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Breeding Dairy Cows to Reduce Greenhouse Gas Emissions

M.J. Bell, R.J. Eckard and J.E. Pryce

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1. Introduction

The dairy industry has made large advances in efficiencies over the past 60 years as a result of changes in breeding, nutrition and management practices [1]. To meet the growing demand for dairy products, which is projected to continue out to the year 2050 [2], milk production per cow has increased over the last thirty years primarily by genetic selection and better nutrition. Genetic selection has tended to focus on mostly production traits (kilograms milk, kilograms fat and protein) rather than fitness (lameness, mastitis, fertility and lifespan) traits, although most countries now include fitness traits in addition to production traits in modern breeding goals. The Holstein Friesian is a popular breed due to its high genetic potential to produce milk; however it is characterised by having a lower body condition score, and reduced fertility and survival compared to other breeds [3]. Even with these negative attributes, in tandem with efficiencies in production in recent decades have come reductions in greenhouse gas (GHG) emissions and resource inputs per unit product [1, 4, 5], while emissions per unit area have increased.

The main GHGs attributed to livestock systems are methane and nitrous oxide emissions [6]. Due to the variability in lifespan of gases in the atmosphere and the ability of gases to reflect and trap radiant energy, the average potential of a GHG to warm the earth's near-surface air is expressed in carbon dioxide equivalents (CO_2-eq.) emissions (its global warming potential). Methane and nitrous oxide are capable of trapping about 25 and 298 times more radiant energy respectively, over a 100-year time horizon, than one kilogram of carbon dioxide [6]. The dairy sector's total CO_2-eq. emissions are estimated to be 4% of total global GHG emissions, of which, about half are methane and a third nitrous oxide emissions [2].

The main benefits of selection to improve production efficiencies are by increased productivity and gross efficiency (i.e. the ratio of yield of milk to resource input) by firstly, diluting the maintenance cost of animals in the system and secondly, less animals are

required to produce the same amount of product [1, 7]. Studies have found [8, 9] that more energy efficient animals produce less waste in the form of methane and nitrogen excretion per unit product. A study in the UK [4] calculated that the genetic improvement in dairy cows by economic and production efficiency in the last 20 years had reduced GHG emissions per unit product by 0.8% per year and would continue to reduce emissions at a rate of 0.5% per year over the next 15 years. A reduction of 0.6% per year in GHG emissions per unit product was found in the US [1] over a 63 year period. Emissions of methane and nitrous oxide per unit product were estimated to have shown large declines of about 1.3% and 1.5% per year respectively over the last 20 years in the UK, and will continue to decline over the next 15 years albeit at a slightly slower rate per year [4]. These rates of decline for methane are similar to those reported in other studies [10] for enteric methane emissions per unit product of 1.1% per year for cows selected on increased milk fat and protein production (Select line cows) and at 1.4% per year for cows selected to represent the UK average for milk fat and protein production over a similar time period.

In this review, we investigate the potential role of selective breeding in reducing GHG emissions.

1.1. Selecting animals for reduced emissions

Level of feed intake and its composition are important factors influencing methane and nitrogen losses. As the feed intake of an animal increases, the percentage of dietary gross energy (GE) intake lost as methane decreases by an average of 1.6% per unit of intake [11]. A higher feed intake level increases its fractional passage rate through the rumen and reduces its retention time, rumen digestion (depending on the diet) and methane production [11, 12, 13]. As rumen retention time decreases with increased feed intake the rate of nitrogen excretion increases, increasing the potential for nitrous oxide emissions [9, 14]. However, if cows are to meet their genetic potential for milk production, they need to maximise their feed intake [15, 16]. At pasture the nutrient intake can vary and impair the milk production potential of the animal, particularly during the peak of lactation [17]. To meet the genetic potential for milk production forage based diets are supplemented with high energy dense feed in the form of concentrate. Supplementing the diet of high milk yielding dairy cows at pasture with concentrate was found [17] to result in a lower rate of pasture intake substitution and a higher response in improved milk yield compared to lower milk yielding cows.

