on DNA extracted from ear-punch tissue. After quality control criteria were applied, genotypes were imputed to the 624,930 single nucleotide polymorphisms used in the growth study. Using these data, genomically estimated breeding values (GEBV) for RFI_{gro} were calculated in the selected cow population based on a genomic prediction for RFI_{gro} estimated in an independent group of growing heifers. Cows were ranked by GEBV and the top and bottom 310 identified for possible purchase. Purchased cows (n = 214) were relocated to research facilities and intake and body weight (BW) measurements were undertaken in 99 "high" and 98 "low" RFI_{gro} animals in 4 consecutive groups [(beginning at d 61 ± 1.0 standard error (SE), 91 ± 0.5 SE, 145 ± 1.3 SE, and 191 ± 1.5 SE d in milk, respectively)] to measure RFI during lactation (RFI_{lac}). Each group of ~50 cows (~25 high and ~25 low RFI_{gro}) was in a feed intake facility for 35 d, fed pasture-alfalfa cubes ad libitum, milked twice daily, and weighed every 2 to 3 d. Milk composition was determined 3 times weekly. Body weight change and BW at trial mid-point were estimated by regression of pre- and posttrial BW measurements. Residual feed intake in lactating cows was estimated from a linear model including BW, BW change, and milk component yield (as MJ/d); RFI_{lac} differed consistently between the high and low selection classes, with the overall means for RFI_{lac} being +0.32 and −0.31 kg of dry matter (DM) per day for the high and low classes, respectively. Further, we found evidence of sire differences for RFI_{lac}, with one sire, in particular, being highly represented in the low RFI_{gro} class, having a mean RFI_{lac} of −0.83 kg of DM per day in 47 daughters. In conclusion, genomic prediction of RFI_{gro} based on RFI measured during growth will discriminate for RFI_{lac} in an independent group of lactating cows.

Key words: residual feed intake, genomic selection, dairy, feed conversion efficiency

INTRODUCTION

Feed conversion efficiency is an important component of profitable dairying and applies both to the feed costs of rearing as well as productive performance. Lifetime feed requirements per unit of milk production decline as the number of lactations increase. Further, within a lactation (or during growth), as productivity increases, feed conversion efficiency increases as the fixed costs of maintenance energy requirements become a smaller proportion of total energy requirements and intake.

Residual feed intake (**RFI**) is a component of feed conversion efficiency, being the difference between actual and predicted intake. This measure of efficiency has been well studied in growing beef animals (and nonruminants) but much less so in dairy cattle. It is more difficult to quantify RFI accurately in lactating, relative to growing, cattle because feed intake is higher and quantification of energy requirements and utilization is problematic when, at some stages of lactation, cows can be in significant negative energy balance. Nevertheless, several reports describe successful measurement of RFI in lactating (Korver et al., 1991; van Arendonk et al., 1991; Ngwerume and Mao, 1992; Nieuwhof et al., 1992; Svendsen et al., 1993; Veerkamp et al., 1995) and growing (Nieuwhof et al., 1992; Williams et al., 2011; Waghorn et al., 2012) dairy cattle.

The physiological basis of RFI is not well understood (see Herd and Arthur, 2009 for review). The causative mechanism may be as simple as the relative proportions of visceral mass to carcass mass, given the relatively

Received June 30, 2013.
Accepted December 5, 2013.
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high metabolic activity of the former (Ferrell, 1988). Alternatively, a general change in metabolism may occur, such as that associated with ion pumps or protein turnover (Herd and Arthur, 2009) that might affect heat production relative to tissue deposition. In both cases, the required quantity of feed energy for maintenance, production, or both may differ from a predicted average for a group or population. Certainly, it can be envisaged that a difference in RFI associated with a difference in maintenance energy could be sustained and measured in both growth and lactation, albeit with more difficulty in lactation. In support of this assertion, genetic and phenotypic variation in maintenance energy requirements in young Hereford bulls was also closely associated with RFI (Herd and Bishop, 2000).

In both beef and dairy animals, RFI is a heritable trait (see reviews by Herd et al., 2003; Berry, 2008; Berry and Crowley, 2013). Estimates of heritability are relatively repeatable at different phases of the growth curve (Kelly et al., 2010) and in both growing and lactating dairy cattle (Nieuwhof et al., 1992). Further, there does not appear to be a strong interaction of RFI with diet used during testing. For example, steers that performed well on high-quality, pelleted rations appeared to maintain superior performance on pasture (Herd et al., 2002).

