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INVITED REVIEW

Genetic mechanisms underlying feed utilization and implementation of genomic selection for improved feed efficiency in dairy cattle

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Abstract: The economic importance of genetically improving feed efficiency has been recognized by cattle producers worldwide. It has the potential to considerably reduce costs, minimize environmental impact, optimize land and resource use efficiency, and improve the overall cattle industry's profitability. Feed efficiency is a genetically complex trait that can be described as units of product output (e.g., milk yield) per unit of feed input. The main objective of this review paper is to present an overview of the main genetic and physiological mechanisms underlying feed utilization in ruminants and the process towards implementation of genomic selection for feed efficiency in dairy cattle. In summary, feed efficiency can be improved via numerous metabolic pathways and biological mechanisms through genetic selection. Various studies have indicated that feed efficiency is heritable, and genomic selection can be successfully implemented in dairy cattle with a large enough training population. In this context, some organizations have worked collaboratively to do research and develop training populations for successful implementation of joint international genomic evaluations. The integration of "-omics" technologies, further investments in high-throughput phenotyping, and identification of novel indicator traits will also be paramount in maximizing the rates of genetic progress for feed efficiency in dairy cattle worldwide.

Key words: environmental footprint, feed efficiency, genomic selection, residual feed intake, rumen microbiome.

Résumé : L'importance économique de l'amélioration génétique de l'indice de consommation a été reconnue par les producteurs de bétail à travers le monde. Elle a le potentiel de considérablement réduire les coûts, minimiser l'impact environnemental, optimiser l'efficacité d'utilisation des terres et des ressources, et améliorer la profitabilité générale de l'industrie du bétail. L'indice de consommation est une caractéristique génétiquement complexe qui peut être décrite comme les unités de produits produites (p. ex., rendement de lait) par unité d'aliments consommés. L'objectif principal de cet article de synthèse est de présenter un survol des principaux mécanismes génétiques et physiologiques sous-jacents à l'utilisation des aliments chez les ruminants ainsi que le processus vers l'implémentation de la sélection génomique pour l'indice de consommation chez les bovins

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laitiers. En résumé, l'indice de consommation peut être amélioré par de nombreuses voies métaboliques et nombreux mécanismes biologiques par sélection génétique. Des études variées ont indiqué que l'indice de consommation est héritable et la sélection génomique peut être implémentée avec succès chez les bovins laitiers avec une population assez grande de formation. Dans ce contexte, certaines organisations ont travaillé en collaboration pour la recherche et le développement des populations de formation pur l'implémentation à succès d'évaluations génomiques internationales conjointes. L'intégration des technologies « -omiques », les investissements ultérieurs pour le phénotypage à haut débit, et l'identification de nouveaux traits indicateurs seront primordiaux pour la maximisation du taux de progrès génétique pour l'indice de consommation chez les bovins laitiers à travers le monde. [Traduit par la Rédaction]

Mots-clés : empreinte écologique, indice de consommation, sélection génomique, consommation résiduelle, microbiome du rumen.

Introduction

The global human population is expected to reach 9.8 billion by 2050 (FAOSTAT 2019), and consequently, there will be a substantial increase in food demand. In addition, the projected reduction in poverty and expansion of the middle class will reflect in a greater demand for larger amounts of high-quality meat and dairy products, produced under exemplary welfare conditions and leaving a minimal environmental footprint. As there are limited land and natural resources for production expansion, there is an urgent need to develop strategies to optimize the efficiency of food production.

The current worldwide cattle population has more than 1.5 billion animals; over 105 million cattle are raised in Canada and the United States alone (FAOSTAT 2019). With feed currently being the largest expense in cattle production (Ho et al. 2013; Connor 2015), a small improvement in nutrient utilization [i.e., better digestibility and (or) greater nutrient absorption] can have major economic and environmental impacts. The reduction in feeding costs will positively impact, not only the cattle producers' profitability, but also the final prices of meat and dairy products available to consumers.

The demand to optimize animal nutrition practices has led to important investments in research over the past decades. Consequently, the science of animal nutrition has evolved rapidly and resulted in major contributions to a better understanding of the nutritional physiology of cattle and its nutrient requirements. This had led to major advancements in diet formulation, supplementation, and techniques for food processing and storage (Eastridge 2006; Coffey et al. 2016; de Ondarza and Tricarico 2017; Tedeschi et al. 2017). Despite the clear effectiveness of these developments, the need for a more permanent and cumulative solution has been envisioned through genetic selection for a long time in various livestock species, including cattle (e.g., Stone et al. 1960; Koch et al. 1963; Freeman 1967; Herd et al. 2003).

The economic importance of selecting for improved feed efficiency has been clearly recognized by cattle producers, due to its potential to reduce costs considerably, minimize environmental impacts (e.g., reduce nutrient loss in manure and methane intensity), optimize land and resource use efficiency, and improve the overall cattle industry profitability (Richardson and Herd 2004; Basarab et al. 2013; Berry and Crowley 2013). However, the inclusion of feed efficiency in cattle selection indexes used in commercial breeding programs has been delayed for various reasons, among them: (1) the limited amount of phenotypic records for feed efficiency and related variables in commercial herds; (2) the differences in feed intake measurement protocols and data sources (e.g., different breeds, lactation stages, parities, and diets); (3) unclear definition of the breeding goal (Berry and Crowley 2013; Pryce et al. 2014; Connor 2015; Hurley et al. 2016); and (4) the lack of research on novel traits evaluated based on a systems biology level that could contribute to improve the accuracy of genomic prediction of breeding values. In the case of beef cattle, there are even some additional challenges, including limited vertical integration of production, large diversity of genetic resources (breeds) within country and internationally, greater use of crossbreeding systems, and reduced use of artificial insemination compared with dairy cattle, which leads to weaker genetic linkage among populations, and consequently, less accurate genomic breeding values.

With the more recent advancements in genomic methods and technologies, selection for feed efficiency has become more feasible, as genomics can be used as a tool to transfer the knowledge generated on research farms to genetically connected commercial populations (Connor 2015). However, selection based on genomic information still requires genotyping of the selection candidates, as well as continued collection of phenotypic and genotype records from genetically representative individual animals (i.e., a training population). The main objective of this review is to present an overview of worldwide research efforts to unravel genetic, molecular, and physiological mechanisms underlying the efficiency of feed utilization in ruminants, current knowledge on host–microbiota interactions, and the implementation process of genomic selection for improved feed efficiency in dairy cattle.

Definitions of Feed Efficiency and Indicator Traits

Dairy cattle breeding programs have been very successful in improving the main traits of interest for the industry (e.g., Miglior et al. 2017). The first step in moving genetic progress in a desired direction for any breeding program is the clear definition of the breeding goal. In this context, a feed-efficient animal has been broadly defined as an animal that eats less without compromising performance, or an animal that produces more while consuming the same amount of feed. In other words, feed efficiency is related to the units of product output (e.g., milk production) per unit of feed input. These units are generally mass, energy, protein, or an economic value (Vandehaar et al. 2016). It is also of interest to dairy cattle breeders to select animals that do not compromise other vital functions, such as reproduction and health, while breeding to achieve greater feed efficiency (Connor 2015).

