Beef on Dairy Genomic Evaluation for Feed Efficiency, Methane Emission and Meat Quality

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Abstract

Improving resource efficiency and meat quality as well as reducing the environmental impact from cattle industry, are important issues. Therefore, the aim of the FutureBeefCross (FBC) project is to show the genetic background of feed efficiency, methane emission and marbling score (MS) in young, crossbred calves. The aim is to implement breeding values for major beef breeds used to inseminate dairy cows. In this project, longitudinal daily dry mater intake (DDMI) and longitudinal body weight (BW) during 100 to 300 days of age were available for 4,400 crossbred animals with either Danish Blue, Charolais, or Angus sires and with Holstein dams. Feed intake is obtained by All feed system from Allflex. In addition, marbling score was obtained using image analysis. The basis was Q FOM™ images on 1,700 crossbred animals of Danish Blue sires and Holstein dams. Longitudinal daily dry matter intake and body weight were analyzed in a bivariate model with Legendre polynomials of days of age at the time of the test with first order for fixed, genetics, and permanent environment effects using Pedigree BLUP. Genetic parameters for marbling score were obtained from a univariate pedigree BLUP model. The genetic residual feed intake was measured as sum of daily dry matter intake minus the body weight gain and the mid body weight during the period of 200 to 280 days of age. The genetic residual feed intake has a moderate heritability of 0.21 and low genetic correlation of -0.12 with body weight gain and zero with mid body weight. The marbling score has low heritability of 0.15 which could be because the measured animals are young (10-12 months at slaughter). Breeding values for all traits will be implemented in 2023 and will act as a decision-making tool for artificial insemination (AI) organizations in selecting beef bulls that can improve farm profitability while meeting consumer demands.

Key words: beef on dairy, feed efficiency, genomics, heritability, meat quality

Introduction

There has been an increase in use of beef semen on dairy cattle in Denmark in the latest 10 years. In 2013 less than 5% of calves born at 2nd or later calving had a beef bull sire, but that number has risen to 34% to 46% in 2023 depending on dam breed. Since 2015 across breed estimated breeding values (EBVs) have been published for beef on dairy (BxD) bulls in Denmark. Later Nordic Cattle Genetic Evaluation (NAV) has developed a joint Nordic multibreed genetic evaluation of BxD bulls (Carlén et al., 2019).

In 2019 the FBC project started, aiming to improve economy, reducing climate impact, and improving meat quality in the production of BxD calves by improving their genetic potential. The basis is to develop new methods to phenotype 12,000 Danish BxD calves from Holstein dams and Danish blue, Angus or Charolais sires for these three traits. The aim of this project is to estimate the genetic parameter for feed efficiency during fattening period and the marbling score (MS) at slaughter. Also, we will shortly present our thought on the outline of the evaluation of

methane emission, where data is not yet available.

Materials and Methods

Data for feed intake

Daily dry mater intake (DDMI) and birth weight (BW) of 4266 crossbred animals during 100 to 300 days of age were available. The crossbred animals were from Danish Blue, Angus, or Charolais sire breeds crossed with Holstein dams.

Data for marbling score

Marbling score MS of 1686 crossbred animal from 65 Danish Blue sires and Holstein dam that were slaughtered between 240 to 360 days of age were available. Marbling score was calculated by Frontmatec by converting parameters obtained from picture of rib eye of between 5th and 6th ribs taken by a handheld camera device (Q FOM™).

Statistical analysis

Bivariate Random regression animal model with Legendre polynomial of the days of age on the test was used to model DDMI and BW. The model for DDMI contained fixed effects of slaughter herd by year by month of slaughter and by gender of animal interaction; sire breeds (Angus, Danish Blue, and Charolais); and start age of the test and its quadratic term. First order polynomial was fitted for fixed part of the model and the additive genetics of animal and the permanent environment effect. For BW, the fixed effects were slaughter herd by year interaction; gender; and sire breeds. The fixed effects were modeled with second order polynomials and the genetics and permanent environment with first order polynomials. For MS, a univariate animal model was used that included the fixed effects of slaughter herd by year by month interaction; gender; slaughter age; and carcass weight. The DMU software package (Madsen and Jensen, 2013) was used for genetic parameter estimation.

Genetic Residual feed intake (RFI) calculationMethodology of Esfandyari and Jensen (2021) and Shirali et al. (2018) was used to make the derivations for genetic RFI and its component traits as well as the genetic regression coefficients. Genetic RFI was obtained as the sum of daily dry matter intake (TDMI) during 200 to 280 days of age minus body weight gain (Gain) and the mid BW (MBW) in that period. Where regression coefficients for body weight gain and mid BW were obtained from the genetic (co)variance matrix.

Results & Discussion

The heritabilities were moderate for TDMI (0.24), Genetic RFI (0.21), Gain (0.21), and MBW (0.35). The genetic correlation between TDMI and RFI was substantially high at 0.82. In addition, RFI explained 72% of variation in TDMI obtained from genetic variance of RFI over the ones from TDMI (484/675). The genetic correlation between TDMI and Gain was favorable (0.43). Due to the modeling of RFI, the genetic correlation between RFI and its component traits of Gain (-0.12) and MBW (0.00) were very low and close to zero. Esfandyari and Jensen (2021) reported a heritability of 0.40 to 0.50 for feed intake and genetic RFI; and between 40% to 80% variance in daily feed intake to be explained by RFI. In literature, heritability of feed intake during growing period is reported to be moderate to high (0.25 to 0.44) (Schenkel et al., 2004; and Retallick et al., 2017).

The heritability for MS was low (0.15). In literature, higher heritabilities for marbling score were reported for example Bedhane et al. (2019), Do et al. (2016), Davis and Simmen (2000), Ríos-Utrera et al. (2005), and Nephawe et al. (2004) (0.49±0.05, 0.28±0.02, 0.27±0.17, 0.40±0.09, 0.46±0.06, respectively) reported moderate to high heritabilities. The genetic correlation between MS and Intramuscular fat

was 0.94 as both measurements are obtained from parameters in the pictures taken from rib eye captured by handheld devices.

For the methane emission trait, we are planning to use the sole ratio between CO_2 and CH_4 directly, as also suggested as a possibility by Madsen et al. (2010). Alternatively, daily methane production could be calculated, from the estimated daily CO_2 production and the ratio between CO_2 and CH_4, as also suggested by Madsen et al. (2010). However, using their method to estimate CO_2, it would require accurate information on weight gain and feed intake. Uncertainty in these data would affect the accuracy of the estimated CO_2 and thereby also the CH_4 production.

Conclusions

The one-step method for calculation of genetic RFI as measure of feed efficiency can act as a good approach to improve modelling of feed efficiency. Moreover, the genetic RFI is suitable for selection of beef bulls and can improve farm efficiency. Marbling score can be utilized to improve the quality of carcass. These new breeding values can be used as additional tools for AI organizations to select beef bulls for use on dairy cattle. The result is that farm productivity increases while consumer satisfactions are met. Adding also a breeding value to reduce methane emission and thereby lower climate impact of these BxD calves, would also increase the acceptance of beef from these BxD calves from a consumer point of view.

Acknowledgments

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