The relationship between RFI measured during growth ($\mathbf{RFI_{gro}}$) and RFI measured during lactation ($\mathbf{RFI_{lac}}$) has not been well established. Groups of cows selected for RFI_{gro} showed divergence for RFI_{lac} on diets of lucerne and pasture cubes with or without supplement of wheat grain (Macdonald et al., 2014). A moderate genetic correlation between RFI_{gro} and RFI_{lac} has been reported (r = 0.58; Nieuwhof et al., 1992). One study linked RFI_{lac} during lactation to RFI_{gro} during growth in beef animals (Arthur et al., 1999). Cows that had a low RFI at weaning appeared to require less feed as mature lactating animals, and cow performance was not compromised. Other work has demonstrated moderate repeatability of RFI at different stages of the growth phase, again in beef cattle (Archer et al., 2002). All of these data indicate that RFI may be a lifetime trait.

The experiment described here is the third in a series to examine RFI in Holstein-Friesian dairy cattle. The first experiment determined RFI at 6 to 9 mo of age (Williams et al., 2011; Pryce et al., 2012; Waghorn et al., 2012) and developed a genomic prediction for RFI. The second experiment examined RFI in the first lactation for 183 cows previously identified during growth to be extreme for high or low RFI (Macdonald et al., 2014). The current experiment used the genomically estimated breeding values (**GEBV**) developed for RFI_{gro} in heifers to predict GEBV for RFI_{gro} in an independent data set of 3,359 cows selected from the general industry population in New Zealand and measure the RFI_{lac} in the predicted extremes. The hypothesis was that genomic markers generated from divergence in RFI_{gro} for growth in Holstein-Friesian heifers would enable identification of mature Holstein-Friesian cows with divergence in RFI_{lac}.

MATERIALS AND METHODS

Animals

Cows (n = 3,359), born in 2005 or 2006 (lactations 3 and 4 at the time of testing) and at least 15/16ths Holstein-Friesian, were identified in 224 commercial dairy herds in the South Auckland and Taranaki regions of New Zealand. Ear tissue samples were taken by an ear-punch and DNA extracted as described previously (Pryce et al., 2012).

Genotyping was undertaken with the Bovine SNP50 BeadChip (Illumina Inc., San Diego, CA), which assayed approximately 54,000 SNP. Quality control was applied to the data in a similar manner to that described by Pryce et al. (2012). The genotypes were imputed (using Beagle software: Browning and Browning, 2009) to the 624,930 SNP used in Pryce et al. (2012) derived from the high-density bovine SNP chip (Illumina Inc.), and the combined information from the New Zealand-Australian heifers as the reference data set.

Using the imputed genotype data, GEBV were calculated for RFI_{gro} based on the SNP estimates that were generated from the BayesA model that was presented by Pryce et al. (2012). Briefly, using the estimated SNP effects, a vector of GEBV was calculated for the 3,359 cows: GEBV = $\mathbf{Xu}$, where $\mathbf{X}$ is a matrix of the cows' genotypes and $\mathbf{u}$ is the vector of SNP effects estimated by the BayesMulti method (Pryce et al., 2012). Correlation of measured RFI with GEBV was 0.31 in the New Zealand heifer data set (Pryce et al., 2012). Animals were ranked by GEBV and the top and bottom 310 identified for possible purchase from 159 farms. After animal health checks (for Johne's disease, enzootic bovine leukemia, mastitis, and bovine viral diarrhea), 214 of these animals, ranked in the top or bottom 10% for GEBV for RFI_{gro}, were purchased from 112 farms (maximum of 3 cows from any 1 farm) and relocated to the research farm in May 2011, at the end of their third or fourth lactation. Genetic merit for lactation traits (breeding worth) was 95 (±3 SE) and 99 (±4 SE) for the low and high RFI_{gro} cows, respectively. This compares with the New Zealand average for Holstein-Friesian cattle in 2010 of 72 (Dairy NZ/LIC, 2010). These cows were tested for RFI during the lactation beginning in spring (July/August) 2011.