Feed efficiency is a complex trait, as feed intake and nutrient utilization are associated with many biological and physical mechanisms. For example, variability in feed efficiency can be due to variation in feed intake levels, digestion of feed and the associated energy costs, absorption of nutrients, metabolism, physiological stage, health status, rumen microbial metabolism, activity, and thermoregulation (Herd et al. 2004; Herd and Arthur 2009; Patience et al. 2015; Li et al. 2016). Due to the challenging nature of measuring feed efficiency, many indicator traits have been proposed and utilized to assess feed efficiency, such as residual feed intake (RFI), residual solids production (RSP), and the use of milk mid-infrared spectroscopy (MIR) (Koch et al. 1963; Coleman et al. 2010; Berry and Crowley 2013; Pryce et al. 2014; Connor 2015; Hurley et al. 2016; de Ondarza and Tricarico 2017).

Koch et al. (1963) suggested the use of RFI as an indicator of feed efficiency. The RFI variable, estimated through a regression model, corresponds to the difference (residual) between the observed and expected feed intake, where the expected feed intake is based on feeding requirements assessed according to metabolic body weight and level or quantity of product outcome. Other physiological activities that are energy demanding, such as maintenance and reproduction, can also be included in the calculations (Berry and Crowley 2013; Pryce et al. 2014). Most commonly, RFI has been used in beef cattle research (Berry and Crowley 2013). More recently, studies in dairy cattle have also been reported (e.g., Waghorn et al. 2012; Connor et al. 2019; Flay et al. 2019).

In dairy cattle, RFI is estimated by regressing dry matter intake (DMI) on a variety of physiological activities, which commonly include production (milk yield or energy-corrected milk), metabolic body weight, changes in body weight or body condition score (BCS), and stage of lactation (Connor 2015; Byskov et al. 2017; Seymour et al. 2019). Other residual traits have also been analyzed in place of RFI to obtain an estimate closer to the biology behind feed efficiency, such as RSP (Coleman et al. 2010). Similar to RFI, RSP represents the difference between observed milk solids production and that estimated via regression based on various activities (Coleman et al. 2010).

Another group of feed efficiency indicators are based on nutrient usage, such as energy and nitrogen efficiency, which considers nutrient partitioning between milk production and other physiological functions (de Ondarza and Tricarico 2017). For instance, energy conversion efficiency is the milk energy output divided by metabolizable energy intake. It has the advantage to consider diverse nutrient efficiency; however, it does not account for mobilization of body reserves. Therefore, to account for body reserve changes, residual energy intake (REI) has been proposed (Mantysaari et al. 2012; Liinamo et al. 2015; Fischer et al. 2018). REI is the actual metabolizable energy intake minus the predicted energy requirement of the cow based on production, bodyweight, changes in bodyweight and (or) BCS, as well as gestational energy needs (Mantysaari et al. 2012; Fischer et al. 2018).

As the costs to measure feed intake on individual animals are still high, alternative approaches to measure feed efficiency have been investigated. For instance, predictor traits that can be measured on a large number of animals for a relatively low cost through milk samples, blood, biosensors, and automated recording systems are of great interest. Some examples of these include infrared thermography (Montanholi et al. 2010), plasma concentrations of insulin-like growth factor-1 (Moore et al. 2005), milk MIR spectrometry (O'Donovan et al. 2014; Wallén et al. 2018), and milk fatty acid composition (Kelly et al. 2010). The use of MIR spectrometry to measure energy balance in dairy cattle began in 2011 (McParland et al. 2012). In addition, MIR is widely used to determine major milk components, such as fat and protein. Shetty et al. (2017) used a partial least-squares approach to estimate DMI based on MIR spectral data. Although further studies are necessary, such models are a promising way to estimate individual energy intake (Dórea et al. 2018; Seymour et al. 2019). In summary, multiple alternatives to quantify individual variability of feed efficiency in dairy cattle have been proposed. As reviewed by de Ondarza and Tricarico (2017), each one of them has advantages and disadvantages. To make a better decision on the indicator trait to be used in a breeding program, it is of utmost value to understand the physiological mechanisms of feed utilization and the genetic architecture of the traits utilized. The next sections of this review will cover these aspects.

An Overview of the Main Physiological Mechanisms Underlying Feed Efficiency

The expected physiological changes arising from genetic selection for improved feed efficiency are dependent on the feed efficiency metric (i.e., indicator trait) used. For example, gross feed efficiency is typically calculated as the ratio of milk output to feed intake. As a result, this trait can be improved by increasing milk yield, decreasing feed intake, or a combination of both strategies. More complex measures of feed efficiency, such as RFI (Koch et al. 1963), REI (Fischer et al. 2018), or net energy efficiency (Seymour et al. 2020), share some commonalities. This includes the concept of categorizing energy expenditures into maintenance, growth, or production activities, and will be the focus of this section. However, regardless of the measure (i.e., trait) used, the physiology of feed efficiency can be partitioned into two main areas: those regulating voluntary feed intake and those regulating the conversion of nutrients into milk. On another layer, the major components affecting feed efficiency can be divided into those that alter maintenance or the portion of net energy that is captured in milk or body tissues (instead of being used for maintenance) and those that alter the conversion of gross energy to net energy (VandeHaar et al. 2016).

All measures of feed efficiency are dependent on the amount of feed consumed, and thus, the regulation of voluntary feed intake is a major determinant of efficiency. The physiological regulation of DMI is a complex and multi-factorial process, and it was comprehensively described by Allen (2000), Allen et al. (2009), and Forbes (2000, 2007). The predominant factors known to affect voluntary feed intake in ruminants are reticulorumen distension due to gut fill, hepatic propionate flux, and the amount of lipid in the diet (Allen 2000). Gut fill is considered to be the major limiting factor of feed intake in early lactation when energy demands are highest, where mechanoreceptors are triggered by reticulorumen wall distension and send negative feedback to the brain via the vagus nerve to reduce feed intake (Allen 2000; Forbes 2000). The hepatic oxidation theory (Allen et al. 2009) postulates that the oxidation of fuels in the liver, such as propionate, acts as a major signal integrator that regulates feed intake in response to whole body energy status. There is a plethora of other signaling mechanisms involved in the regulation of feed intake, and a single stimulus may act through multiple pathways (polymodality) as well as at different sites (polytopicity; Forbes 2007).

