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Gastrointestinal tract size, total-tract digestibility, and rumen microflora in different dairy cow genotypes

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ABSTRACT

The superior milk production efficiency of Jersey (JE) and Jersey × Holstein-Friesian (JE × HF) cows compared with Holstein-Friesian (HF) has been widely published. The biological differences among dairy cow genotypes, which could contribute to the milk production efficiency differences, have not been as widely studied however. A series of component studies were conducted using cows sourced from a longer-term genotype comparison study (JE, JE × HF, and HF). The objectives were to (1) determine if differences exist among genotypes regarding gastrointestinal tract (GIT) weight, (2) assess and quantify whether the genotypes tested differ in their ability to digest perennial ryegrass, and (3) examine the relative abundance of specific rumen microbial populations potentially relating to feed digestibility. Over 3 yr, the GIT weight was obtained from 33 HF, 35 JE, and 27 JE × HF nonlactating cows postslaughter. During the dry period the cows were offered a perennial ryegrass silage diet at maintenance level. The unadjusted GIT weight was heavier for the HF than for JE and JE × HF. When expressed as a proportion of body weight (BW), JE and JE × HF had a heavier GIT weight than HF. In vivo digestibility was evaluated on 16 each of JE, JE × HF, and HF lactating dairy cows. Cows were individually stalled, allowing for the total collection of feces and were offered freshly cut grass twice daily. During this time, daily milk yield, BW, and dry matter intake (DMI) were greater for HF and JE × HF than for JE; milk fat and protein concentration ranked oppositely. Daily milk solids yield did not differ among the 3 genotypes. Intake capacity, expressed as DMI per BW, tended to be different among treatments, with JE having the greatest DMI per BW, HF the lowest, and JE × HF being intermediate. Production efficiency, expressed as milk solids per DMI, was higher for JE than HF and JE × HF. Digestive efficiency, expressed as digestibility of dry matter, organic matter, N, neutral detergent fiber, and acid detergent fiber, was higher for JE than HF. In grazing cows ($n = 15$ per genotype) samples of rumen fluid, collected using a transesophageal sampling device, were analyzed to determine the relative abundance of rumen microbial populations of cellulolytic bacteria, protozoa, and fungi. These are critically important for fermentation of feed into short-chain fatty acids. A decrease was observed in the relative abundance of *Ruminococcus flavefaciens* in the JE rumen compared with HF and JE × HF. We can deduce from this study that the JE genotype has greater digestibility and a different rumen microbial population than HF. Jersey and JE × HF cows had a proportionally greater GIT weight than HF. These differences are likely to contribute to the production efficiency differences among genotypes previously reported.

Key words: digestibility, breed, rumen microflora, production efficiency

INTRODUCTION

The topic of production efficiency, within the context of livestock production systems, has received renewed attention in recent years (Spurlock et al., 2012; Berry and Crowley, 2013; Connor et al., 2013). The great debate concerning land use for ruminant production versus production of human edible feed is a primary driver for this renewed interest in production efficiency (Wilkinson, 2011). Opportunities to directly select for improved efficiency are limited, as DMI measurements from individual cows, required to generate breeding values for traits related to efficiency, are not routinely available. However, genetic diversity within feed efficiency has been demonstrated to exist. In a review of genetic parameters for the trait, Berry and Crowley (2013) reported heritability estimates for feed

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efficiency-related traits in cows (residual feed intake or feed conversion ratio) ranging from 0.00 (Svendsen et al., 1993) to 0.38 (Veerkamp et al., 1995). A review by Goddard and Grainger (2004), and more recently studies by Buckley et al. (2007) and Prendiville et al. (2011a), indicated genotype or strain within genotype variation for DMI capacity and milk production efficiency. Milk production efficiency can be defined in many ways. The present study uses the definition of milk solids yield (kilograms of fat and protein) per unit of DMI (Lopez-Villalobos et al., 2008). Whereas such variation in milk production efficiency has been demonstrated, the biological differences among dairy cow genotypes, which could contribute to the milk production efficiency differences measured, have not been as widely studied. Previous studies are either dated or use beef cattle (Smith and Baldwin, 1974; Richardson and Herd, 2004). Hence, further evidence of biological differences among the genotypes is warranted to enhance the understanding of the production efficiency differences and the potential to select for this increasingly important trait.

