ABSTRACT: It has long been appreciated that animals fed the same diet may perform differently. This is due to the ability of nutrients to interact with and affect molecular pathways that result in differences in BW gain, production performance, or disease resistance. To understand these effects, studies are being undertaken to discover how the differential expression and function of genes occur with different diets. These studies are using new technologies, genomic resources, and analysis techniques that have recently become available for domestic animals. Nutrigenomics and nutrigenetics are new research approaches that strive to optimize health by looking beyond the diet to understand the effects of food at the genetic and epigenetic levels. Nutrigenomics is focused on the effects of diet on health through an understanding of how bioactive chemicals in foods and supplements alter gene expression or the structure of the genome of an animal. Nutrigenetics focuses on how the genetic composition (i.e., genetic variation) of an animal influences their response to a given diet. Results from these studies will aid in formulating nutritionally appropriate diets that may be optimized for animals based on their genomic underpinnings. Nutrigenomics and nutrigenetics unite many fields: nutrition, bioinformatics, molecular biology, genomics, functional genomics, epidemiology, and epigenomics. The use of multi-disciplinary tools promises new opportunities to investigate the complex interactions of the genome and the diet of an animal. Through these new approaches, the partnerships of the genome and nutrition will be revealed resulting in improved efficiency of diets, enhanced sustainability of animals as a protein source, and improved methods for preventing illnesses.

KEY WORDS: nutrigenetics, nutrigenomics


INTRODUCTION

The genome is the haploid complement of DNA inherited from a parent of the offspring. Genomics encompasses the genomic variation within an individual animal and how these differences result in unique functions and interactions of the genes within the genome. The human genome project has propelled the agricultural livestock community forward with the development of new tools to characterize genomic diversity.

The reduced cost of sequencing, the development of computational tools to align nucleotide sequences, and the annotation of the genomes have accelerated the rate at which SNP assays that cover the whole genome of livestock species have been developed. These assays have been instrumental in providing the foundation upon which the genetic diversity of livestock can be explored in the context of disease, production traits, and nutrition. Nutrition is an environmental factor of major importance in animal agriculture. Nutrients interact with the genome to set the nutrient requirements and the performance potential for each individual animal. This interaction is dynamic: it can be reset through epigenetic changes at key points in the life of an individual animal.

The focus of how the relationship between nutrients and the genome is studied differs between the fields of nutrigenetics and nutrigenomics. Nutrigenetics addresses how the genome, proteome, and metabolome of the host influence the response
of an individual animal to a given diet. Nutrigenomics applies genomic technology to study how nutrients affect the expression of genes. These 2 fields are based on 3 premises: 1) that there is genomic diversity among individuals of a species (i.e., within and across breeds) that affects nutrient bioavailability and metabolism; 2) nutrient availability varies greatly depending on feedstuffs available, cost, and palatability; and 3) deficiency or excess of nutrients affects gene expression and genome stability (or the ability to resist damage). The objective of these fields is to integrate information coded in the genome in response to nutrients to optimize health and performance in all animals. This article is organized to provide examples of how nutrigenomics and nutrigenetics are expanding our knowledge of the complex relationships between nutrition and the genome.

**NUTRIGENETICS**

Nutrigenetics begins with the variation present within or modification to the genome of an animal. The study of nutrigenetics is concerned with the variation within the nucleotide sequence or the modification of the DNA through epigenetic processes as it applies to the diet of an animal. This approach is in contrast to historical epidemiological approaches in which populations, rather than individuals, were studied to identify nutritional requirements or responses to feedstuffs (Malloy et al., 1997; Zeisel, 2008). In cattle, breed differences in dietary mineral requirements indicate that genetic variation influences individual dietary requirements. Simmental heifers had less plasma copper concentrations than Angus heifers housed together during gestation and early lactation, indicating that Angus heifers have a reduced copper requirement compared with Simmental heifers (Mullis et al., 2003). The individual nucleotide or epigenetic differences in the DNA of cattle responsible for these and other differences in dietary nutritional requirements for cattle are beginning to be explored. However, in the literature about humans, there are more examples in which the nucleotide differences that alter the nutritional requirements of individuals have been identified. One example is a variation in the nucleotide sequence of the folate-related enzyme 5,10-methylenetetrahydrofolate reductase gene (MTHFR).