After consuming feed, the animal's available energy is divided into various processes, which are normally categorized into maintenance, growth, reproduction, and production. In general, animals which partition a greater proportion of energy towards productive purposes are considered to be more feed efficient. The biological processes governing anabolic and catabolic processes are generally considered to be highly regulated and subject to strict thermodynamic constraints (Baldwin et al. 1980; Seymour et al. 2020), making genetic selection for improved efficiency of these pathways somewhat challenging. However, Bottje (2019) has recently provided support for the theory that defective proteins in the electron transport chain may lead to suboptimal mitochondrial function and reduce the overall energetic efficiency of the animal. If the genes associated with these protein defects could be identified, genomic variants [e.g., single-nucleotide polymorphisms (SNPs)] could be given greater weight in sophisticated genomic prediction methods that are currently available. However, this would likely necessitate increased selection intensity on dam of dam lines, as mitochondrial DNA is strictly maternal in origin.

An important physiological change associated with improved feed efficiency (RFI) in dairy cattle is a reduction in body size appropriate for the specific production system, as proposed by Dickerson (1978) and Vandehaar et al. (2016). This would serve to reduce the total energy partitioned towards maintenance processes, allowing for a greater proportion of energy to be directed towards productive purposes. Although this will reduce milk yield and feed intake, selection for improved lactation persistency and management for extended lactations would help maintain total lactation milk yield (Capuco et al. 2006; Santschi et al. 2011*a*, 2011*b*). Additionally, it is generally accepted that smaller body size is associated with improved fertility. Thus, animals would remain in the herd longer, which would result in fewer animals needed to produce a given volume of milk in a specific time period. Overall, these outcomes would likely improve the efficiency of both the individual animal and the overall herd. The nutritional management system in each farm also needs to be considered. As described by Vandehaar et al. (2016), under limited feeding and management, significant gains in feed efficiency can be captured by further diluting maintenance (e.g., smaller cows). In this context, similar genetic improvement is expected if animals are selected to produce more milk at a specific body weight, or the same milk yield with smaller body weight (Vandehaar et al. 2016).

Genetic Architecture of Feed Efficiency

Genetic parameters for feed efficiency traits

Before including a trait in a genetic selection index, it is important to evaluate its heritability (h^2) and genetic variance in the population of interest, as well as its genetic correlation with other economically important traits. These genetic parameters give insights into the rate of genetic progress that can be achieved per generation and contribute to better designing the genetic evaluation systems. Studies have indicated that feed efficiency, assessed in different ways using indicator traits, is moderately heritable (Table 1). For example, Williams et al. (2011) reported that genetic variation in RFI exists in dairy heifers, and this could be an alternative to indirectly selecting dairy cows for improved feed efficiency, as it is easier to record feed intake in heifers (similar production and data collection systems as in beef cattle). Spurlock et al. (2012) estimated genetic parameters and made recommendations regarding traits related to energy balance, including DMI, bodyweight, BCS, energy-corrected milk production, and gross feed efficiency.

Table 1. Heritability (h^2) estimates for different indicator traits of feed efficiency in dairy cattle.

Trait	Reference	$h^2 \pm$ SE	Breed
Dry matter intake	Vallimont et al. 2010	0.18 ± 0.06	Holstein
	Williams et al. 2011	0.17 ± 0.10	Holstein Friesian
	Liinamo et al. 2015	0.23 ± 0.12	Nordic Red dairy cattle
	Tetens et al. 2014	0.37 ± 0.04	Holstein
	Shonka et al. 2015	0.52 ± 0.13	Holstein
	Bilal et al. 2016	0.12 ± 0.01	Canadian Holstein
	Byskov et al. 2017	0.37 ± 0.06	Holstein
	Lu et al. 2018	0.23 ± 0.02	NA
Energy intake	Köck et al. 2018	0.07 ± 0.03 to 0.13 ± 0.02	Fleckvieh, Brown Swiss, and Holstein
Energy-corrected milk	Köck et al. 2018	0.08 ± 0.03 to 0.12 ± 0.02	Fleckvieh, Brown Swiss, and Holstein
Residual feed intake	Hurley et al. 2016	0.04 ± 0.08 to 0.11 ± 0.08	Holstein Friesian
	Van Arendonk et al. 1991	0.19 ± 0.12	Dutch and Holstein Friesian
	Korver et al. 1991	0.22 ± 0.11	Dairy cattle raised in the Netherlands (breed not specified)
	Jensen et al. 1995	0.36 ± 0.17	Red Danish, Danish Friesian, Danish Red and White, and Jersey
	Svendsen et al. 1993	0.02 ± 0.08	Dual-purpose Norwegian cattle
	Vallimont et al. 2011	0.01 ± 0.05	Holstein
	Williams et al. 2011	0.27 ± 0.12	Holstein Friesian
	Byskov et al. 2017	0.23 ± 0.05	Holstein
	Lu et al. 2018	0.16 ± 0.02	NA

Note: SE, standard error; NA, data from international dairy consortium, included several breeds (not specified).

The h^2 estimates presented in Table 1 indicate that feed efficiency can be improved through genetic selection. The wide range of h^2 estimates reported in the literature is related to the different populations used in each study, as genetic parameters (such as h^2 estimates) are population specific. Thus, this suggests the importance of (re-)estimating genetic parameters for each population. It is worth noting that selection for improved feed efficiency might also impact other economically important traits, due to genetic correlations between them. Examples of genetic correlations reported in the literature for different indicator traits of feed efficiency and some important economic traits in dairy cattle are summarized in Table 2. A detailed description of genetic correlations between feed efficiency indicators and other relevant traits can be found in Berry and Crowley (2013) and Manafiazar et al. (2016).

Functional candidate genes associated with feed efficiency

The development and availability of high-throughput "-omics" technologies (e.g., genomics, transcriptomics, proteomics, metabolomics, and metagenomics) have enabled the identification of numerous candidate regions associated with economically relevant traits (Cánovas et al. 2017). In this context, genome-wide association studies (GWAS) and transcriptomics using RNA-sequencing (RNA-Seq) technology have contributed to the identification of functional candidate genes and genetic variants [e.g., SNPs, copy number of variations (CNVs), and insertions and deletions; Cánovas et al. 2010; Wickramasinghe et al. 2014]. In beef cattle, GWAS and transcriptomics studies using RNA-Seq have enabled the identification of key regulators of biological processes and pathways linked to feed efficiency variability, including lipid and protein metabolism, ion transport, protein and amino acid glycosylation, as well as valine, leucine, and isoleucine degradation (Rolf et al. 2012; Abo-Ismail et al. 2014; Olivieri et al. 2016; Duarte et al. 2019).

The integration of multiple "-omics" technologies through a systems biology approach is a powerful strategy for precisely identifying functional variants mapped in key regulator genes involved in the metabolic pathways affecting feed efficiency (Cánovas et al. 2017). Despite the low number of GWAS and RNA-Seq studies evaluating feed efficiency in dairy cattle, the combination of these results can be integrated to better understand the genetic architecture of feed efficiency in dairy cattle.