Cows with a high body weight have been found to have a greater bite weight when eating and therefore are more efficient in their use of time spent feeding [16]. The larger North American Holstein genotype has been found to produce between 8 to 11% less methane as a percentage of GE intake, on both a total mixed ration and pasture-based diet, than a small New Zealand Holstein [18], presumably due to differences in level of feed intake. However, larger cows have greater maintenance requirements. For the same level of production, a smaller cow is obviously a more efficient converter of feed into milk. This is why selection programmes in both New Zealand and Australia, in particular have focused on increasing the rate of genetic gain in traits that contribute to profitability per unit of feed eaten [19].

Selecting dairy animals for efficient feed use could bring both higher production and reduced resource requirements. In comparison to other mitigation strategies, selective breeding offers a medium to long-term approach to GHG mitigation, which can be cost effective [20]. The response from selective breeding depends on the selection intensity, genetic variation, generation interval and the economic importance of the trait, with annual rates of response typically being between 1% and 3% [7] of the mean in the trait under selection. In intensive poultry and pig production, profitability on cereal-based diets has encouraged selection for feed efficiency (ranging from 1.7 to 2.4 kg cereal feed per kg animal weight) compared to ruminant systems [21]. The improvement in feed conversion efficiency in non-ruminants has been quite remarkable, for example, it has been reported [22] that the feed conversion efficiency (kg lean meat/t of feed) in pigs has nearly doubled from 85 kg/t in the 1960s to 170 kg/t in 2005. It is reasonable to assume that in non-ruminant animals where selection on feed use efficiency has been made that current selection goals will account for a moderate to high proportion of any genetic variation in methane output or nitrogen use efficiency.

Average daily dry matter intake and milk yield are moderately heritable in dairy cows at about 0.30 [15, 23] compared to about 0 to 0.15 for health and fertility traits [24]. Therefore, genetic improvement in dry matter intake and milk production traits is easier to achieve than for health and fertility. Increasing the genetic potential of a cow to produce milk increases total system GHG emissions, due a higher feed intake [25]. However, the milk produced per unit of feed eaten is likely to reduce due to improvements in gross efficiency. For example, the genetic correlation between intake and milk yield has been found [15] to account for just less than half the genetic improvement in milk production being covered by an increase in dry matter intake. This implies that the apparent improvement in gross efficiency is partly due to feed conversion efficiency. The remainder could be due to increased reliance of body tissue mobilisation.

The direct selection of animals on a trait such as methane production in ruminants may be of little importance given its relationship with feed intake [26, 27], which is a more easily measured trait. The additional benefit from directly measuring GHG emissions from animals would be if selection on a measure of feed use efficiency was not possible. Whether breeding goals are able to account for all the genetic variation in methane output or nitrogen efficiency is unlikely, and therefore there may be some benefit to directly selecting on these traits if possible. In ruminants, measurements of methane output, nitrogen efficiency and overall feed efficiency are difficult and costly to obtain, which has limited the direct selection of these traits in the past. A large part of the variation in methane emissions from dairy cows has been found to be genetic, with a heritability of 0.35 for methane output and 0.58 for methane output per unit product [28], presumably due to a prediction of methane being used and its close unity correlation with feed intake. In comparison, a lower heritability of 0.13 has been found [29] in sheep for methane output. Once individual measurements for total animal methane emissions become more affordable to carry out for a large number of animals, selecting animals on methane output will become possible.

Variation in feed use efficiency and enteric methane emissions between-animals, breeds and over time means there is potential to reduce GHG emissions through genetic selection [30, 31, 32]. With a positive genetic correlation between feed efficiency and methane output, with an estimated range from 0.18 to 0.84 [28], it can be inferred that selecting cows that are more efficient will reduce methane production, possibly in the order of 1.1% to 2.6% per year. From a range of production and fitness traits, breeding studies [4, 14] found feed efficiency to have a large impact on reducing the GHG emissions from dairy systems compared to other production or fitness traits. Feed efficiency can be assessed by feed intake required per unit product (gross efficiency) or by net or metabolic efficiency commonly calculated as residual feed intake [4]. Residual feed intake is the difference between the observed and predicted feed intake; where the predicted feed intake is often calculated as energy requirements. Studies [31, 33, 34] looking at selecting beef cattle based on a lower residual feed intake (difference between actual and expected feed intake) found that growth performance was not compromised and the lower expected feed intake resulted in less methane produced. Heritability estimates for feed efficiency tend to be moderate (0.16 to 0.46; [4]). Low correlations between residual feed intake and other production traits imply that little or no genetic improvement has previously been made in residual intake in beef cattle as a result of selection on production traits [4]. In dairy cows, calculating residual feed intake accurately is difficult as changes in body tissue composition need to be fully accounted for. This is because without accounting for body composition changes, residual feed intake is mathematically equivalent to energy balance [35]. Negative energy balance (often considered to be very similar to condition score loss) in early lactation has been the subject of intense phenotypic (and genetic) investigation [36]. Mobilisation of body tissue, or low body condition score is associated with reductions in fertility [37].