Hyperhomocysteinaemia, homocystinuria, and hypermethioninaemia result in humans with a severe deficiency of MTHFR. Infants or adolescents with this disorder have about 50% of the normal enzyme activity and present with developmental delay, motor and gait dysfunction, seizures, psychiatric disturbances, and a risk for vascular disease such as coronary artery stenosis (Kang et al., 1995; Van der Put et al., 1995). This MTHFR variant results in a thermolabile form of reductase that has been reported in approximately 17% of North American patients with coronary artery disease (Kang et al., 1991). In the Netherlands, 7% of patients with vascular disease and 28% of patients with hyperhomocysteinemia carry the mutation in MTHFR (Engbersen et al., 1995). The mutation responsible for the thermolabile enzyme form differs from a second nucleotide variant in MTHFR that results in less than 2% of the normal enzyme activity, is not thermolabile, and is characterized by neurological abnormalities, atherosclerotic changes, and thromboembolism (Rosenblatt, 1989).

The biochemical consequences of hyperhomocysteinuria are reduced methionine concentrations in plasma, decreased plasma folate concentrations, and very low 5,10-methylenetetrahydrofolate reductase enzyme activity in fibroblasts and lymphocytes. Frosst et al. (1995) identified a C to T substitution at nucleotide 677 in MTHFR (MTHFR, C677T), which converts an alanine to a valine residue. The allele frequency of this mutation was 0.38 in 114 randomly selected French Canadians (Frosst et al., 1995). Those individuals homozygous for the alanine to valine substitution had approximately 30% of the mean activity of those that were homozygous for the normal valine form of the enzyme. Heterozygotes had a mean enzyme activity level of 65% of normal (Frosst et al., 1995). This mutation corresponds with the region in MTHFR involved in folate binding that stabilizes the enzyme. The administration of folic acid corrects hyperhomocysteinemia in individuals with thermolabile MTHFR and premature vascular disease (Kang et al., 1988; Franken et al., 1994).

The pathways that connect choline, methionine, and methyltetrahydrofolate and vitamins B6 and B12 intersect at the formation of methionine from homocysteine. The deprivation of choline results in an increased requirement of methyltetrahydrofolate to methylate homocysteine in the liver therefore increasing the dietary requirement for choline (Niculescu and Zeisel, 2002). Total hepatic folate content declined more than 30% in rats fed a choline-deficient diet. Similarly, when dietary folate is deficient in rats, hepatic choline concentrations also decline (Kim et al., 1994). Therefore, genetic differences in either of these key pathways would likely alter the dietary requirements for folate, choline, and methionine. It is unknown how many cattle are affected by nucleotide variants in these 3 pathways, but a quick survey identified over 50 noncoding variants within MTHFR associated with dietary folate requirements; and a missense mutation (rs135340897) in the gene phosphatidylethanolamine N-methyltransferase, associated with dietary choline requirements, indicates that individual cattle may have different dietary requirements for folate, choline, and methionine than currently appreciated.
The genomic tools recently made available to the cattle community will facilitate the association of genetic variation with a specific dietary environment. The cattle community has enjoyed access to several genome-wide SNP-based assays. Illumina (San Diego, CA) has 3 SNP assays: the Illumina BovineHD, which contains more than 777,000 SNP markers; the SNP50 BeadChip, which contains more than 50,000 SNP markers; and the Bovine 3K GoldenGate BeadChip, which contains more than 3,000 SNP markers throughout the genome. Affymetrix’s (Santa Clara, CA) new Axiom Genome-Wide BOS 1 Array offers 648,000 SNP markers, and Affymetrix also offered an earlier bovine SNP array with over 25,000 markers. These tools are used to test for segregation of a phenotype with genomic regions through linkage disequilibrium in unrelated animals (i.e., animals that do not share common ancestors within 4 generations) or with linkage within families.

Linkage disequilibrium is the nonrandom distribution of alleles on a chromosome in the individuals within a population. Genome-wide association studies are commonly done in populations of unrelated individuals in which the allele frequencies of each marker are compared with a phenotype. The availability of genome-wide SNP assays makes association analysis the most powerful approach for identifying loci associated with disease or complex traits (Risch and Merikangas, 1996). This method of analysis relies upon linkage disequilibrium or the nonrandom association of alleles at 2 or more loci to detect associations between neutral markers and causal loci (King and Stans, 2002). Association studies do not require structured breeds or pedigreed populations of cattle in which the genotyped animals are separated by only a few pedigreed generations as in linkage studies, but instead use a sampling of the independent meioses present within a cattle population. Association studies require the use of high-throughput, high-density SNP genotyping assays, which dramatically decreases cost and increases study power.