In this section, we summarize the main studies, published up to date, that have applied GWAS and RNA-Seq to investigate the genetic mechanisms underlying feed efficiency. Table 3 presents the descriptive details of GWAS studies for feed efficiency in dairy cattle: breed(s), sample size, indicator trait, number of genetic markers, statistical method used, significance threshold, and number of significantly associated markers. Similarly, Table 4 presents the descriptive details of transcriptomics studies using RNA-Seq comparing divergently selected feed-efficient dairy cattle: breed(s), sample size, tissue analysed, indicator trait, statistical analysis, p value threshold, and number of differentially expressed genes. Seven GWAS for feed efficiency indicator traits (e.g., RFI, DMI, milk energy, and metabolic body weight) and three RNA-Seq studies comparing

Table 2. Examples of genetic correlations between different indicator traits of feed efficiency and production, as well as production-related traits, in dairy cattle.

Feed efficiency trait	Trait	Reference	$r_g \pm$ SE
Dry matter intake	Milk yield	Gonzalez-Recio et al. 2014	0.10 ± 0.11
		Vallimont et al. 2010	0.51 ± 0.32
	Fat- and protein-corrected milk yield	Difford et al. 2020	0.83 ± 0.04
	Fat yield	Gonzalez-Recio et al. 2014	−0.03 ± 0.10
		Vallimont et al. 2010	0.53 ± 0.34
	Protein yield	Gonzalez-Recio et al. 2014	−0.11 ± 0.08
		Vallimont et al. 2010	0.55 ± 0.37
	Somatic cell score	Vallimont et al. 2010	−0.15 ± 0.28
	Bodyweight	Liinamo et al. 2015	0.54 to 1.00
		Vallimont et al. 2010	0.52 ± 0.35
	Natural logarithm of methane	Difford et al. 2020	0.60 ± 0.13
	Natural logarithm of carbon dioxide	Difford et al. 2020	0.42 ± 0.13
	Productive life	Vallimont et al. 2013	0.49 ± 0.18
	Meal size	Lin et al. 2013	0.18 ± 0.15
	Eating rate	Lin et al. 2013	0.11 ± 0.14
	Feeding duration	Lin et al. 2013	0.48 ± 0.12
	Number of meals	Lin et al. 2013	0.03 ± 0.16
	Days open	Vallimont et al. 2013	−0.14 ± 0.29
	Body condition score	Gonzalez-Recio et al. 2014	0.37 ± 0.32
		Liinamo et al. 2015	0.11 to 0.45
		Vallimont et al. 2010	0.37 ± 0.46
Residual feed intake	Milk yield	Veerkamp et al. 1994	−0.11 to 0.07
		Gonzalez-Recio et al. 2014	0.07 ± 0.08
	Fat yield	Gonzalez-Recio et al. 2014	0.02 ± 0.07
	Protein yield	Gonzalez-Recio et al. 2014	0.03 ± 0.07
		Veerkamp et al. 1994	−0.11 to −0.02
	Lactose	Veerkamp et al. 1994	−0.19 to −0.05
	Bodyweight	Korver et al. 1991	0.03
		Van Arendonk et al. 1991	0.01
	Natural logarithm of methane	Difford et al. 2020	0.42 ± 0.23
	Natural logarithm of carbon dioxide	Difford et al. 2020	0.48 ± 0.24
	Productive life	Vallimont et al. 2013	−0.23 ± 0.29
	Days open	Vallimont et al. 2013	−0.50 ± 0.40
	Meal size	Lin et al. 2013	−0.06 ± 0.16
	Eating rate	Lin et al. 2013	0.06 ± 0.16
	Feeding duration	Lin et al. 2013	0.27 ± 0.15
	Number of meals	Lin et al. 2013	−0.07 ± 0.17
	Body condition score	Gonzalez-Recio et al. 2014	0.71 ± 0.32
		Veerkamp et al. 1994	0.33 to 0.36

Note: r_g, additive genetic correlation; SE, standard error.

two divergent groups of feed-efficient animals were found in the literature (Tables 3 and 4). The majority of these studies focused on the Holstein breed, which is the most commonly raised breed for milk production around the world. However, Salleh et al. (2018) studied Jersey breed animals, in addition to a subset of Holstein cows. As there are breed differences for feed utilization performance (Berry and Crowley 2013), one can assume that there would be differences at the gene expression level as well. However, the number of transcriptomics studies available using RNA-Seq is still too limited to draw such conclusions.

The integration and evaluation of multiple levels of -omics data can provide a better understanding of the physiological processes underlying feed efficiency. In addition to transcriptomics, the combination of proteomic and metabolomic analysis is important to determine causal effect and provide functional validation. When considering the application of -omics in livestock studies, there is a lack of information on feed efficiency and, more specifically, in dairy cattle. Few studies have evaluated feed efficiency in dairy cattle using metabolomics and proteomics. Due to the lack of studies integrating multiple -omics technologies to study feed efficiency in dairy cattle, it is difficult to assess the consistency across studies. For instance, proteomics and metabolomics have only recently been performed to study feed efficiency in dairy cattle (Wang and Kadarmideen 2019;

Table 3. Summary of genome-wide association studies (GWAS) performed in dairy cows to identify genomic regions associated with feed efficiency traits.

Breed, country, and reference	*N*	Trait	*N* of SNPs	Statistical analysis	Significance threshold	*N* of significant markers
Holstein, USA (B. Li et al. 2019)	5610	RFI	278 254 (after quality control)	Single-step GWAS	Top-20 SNPs and 5-SNP sliding windows	20 single-SNPs 20 five-SNPs sliding windows
Holstein, Scotland, the Netherlands, Canada, and USA (Lu et al. 2018)	4916	RFI based on classical model and MT model (Lu et al. 2015) using DMI, MILKE, and MBW	57 347 (after quality control)	Single-SNP marker association and windows-based association (1 Mb non-overlapping windows)	Multiples, based on Bonferroni adjustment at genome-wide type I error rate of 5%	MBW = 4 SNPs, 3 windows RFI = 2 windows MT = 2 windows DMI = 2 windows MILKE = 1 window MBW = 3 windows
Holstein, USA (Zhou et al. 2018)	473	RFI and DMI	454 CNVs	Multiple linear regression	$p < 0.05$ after FDR correction	RFI = 10 CNVs DMI = 1 CNV
Holstein, USA, Canada, the Netherlands and United Kingdom (Hardie et al. 2017)	4916	RFI was calculated as the residual of the regression of DMI on MILKE, MBW, change in body weight, and systematic effects. For RFI, DMI, MILKE, and MBW, bivariate analyses were performed for each trait as a separate trait within parity group	60 671 markers	Bayes B and Bayes C	Top-10 genomic windows	RFI = 5.38% (PM) and 4.80% (MP) of total genetic variance explained by the top 10 windows DMI = 9.18% (PM) and 5.54% (MP) MILKE = 7.12% (PM) and 5.08% (MP) MBW = 9.31% (PM) and 9.8% (MP)
Holstein, Germany (Tetens et al. 2014)	681	DMI 11, 30, 80, 130, and 180	40 407 (after pruning for loci >10% of missing genotypes, MAF < 0.05 and markers without position)	Linear mixed model approach implemented in the package GEMMA	$p < 0.05$ after Bonferroni correction	DMI11 = 4 markers DMI30 = 8 markers DMI80 = 3 markers DMI130 = 5 markers DMI180 = 7 markers
Holstein, USA (Yao et al. 2013)	395	Daily RFI from 50 to 150 d postpartum	42 275	Random Forest algorithm	Importance score (ΔMSE%)	188 markers
Holstein, Australia and New Zealand (Pryce et al. 2012)	1782	RFI	624 930	Bayes A and Bayes	The 1000 largest SNP effects ranked on absolute value were selected	1000 markers