Taking direct feed intake measurements can be costly due to the equipment required, therefore an indirect measure of feed efficiency may be a more appropriate option for dairy animals, but further research is required to investigate measures that might be correlated with intake. Biologically inactive markers released in the rumen (such as n-alkanes) have successfully been used to predict feed intake, however, as with other markers released in this way (i.e. such as SF_6) there are concerns about the consistency of the marker release rate (see [38] for a review). A new technology, known as genomic selection is especially promising for difficult or expensive to measure traits, as measurements need only to be made on a representative sample of the population. Genomic breeding values are calculated as the sum of the effects of dense genetic markers that are approximately equally spaced across the entire genome, thereby potentially capturing most of the genetic variation in a trait. Here the prediction equation is formed in a reference population with genotype and phenotype data. The prediction equation can be used to predict breeding values in animals that are genotyped but without phenotype data. The availability of SNP chips at affordable prices has made implementation of this technology commercially feasible. For example, many countries now publish genomic breeding values for bulls on a range of traits of economic importance.

Recently, there has been interest in estimating genomic breeding values for traits in the feed conversion efficiency complex. The estimated accuracy of genomic prediction of RFI calculated in a population of 1000 New Zealand and 1000 Australian non-lactating heifers was around 0.4 [39]. The accuracy of the genomic prediction could be increased further still if countries were to pool together their phenotypes that are expensive to record and their genotype resources, as these data could be used to increase the accuracy of genomic selection further still. Collaborative efforts between research organizations in the Netherlands, the UK and Australia have already demonstrated that the accuracy of genomic predictions of dry matter intake can be increased by combining datasets (de Haas submitted, 2012). The ultimate aim of these collaborative research efforts is to develop genomic breeding values for dry matter intake or a feed conversion efficiency trait that could be used in breeding programs to improve efficiency and mitigate emissions.

1.2. Breeding x feeding system

Due to the profitability of Holstein cows, Holstein genes are present in a large proportion of dairy cows globally, particularly North American. Larger North American Holstein-Friesian cows have been found to show a better response in milk yield with a higher proportion of concentrate in their diet than smaller genotypes like the New Zealand Holstein-Friesian, which have been selected for higher milk yield performance from pasture [16]. Cows which were ~88% North American Holstein and selected on increased milk fat and protein production (Select line cows) were found to grow faster and had increased kg milk per kg dry matter intake during their productive life when on a high energy dense diet, compared to cows selected to represent the UK average for milk fat and protein production on the same diet [10]. Select genetic line animals have a high genetic potential for mobilising body energy reserves for production, which has been found to have deleterious effects on health and fertility [3, 24], particularly later in life [7]. However, it was found [14] that Select line cows responded to a diet containing a low proportion of forage, rather than a high forage diet, by having a significantly shorter calving interval. Select line animals on a low forage diet also produced lower CO_2-eq. emissions per energy corrected milk compared to non-select and cows on a high forage diet over their lifetime (Figure 1).