Prendiville et al. (2010) concluded that differences in grazing behavior contributed little to differences in DMI capacity among lactating dairy cow genotypes. They speculated that the higher DMI capacity expressed as DMI per BW observed with Jersey (**JE**) and Jersey × Holstein-Friesian (**JE × HF**) compared with Holstein-Friesian (**HF**) was likely a function of physical differences associated with gastrointestinal tract (**GIT**) size. Two studies exist that support this speculation, but their relevance in the context of modern HF and JE genetics is questionable, as one study is almost 40 yr old (Smith and Baldwin, 1974) and the other (Nagel and Piatkowski, 1988) compared JE to German Black-Pied cattle. Both studies are limited by very small numbers of lactating animals and neither compared the genotypes consuming a grass-based diet.

Differences in digestibility among beef steers are reported to account for 10% of the variation in feed efficiency, with more efficient animals capable of digesting more of the diet (Richardson and Herd, 2004). Genetic variation among dairy cows in their ability to digest a predominately grazed grass diet ranges from 0.08 to 0.45, but digestibility was predicted using the n-alkane method (Berry et al., 2007). The accuracy of the n-alkane method is questionable, as errors can arise from estimation of the alkane concentration, herbage sampling errors, or analytical errors (Rymer, 2000). Digestibility measured in vivo is the most accepted method. Digestibility and DMI are related, as increasing DMI can result in a quicker passage rate (Thornton and Minson, 1972; Colucci et al., 1982) resulting in decreased digestibility (Tyrrell and Moe, 1975). Yet JE animals have been shown to have both a greater DMI capacity (Goddard and Grainger, 2004; Prendiville et al., 2009) and a higher NDF digestibility than HF cows, resulting in JE producing a greater milk energy output per kilogram of DMI (Aikman et al., 2008). However, animals in the latter study were offered a TMR diet. Differences in digestibility among dairy cows offered a predominately grass-based diet warrants further research to accurately determine the digestibility differences in vivo among genotypes.

Approximately 65% of digestion occurs in the rumen (Hogan and Weston, 1967). Rumen microorganisms control rumen pH (Williams and Coleman, 1997) and the fermentation of cellulose, hemicellulose, and fiber into short-chain FA (Van Soest, 1994; Gordon and Phillips, 1998), which are used by the host for maintenance, growth, and performance. Previous work has shown that diet has a large influence on the rumen microbial population, affecting the bacteria (e.g., *Bacteroidetes* and *Firmicutes*) and archaeal populations (de Menezes et al., 2011), whereas the cellulolytic bacteria (e.g., *Fibrobacter succinogenes, Ruminococcus flavefaciens*, and *Ruminococcus albus*) are affected more by the individual host cow than by diet (Weimer et al., 1999). Data suggest that variation in feed efficiency in beef cattle may be explained by rumen microbial density and diversity (Guan et al., 2008; Carberry et al., 2012). However, no information is available comparing the rumen microbial populations among dairy cow genotypes consuming a grass diet. The objectives of the present study were to (1) determine if differences exist among dairy cow genotypes regarding GIT weight, (2) assess if JE, and by extension JE × HF, differ from HF in their ability to digest perennial ryegrass, and (3) examine the relative abundance of specific rumen microbial populations potentially relating to feed digestibility among dairy cow genotypes.

MATERIALS AND METHODS

All sampling procedures described as part of the present experiment were executed in accordance with guidelines set by the Irish Minister for Health and Children under section 8 of the Cruelty to Animals Act (1876). This study comprised a series of component studies conducted using cows sourced from a longer term genotype comparison study (JE, JE × HF, and HF) based at the Teagasc, Animal and Grassland Research and Innovation Centre, Moorepark, Fermoy, Co. Cork, Ireland (52°09′N; 8°16′W). The longer term study was established in 2006 to evaluate the performance and profit potential of JE, JE × HF, and HF under an