Note: SNP, single-nucleotide polymorphism; RFI, residual feed intake; MT, multiple trait; DMI, dry matter intake; MILKE, milk energy; MBW, metabolic body weight; CNV, copy number variant; MAF, minor allele frequency; FDR, false discovery rate; MSE, mean squared error; PM, primiparous cows; MP, multiparous cows.

Table 4. Summary of RNA-sequencing studies comparing divergent feed efficient groups [based on residual feed intake (RFI)] in dairy cattle.

Breed, country	Sample size	Tissue	Significance threshold	*N* of differentially expressed genes	Reference
H and J, Denmark	High RFI[a] = 5 H and 5 J Low RFI[a] = 4 H and 5 J	Liver	$p < 0.05$	H: 11 modules of co-expressed genes J: 4 modules of co-expressed genes	Salleh et al. 2018
H and J, Denmark	High RFI[a] = 5 H and 5 J Low RFI[a] = 4 H and 5 J	Liver	FDR < 5%	70 (H for model 1) 19 (J for model 1) 2 (J for model 2)	Salleh et al. 2017
H, Australia	High RFI[b] = 9 animals Low RFI[b] = 10 animals	Liver and WBC	FDR < 5%	Liver RFI = 473 Liver GEBV = 526 WBC RFI = 4817 WBC GEBV = 137	Khansefid et al. 2017

Note: H, Holstein; J, Jersey; WBC, white blood cells; GEBV, genomic estimated breeding values.

[a] RFI groups were defined based on the ranking of random effects solutions [from a fixed linear regression on metabolic body weight, daily live weight change, daily body condition score change (fitted with a Legendre polynomial), and energy corrected milk yield] for 200 animals, where the top and bottom animals were selected.

[b] RFI groups were defined using the top and bottom 10% animals from the RFI distribution in a population composed by 843 animals (average RFI = 0 and standard deviation = 0.19; Williams et al. 2011).

Zhang et al. 2019). Metabolic profiling of blood plasma has been performed in Holstein and Jersey cattle, revealing multiple fatty acids with significantly different profiles between divergent feed efficiency groups and were functionally enriched for biological pathways associated with energy use and production (Wang and Kadarmideen 2019). The integration of hepatic metabolomic and proteomic data of Holstein heifers divergent for feed efficiency has revealed 29 metabolites and 60 proteins that were significantly different between low and high feed-efficient heifers (Zhang et al. 2019). These studies provide useful biomarkers as indicators for feed efficiency in dairy cattle; however, integration and evaluation of multiple -omics technologies to study feed efficiency can improve the understanding of the whole biological system underlying feed efficiency through functional validation.

Regarding the study of feed efficiency in dairy cattle at the whole genome level using GWAS, a large number of regions were identified to be associated with feed efficiency traits, but the effect of each genomic region was small, indicating that feed efficiency is a polygenic trait. For instance, Hardie et al. (2017) reported that the 10 genomic windows explaining the majority of the genetic variance for RFI, accounted for only 5.38% and 4.80% of the genetic variance for RFI in first-parity and multiparous cows, respectively.

The transcriptomics analyses performed using RNA-Seq technology (Table 4) compared gene expression measured in the whole transcriptome between two divergently selected groups of animals based on feed efficiency. It is worth highlighting that Salleh et al. (2017, 2018) evaluated liver biopsies from the same set of animals (high RFI = five Holstein and five Jersey cows; low RFI = four Holstein and five Jersey cows) but used distinct statistical approaches. In all studies, RNA-Seq was performed using liver tissue samples due to the key role of this organ in energy conversion and metabolic efficiency. In addition, Khansefid et al. (2017) also evaluated gene expression in white blood cells of divergently selected cattle for RFI. The number of differentially expressed genes (DEG) varied substantially across studies. These results reinforce the polygenic nature of feed efficiency (as described by Salleh et al. 2018; Seymour et al. 2018). The use of methodologies such as the weighted gene co-expression network analysis is a good alternative to identify hidden patterns of interactions between genes and consequently, contribute to further understanding the biological processes associated with feed efficiency. This methodology is useful due to the fact that the individual identification of DEG can underestimate the complexity of the genetic architecture of quantitative traits, especially when the expression of genes acting in the biological processes tends to be correlated (Langfelder and Horvath 2008). To date, no studies have exploited the identification of functional variants associated with feed efficiency traits using RNA-Seq data.

The level of overlapping and cross-validation among studies can greatly vary depending on the methodology used to perform the analyses. One of the main causes of the non-validation across studies is the lack of homogeneity in the population structure, phenotypes, statistical models, quality control thresholds, among others. For example, Fonseca et al. (2018) described a strong stratification for the list of positional and functional candidate genes as a function of the purpose of the breed (dairy or beef) and the phenotype evaluated when GWAS for male fertility traits were functionally integrated. Even though all the studies summarized in this current review were focused on feed efficiency, different phenotypes were used to access the feed efficiency in each study: RFI (using different models), daily RFI, and DMI. As each one of these phenotypes might be representing a different portion of the total feed efficiency of the animals, the candidate regions and genes can be expected to be different for each trait phenotype. Additionally, the population structure and the statistical models applied in each study can substantially impact the detection power. Therefore, a very precise and careful approach must be performed to discuss and to point possible similarities and differences across the studies. This may be achieved by a proper meta-analysis, as more studies become available.

Despite the reduced number of GWAS and transcriptomics studies using RNA-Seq evaluating feed efficiency in dairy cattle, the findings currently reported are similar to those observed in beef cattle (Table 3). The similarities in results from beef and dairy cattle-based studies creates an opportunity to perform integrative analyses (e.g., meta-analyses and functional analyses) to reduce the number of false-positive associations, and consequently, fine map those variants with the strongest effects. Thereafter, the identification of functional candidate genes can be performed in a more efficient way. Once candidate genes are identified, the prospection of causal variants mapped within these genes can contribute to increasing the predictive ability of feed efficiency through the use of specific markers used in sophisticated genomic selection approaches (Hayes et al. 2013; Goddard et al. 2016; VanRaden et al. 2017*a*).