Systems emissions can be minimised by improvements in herd health and fertility (improving longevity and productivity), and by reducing the number of replacement animals retained on the farm to reduce wastage [13, 40, 41]. Improving herd fertility in the UK back to 1995 levels could amount to a 24% reduction in methane emissions per cow by improved efficiencies of reduced herd replacements and calving interval length [40]. Cows of predominantly North American Holstein genes may be better suited to a high energy dense feeding system, typically found in the US, rather than a diet containing a high proportion of forage. In contrast, the performance of animals of New

Zealand origin had higher yields of milk solids and better fertility compared to animals of North American origin when compared on a range of New Zealand grazing systems [42]. Therefore, selecting animals for an environment is important. In a study in the US [1], good health and welfare in modern high input systems (cows of 90% Holstein genes) was reported, with better production efficiency and CO_2-eq. emissions per unit product compared to the past. This may be explained by optimal nutrition being provided to these animals, which may not hold true for the same cows on a lower quality forage diet.
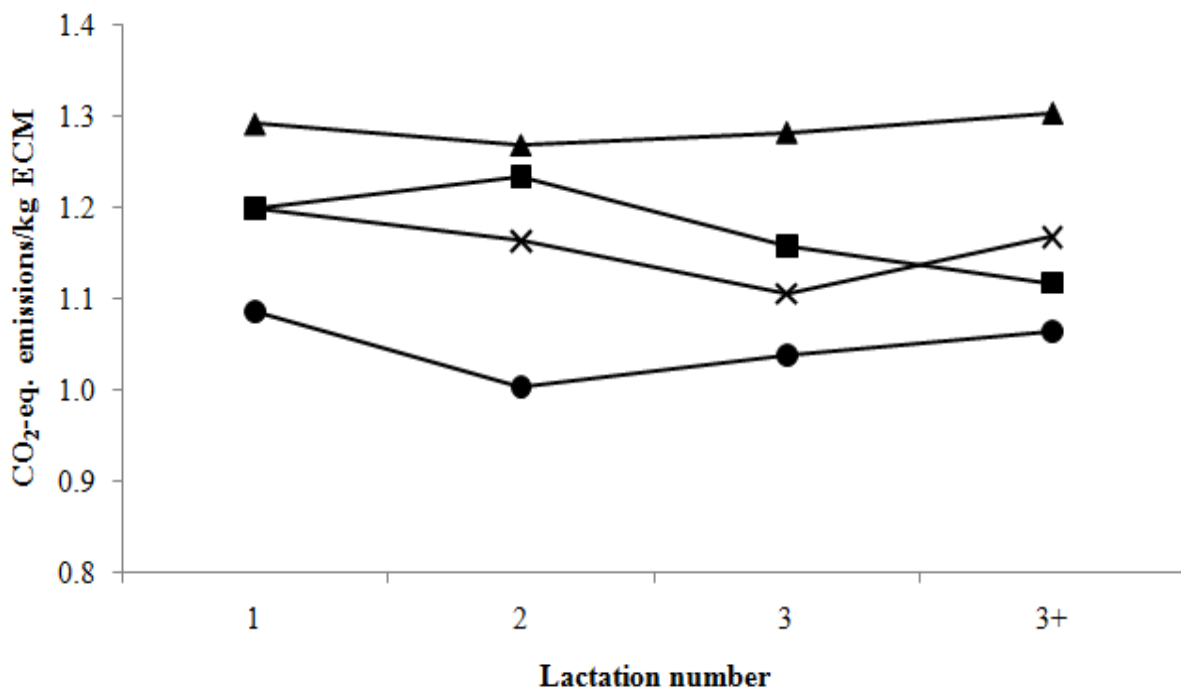

Figure 1. Carbon dioxide equivalent (CO_2-eq.) emissions per kg energy corrected milk (ECM) for cows selected for increased milk fat and protein fed a low proportion of forage (●) and a high proportion (×) of forage in their diet and cows selected to represent the average for milk fat and protein production fed a low proportion of forage (■) and a high proportion (▲) of forage in their diet (from [5]).

To bring about reductions in livestock GHG emissions, it has been suggested [21] that significant technological innovations will be required in the future, in addition to managing our consumption of meat and milk products. Technologies that can bring affordable efficiencies to production are being developed. Using genomic information, such as through genomic breeding values for feed related traits, described previously, and sexed semen [43] offer the potential for better selective breeding.