The additional value of whole-genome sequence data

The use of genomic information derived from SNP chip arrays in genetic evaluation schemes is very efficient for multiple purposes (e.g., Georges et al. 2019). However, the inclusion of information from denser SNP arrays or whole-genome sequence data (WGS) is yet to be shown as advantageous. In this context, more recently, there has been an interest in selecting variants based on WGS-based GWAS analyses and the incorporation of structural variants, especially CNVs, in GWAS and genomic predictions.

The identification of SNPs related to feed efficiency through WGS-based GWAS followed by functional analyses will enable the identification of variants with direct impact on feed efficiency. Therefore, the causal mutations can be included in the genomic predictions without the need to rely on linkage disequilibrium (MacLeod et al. 2014). For instance, VanRaden et al. (2017*a*) reported an increase of 2.7% in the accuracy of genomic estimated breeding values (GEBVs) when performing WGS variant selection based on their estimated effect on a given trait.

Mielczarek et al. (2018) reported CNV variations within and between multiple European dairy cattle breeds. This variability in CNV might enable more accurate selection of animals with greater genetic merit for feed efficiency. Although few CNV studies have been performed in dairy cattle, those conducted reported identified multiple genomic regions associated with feed efficiency and other traits of interest. Based on 147 high-density Holstein genotypes, Hou et al. (2012) identified and partially validated CNVs that were only observed in high- or low-feed-efficient animals. The authors also linked those CNVs with important metabolic pathways involved in feed utilization. However, the power of the study was small due to limited sample size. In addition, Zhou et al. (2018) identified 10 CNVs (based on the UMD3.1 reference assembly; Zimin et al. 2009) in Holstein cattle associated with RFI. One of these CNVs (BTA4: 108 225 979–108 252 635 bp) was also associated with DMI. In addition, multiple regions were harboring olfactory receptor genes (e.g., *RXFP4*), which are likely indirectly related to feed efficiency through changes in feeding behavior (Soria-Gomez et al. 2014). For instance, the *RXFP4* gene is known to be related to appetite regulation and metabolism, providing a direct link to efficiency (Ang et al. 2017). Lastly, a region overlapping with a quantitative trait loci associated with average daily gain on BTA7 (42 745 346–42 788 788) was also associated with RFI. The release of a better-quality reference genome assembly, i.e., ARS-UCD1.2 (Rosen et al. 2018), will enable the discovery of additional CNVs associated with feed efficiency. Furthermore, there are limitations on the number of individuals with phenotypic and WGS information. As more animals have phenotypes and WGS data become available on a larger number of individuals, more accurate results are expected to be obtained.

In addition to the individual genetic merit of dairy cattle, there are other factors that contribute to variability in feed efficiency. The next section will describe the role of the rumen microbiome on the efficiency of feed utilization in dairy cattle as well as its interaction with the genetic makeup of the individual host.

The Role of Rumen Microbiome on Feed Efficiency

The rumen microbial community is a complex ecosystem composed mainly of bacteria, ciliate protozoa, fungi, and archaea, which interact with each other to digest fibrous feed (Williams and Coleman 1997). Ruminants are dependent on the rumen microbial community to produce and serve as metabolic energy products to survive, and in return, the microbial community depends on the ruminant for a habitat to survive, resulting in a symbiotic host–microbial relationship. The function of the rumen to extract nutrients from feed and deliver metabolites to productive tissues represents its large role in nutrient economy and whole-body metabolism (Baldwin and Connor 2017). As feed efficiency is largely dependent on better partitioning of metabolic energy, the metabolic efficiency of the rumen microbiota is known to influence feed utilization, due to its large role in energy production and delivery to the host (Myer et al. 2015; Shabat et al. 2016).

The near-total exchange of rumen contents between two cows has revealed that ruminal pH and volatile fatty acid concentration rapidly stabilizes within 24 h after rumen content exchange. This implies that the rumen microbial community has the ability to adapt rapidly (Weimer et al. 2010), and the assembly of the microbial community could be partially determined by the host (Benson et al. 2010; Sasson et al. 2017; Difford et al. 2018; F. Li et al. 2019; Wallace et al. 2019). This suggests that ruminants may exhibit individual rumen microbial profiles, and that there could be a potential for genetic selection for a desirable rumen microbiome profile in combination with management of other environmental factors (e.g., diet). However, the understanding of the genetic basis underlying the interactions between the host's genetics and the rumen microbiome, along with its overall influence on feed efficiency is limited. This has led to recent studies using transcriptomics, meta-transcriptomic, and metagenomics to investigate the role of the rumen microbiome, which is considered as "all the microbial genomes within the rumen microbial community".

Studying the rumen microbiome using "-omics" technologies

Previous studies have used metagenomic and meta-transcriptomic approaches to quantify microbial content/abundance and microbial gene expression, respectively, and its potential link to feed efficiency in cattle (Shabat et al. 2016; Li and Guan 2017; Paz et al. 2018). Research investigating the rumen metagenome and its association with feed efficiency has revealed differential bacteria abundances across divergent rumen metabolic efficiencies by classifying specific bacteria using operational taxonomic units (OTU; Paz et al. 2018), which measure various microbial species and their abundance. Specific OTU have been characterized in beef cattle across divergent feed efficiency groups and revealed that specific OTU abundance from bacterial families, including Prevotellaceae and Lachnospiraceae, were associated with feed efficiency in beef steers (Paz et al. 2018). Feed efficiency and rumen microbiome have been previously associated (Hayes et al. 2013; Sasson et al. 2017; Paz et al. 2018), revealing that models used to explain feed efficiency traits (e.g., DMI, average daily gain, and gain to feed ratio) explained up to 20% of the total variation in feed utilization when including OTU abundance parameters (Paz et al. 2018). This evidence suggests that microbial OTU abundance may serve as a predictor of feed efficiency (Paz et al. 2018).

The study of rumen meta-transcriptome has indicated that less efficient cattle exhibit more diverse microbial activities (Li and Guan 2017). This supports the findings by Shabat et al. (2016), in which less feed efficient beef cattle exhibited higher richness of microbial gene content compared with more feed efficient beef cattle. These studies suggest that rumen microbiome content and function/activity may serve as a microbiome feature to genetically improve feed efficiency (Shabat et al. 2016; Li and Guan 2017). To further improve the understanding of the associations between the rumen microbiome and host phenotypes, other "-omics" platforms should be considered, including meta-proteomics and metabolomics (de Almeida et al. 2018; Hart et al. 2018).

Estimates of h^2 on rumen microbial features

The nature of the diverse community of the rumen microbiome has led to variation in characterizing and defining consistent rumen microbiome traits to estimate h^2 and investigate correlations with production traits. The h^2 of the rumen microbiome has primarily been estimated using taxonomic profiles, on an OTU abundance basis (Sasson et al. 2017; Difford et al. 2018; F. Li et al. 2019; Wallace et al. 2019). Additionally, more recent traits used to estimate h^2 of the rumen microbiome include microbial diversity indices and ratios between microbial groups (F. Li et al. 2019).

Using specific bacteria OTU abundance, a study on 78 Holstein-Friesian dairy cows estimated h^2 of that trait at approximately 0.70 (Sasson et al. 2017). Furthermore, bacteria and archaea OTU abundance had h^2 estimates ranged between 0.17 and 0.25, when the association between methane emissions (a trait correlated with efficiency of nutrient utilization) and rumen microbiome in lactating Holstein cows was analyzed (Difford et al. 2018). In Holstein and Nordic Red lactating dairy cows, Wallace et al. (2019) identified 39 heritable core (few specific targeted microorganisms) microbial OTUs, with h^2 estimates ranging from 0.20 to 0.60.

Estimates of h^2 on rumen microbial traits have also been studied in beef cattle. For instance, the h^2 of rumen bacterial diversity indices were estimated in Angus, Charolais, and Crossbreed, revealing h^2 estimates of 0.23 (Shannon index) and 0.19 (Simpson index) (F. Li et al. 2019). In the same study, the h^2 of bacterial or archaeal community component differences ranged from 0.15 to 0.25. Similarly, moderate h^2 estimates were observed for total bacterial abundance (0.16), whereas h^2 estimates for total archaeal abundance was lower (0.05). A wide range of h^2 estimates have been reported for various microbial features, mainly due to differences across breeds, populations, analytical methods, and diets (Sasson et al. 2017; F. Li et al. 2019; Wallace et al. 2019).

Host–microbiome genetic interactions and influence on production traits in dairy cattle

Advances in transcriptomic, meta-transcriptomic (the measurement of host and microbial gene expression using RNA-Seq technology; Li and Guan 2017), and metagenomic (amplicon-sequencing to measure microbial content/abundance; Sasson et al. 2017; Wallace et al. 2019) sequencing approaches have led to opportunities to better understand rumen microbiome parameters and their relationship with host phenotypic expression. F. Li et al. (2019) reported 19 SNPs in the host genome associated with 14 rumen microbial taxa. Out of those 19 SNPs, five are located in known quantitative trait loci for cattle feed efficiency. Host–microbiome interactions have been widely studied in mice, flies, and humans (Benson et al. 2010; Turpin et al. 2016; Fromont et al. 2019). However, to our best knowledge, F. Li et al. (2019) is the first report on the characterization of the link between the cattle genetic makeup and heritable microbial features. This is a research area in great expansion at the moment, and therefore, major breakthroughs in this field are expected over the next few years.

Data Collection and Implementation of Genomic Evaluations

Genomic selection for improved feed efficiency

As previously outlined, the costs and feasibility of measuring individual feed intake (and related traits, such as bodyweight) in a large number of animals with pedigree information has limited the implementation of genetic selection for feed efficiency. Genomic selection has become widely available in the dairy cattle industry and enabled selection of breeding candidates based on their predicted genetic merit for feed efficiency. This is because animals from research herds can be used as a training population to estimate SNP effects, which are then used to predict GEBVs for selection candidates based on their own genotype (Veerkamp et al. 2015). In brief, genomic selection refers to the use of genome-wide genetic markers to predict breeding values of selection candidates (Meuwissen et al. 2001).

The accurate calculation of GEBVs depends on the estimation of SNP effects based on genomic and phenotypic datasets (i.e., training population). The size of the training population directly affects the GEBV accuracies (Hayes and Goddard 2008; Goddard 2009). However, the size of training population for feed efficiency in dairy cattle is still limited. Other factors that impact GEBV accuracy are SNP panel density, trait heritability (Daetwyler et al. 2008; Goddard 2009), the extent of the linkage disequilibrium between SNP and quantitative trait loci (Hayes et al. 2009; VanRaden et al. 2009), and the relationship between the training and validation or target populations (Habier et al. 2010; Pszczola et al. 2012).

As previously discussed, RFI is one of the most common indicator traits of feed efficiency in research settings. Genomic selection for RFI has been shown to be feasible, but the accuracies are still lower compared with other traits (Table 5; Calus et al. 2013; Gonzalez-Recio et al. 2014). Some studies have reported that a training population containing more than 30 000 individuals would be required to achieve satisfactory reliabilities for traits with h^2 estimates of 0.2 such as RFI (Calus et al. 2013; Gonzalez-Recio et al. 2014; Connor 2015). Despite the fact that GEBV accuracies for RFI in dairy cows are usually lower than the accuracies obtained for production traits, they are expected to increase as the training populations keep growing. For instance, Pryce et al. (2012) reported GEBV accuracies for RFI of 0.31–0.37, when using a high-density SNP panel and independent cross-validation datasets from Australia and New Zealand, respectively.

Gonzalez-Recio et al. (2014) described the implementation of heifer feed efficiency in the Australian selection index, using genomic selection and its impact in the industry. In 2015, the same research group (Pryce et al. 2015) defined and described the implementation of genetic evaluation for "feed saved" as a new indicator of feed efficiency in dairy cows. Feed saved combines RFI with mature bodyweight estimated using estimated breeding values for predicting maintenance costs, so that feed requirements are quantified in a single breeding value. Since April 2015, feed saved has been included as part of the Australian national selection index.

Negussie et al. (2019) used simulated data to estimate accuracies of genomic prediction for different DMI recording scenarios (once weekly, once monthly, every 2, 3 and 4 mo) using different sizes of training populations in dairy cattle to develop future innovative phenotyping strategies of recording DMI. The authors reported that the accuracy of genomic predictions associated with the five recording scenarios indicated that the use of a large training population and the adoption of a less-frequent DMI sampling scenario is an advantageous strategy when considering accuracy, logistic, and cost implications. The GEBV accuracies for DMI and RFI that have been reported in the literature are summarized in Table 5. These results indicate that there is still room for improving the prediction of GEBVs.

Some alternatives have been investigated to increase the training population for feed efficiency, including the use of data from nutrition studies (Veerkamp et al. 2014; Tempelman et al. 2015) and combining data from different countries (Banos and Coffey 2012; de Haas et al. 2012; Pryce et al. 2012; Berry et al. 2014; Tempelman et al. 2015) or breeds (Khansefid et al. 2014). It is worth noting that in the last few years, a collaboration group named the global dry matter initiative (gDMI) has been created to combine feed intake records, which included 10 research herds from nine countries (Berry et al. 2014; de Haas et al. 2015).

Table 5. Accuracies of genomic predictions for indicator traits of feed efficiency.