2. Conclusions

Reductions in GHG emissions by genetic selection of dairy cows in the past has been achieved largely by increased productivity and gross efficiency, whereby the maintenance cost of animals in the system has been reduced and less animals are required to produce the same amount of product. Based on current breeding goals, a similar rate of reduction in emissions intensity can be expected in the near future. Selecting dairy cows on feed efficiency, and possibly methane and nitrogen losses, will have a large impact on the environmental footprint of milk production, once implemented in breeding schemes. Further research and development of novel technologies to better understand the physiological and genetic differences between animals that lead to differences in energy and nitrogen efficiencies (or overall feed use efficiency) are still required.

Dairy farming is a highly managed system and has the potential to make reductions in GHG emissions intensity through increased efficiencies, such as optimum animal performance (less non-productive and ill animals) and reduced inputs as shown in Figure 2, whilst still maintaining productivity.
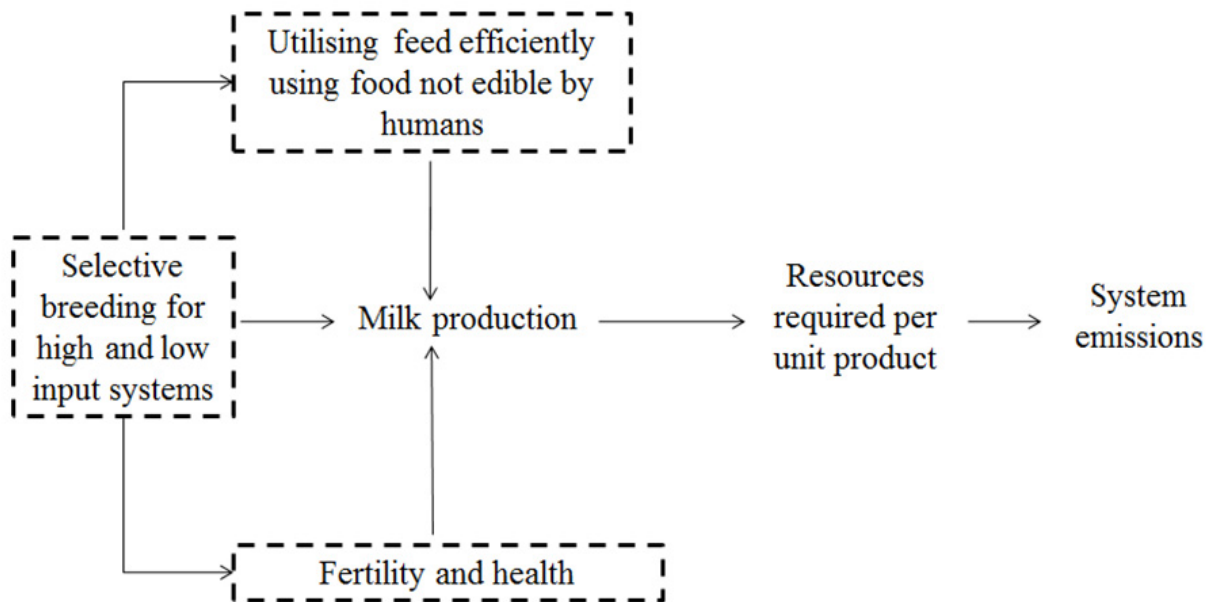

Figure 2. Production efficiencies using management (---) that can reduce GHG emissions beginning with selective breeding of a genotype for a particular system (from [5]).

Genetic improvement is a relatively cost-effective mechanism by which to achieve reductions in emissions, as the effect is cumulative and permanent. Many of the strategies for minimising emissions bring economic benefits to dairy farming through a reduction in production costs, with the added benefit of also reducing GHG emissions at little extra cost. The success of selective breeding as a mitigation strategy however, is dependent on producers being committed to its implementation.

Until direct measurements on GHG traits become available on sufficiently large numbers of animals, selecting for improved efficiency, RFI, or a measure of gross efficiency (unit of output per unit of feed eaten) offer attractive ways of reducing GHG emissions. However, the direct impact on GHG emissions is currently approximate and more research is needed to accurately assess the impact. Furthermore, selection strategies in dairy cattle need to be considered in a multi-trait framework, so that unfavourable correlated responses to selection (such as reduced fertility and excessive mobilisation of body reserves) are avoided.

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