Trait	Reference	Average accuracy
Dry matter intake	de Haas et al. 2012	0.35
	de Haas et al. 2015	0.37
	Mujibi et al. 2011	0.20
	Bolormaa et al. 2013	0.32
	Negussie et al. 2019	0.42 to 0.57 (simulation based)
Residual feed intake	Pryce et al. 2012	0.40
	Mujibi et al. 2011	0.43
	Bolormaa et al. 2013	0.43
	VanRaden et al. 2017*b*	0.44
	Negussie et al. 2019	0.22 to 0.50 (simulation based)

Data collection and international collaborations for data sharing

To genetically select animals for improved feed efficiency, pedigree information and individual phenotypic records associated with feed intake and production traits are required. The simplest way to record DMI is based on the amount of feed offered and refused by each cow per day, with the associated dry matter percentage (Seymour et al. 2019). Other important variables to be recorded for assessment of feed efficiency are milk production and composition, lactation stage, water intake, diet composition, bodyweight and BCS over the course of lactation, health/disease events, and reproductive performance traits. It is important to notice that even if not all these variables are used in the genetic/genomic evaluations, they might be useful in the future for research and also selection purposes. Furthermore, the costs to record these additional traits are low compared with the cost of individual feed intake recording (Veerkamp et al. 2015).

There are various automated systems available for feed intake recording, including Calan Broadbent (American Calan Inc., Northwood, NH, USA), Gallagher Animal Management Systems (Hamilton, New Zealand), GrowSafe® Feed Intake System (GrowSafe Systems, Ltd., Airdrie, AB, Canada), and the RIC system (i.e., Insentec; Hokofarm Group B.V., Marknesse, the Netherlands). These systems are mostly based on radio-frequency identification to track and record individual feed intake as well as feeding behavior (e.g., number of visits per day, intake duration, and time of intake). As discussed by Connor (2015), the use of these systems in dairy cattle has been limited to research herds or growing heifers. The use of automated feed monitoring systems in larger groups of lactating cows is hindered by the limited feeding capacity of the automated feed bunks, meaning that significantly fewer cows can be fed from a single bunk relative to growing cattle to accommodate substantially greater intakes of lactating cows (Connor 2015).

It is well established that the success and long-term sustainability of any livestock breeding program is largely dependent on the amount and quality of pedigree, phenotypic and genotypic data available for genetic and genomic evaluations. As feed efficiency is difficult and expensive to measure, a global effort to enlarge training population for genomic evaluations is crucial, and it has the potential to greatly benefit all groups involved in the project. In addition to gDMI, the efficient dairy genome project (EDGP, http://genomedairy.ualberta.ca/) is a large international research project led by Canadian institutions aiming to develop strategic research, tools, and the whole infrastructure to implement genetic and genomic evaluations for improved feed efficiency and reduced methane emissions in dairy cattle. In this regard, the EDGP database was developed in 2017 to allow data sharing among international collaborators from six countries (Australia, Canada, Denmark, Switzerland, United Kingdom, and United States) to facilitate development of an international genetic evaluation for feed efficiency. This goal is likely possible due to the high level of relatedness of the Holstein population, the most common dairy breed with records for feed efficiency. Moreover, all collaborators are members of the International Committee for Animal Recording (www.icar.org), which provides standardized information on production records.

Incorporating feed efficiency into breeding programs

National organizations and private companies began implementing the selection of feed efficiency into their breeding programs in 2014 (Pryce et al. 2014). Each organization incorporated indirect measures of feed efficiency such as production levels, body weight (or predicted body weight), and conformation traits into their selection indexes (VanRaden et al. 2007; Veerkamp et al. 2013; Pryce et al. 2014, 2015). In Australia, animals that are one standard deviation above the mean for the feed saved trait consume 65 kg less feed per year, while maintaining the same levels of production (Pryce et al. 2018). The USA developed a composite index into their national evaluation, which uses milk, fat, protein, and predicted body weight, to predict feed efficiency (Holstein Association USA 2017). New Zealand indirectly selects for feed efficiency by selecting on milk production, live weight, and BCS simultaneously (Pryce et al. 2014; DairyNZ 2016). In the Netherlands, GEBVs for saved feed costs have been available since December 2017 (CRV 2018). This value is expressed in euros per cow per lactation, where the feed for both production and maintenance are considered (de Jong et al. 2019). Furthermore, there are many other countries worldwide, including Canada, which are working towards including feed efficiency into their national breeding programs.

The inclusion of feed efficiency into breeding objectives is not exclusive to national organizations. Private breeding companies (e.g., CRV, Select Sires, GENEX, STGenetics, and VikingGenetics) are also promoting GEBVs for more efficient cows through their own selection strategies. For instance, CRV generates the NVI, which is the total merit index used in the Netherlands and Flanders, which includes a saved-feed-cost trait. In other countries, such as the USA, CRV offers the Better Life Efficiency program, which identifies bulls that have a high lifetime production to lifetime feed intake ratio (CRV 2019). Recently, VikingGenetics also released a saved feed index. They are working towards implementing an index based on two indicator traits: maintenance efficiency, which captures the energy requirements for maintenance; and metabolic efficiency, which reflects how efficiently the eaten feed is utilized (VikingGenetics 2019). Bulls with a score of 5% for better life efficiency have been reported to have daughters that can produce an additional 680 kg of milk with the same amount of feed, which would translate into an additional $295 per cow per lifetime. Select Sires also developed a selection index, FeedPRO® that focuses on producing moderately sized cows while maintaining production levels (Select Sires Inc. 2019). Daughters of FeedPRO® bulls have been reported to produce on average 13–18 cents more per day (Select Sires Inc. 2019). The FeedPRO® index is also correlated at 0.90 to TPI, a total selection index in the USA. Production efficiency (PREF$), an index from GENEX, has also been reported to result in higher yielding cows with lower feed costs. This subindex makes up 47% of the ICC$™ index, with emphasis on marginal feed costs, fat, protein, and milk yield (Genex Cooperative 2018). EcoFeed™, a feed efficiency index developed by STgenetics, is designed to encompass environmental, metabolic, and genomic factors affecting dairy cattle profitability from birth to culling (STgenetics 2018). Daughters of bulls that are five points above the average are reported to consume 0.45 kg less feed per day, while maintaining similar production levels (STgenetics 2018). Although many companies and national breeding organizations are moving towards the inclusion of feed efficiency into their breeding programs, there is no consensus on the optimal way to include these traits. It is worth mentioning that the descriptions of the selection indexes mentioned above were provided by the companies, and some details might have been omitted by them. Further research is required to compare different approaches and define an optimal strategy.

Conclusions

Feed efficiency, assessed based on different indicators, is a heritable trait and can be improved through genetic and genomic selection. The breeding goal needs to be refined and indicator traits that can be easily measured at low cost should be identified. Feed efficiency is a polygenic trait influenced by many genetic variants, regulator genes, and structural variations. With the important role of the rumen microbiota on feed efficiency and evidence of host genetic influence on the rumen microbiome profile, further evaluation of rumen microbial features may lead to its prospective use as an indicator trait, or use in future genomic selection models. The accuracy of genomic predictions for feed efficiency are still low but are expected to increase as training populations are enlarged, and additional functional information could be included from transcriptomics and other "-omics" technologies. In this regard, various groups around the world are collaboratively working to refine the methods used in the evaluations as well as enlarging the datasets used for genomic evaluations.

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