High-density SNP genotyping assays are also useful to integrate genomic variation, gene expression data, and biological pathway information together to identify molecules that are critical in a physiological process. Pathways and enriched gene sets are composed of genes that interact with one another, act together, and are involved in similar functions or are located close to one another (Holden et al., 2008). The correlation analysis of associated genes can have much greater statistical significance than analysis of the single genes, with the obvious limitation that the association must be functionally meaningful. Gene set enrichment analysis SNP is particularly useful for identifying candidate genes that produce modest effects with different diets and biological processes associated with complex phenotypes in cattle (Neibergs et al., 2010). The use of pathways to determine how the diet has affected the genome, rather than how the genome has affected the dietary requirements, is the approach taken by nutrigenomics.

**NUTRIGENOMICS**

Nutrigenomics focuses on the influence of the diet on the genome of an animal and how that results in a particular phenotype (Ordovas and Moser, 2004). This approach uses genomic tools to investigate biological pathways to understand how nutritional molecules affect gene expression, metabolism, and health after ingestion of feedstuffs. Access to new genomic, database, and computational resources has provided the foundations for nutrigenomics. Resources such as the online database dbSNP (http://www.ncbi.nlm.nih.gov/projects/SNP/), gene ontology (http://www.geneontology.org/), Kyoto Encyclopedia of Genes and Genomes (http://www.genome.jp/kegg/), carbohydrate active enzymes (http://www.cazy.org/), peptidase database (http://merops.sanger.ac.uk/), gene cards (http://www.genecards.org/), and the bovine gene atlas (http://bovineatlas.msstate.edu/), as well as sites hosting the bovine gene sequence, are proving to be invaluable when coupled with computational biology expertise.

**Nutrient Restriction**

Nutrients affect gene expression in cattle long after ample feed is provided. Nutrient restriction during early gestation in beef heifers affects their calves through expression of genes controlling fatty acid transport in adipose tissue and muscle (Long et al., 2010). Angus × Hereford heifers at 32 d of gestation were fed a diet consisting of 55% of NRC (1996) requirements or fed 100% of NRC (1996) requirements for 83 d followed by a diet that exceeded 100% of NRC (1996) requirements (Long et al., 2010). Nutrient restriction did not influence birth weight or ADG of calves; however, complexus muscle from steers whose dams were restricted had an increase in muscle fiber but a reduction in mRNA of genes associated with adipogenesis (i.e., fatty acid binding protein 4, fatty acid translocase, and glucose transporter 4) in pelvic fat compared with steers whose dams were not diet restricted during gestation (Long et al., 2010). When dams on pasture were protein restricted, they produced steers that were lighter at slaughter, were less tender, and had less subcutaneous fat at the 12th rib than steers of dams with greater dietary protein intake during mid-late gestation (Underwood et al., 2010).

The timing of the diet restriction of dams is also important in the subsequent effect in the calves. Diet restriction of the dams before the last trimester of gestation does not result in lighter birth weights, gestational length, or BW gain in calves (Doornobos et al., 1984; Goehrings et al., 1989; Houghton et al., 1990). In contrast, cows and heifers that are diet restricted during the
last trimester of gestation delivered calves with lighter calf birth weights (Houghton et al., 1990; Spitzer et al., 1995). The effect of the diet on the genome can directly affect the nucleotide sequence by causing damage to nuclear and mitochondrial DNA by influencing DNA repair and DNA synthesis or through epigenetic changes (Fenech, 2010; Kussmann and Van Bladeren, 2011).

Compensatory BW gains are the result of dietary restriction followed by an increase in nutrient availability and a subsequent increase in BW gain. The use of compensatory BW gain to improve meat quality has been investigated in several species. The optimal length of the compensatory period for swine was between 42 and 70 d before slaughter to reach optimal increased protein degradation levels associated with meat tenderness (Therkildsen et al., 2002). To measure protein degradation, μ-calpain, m-calpain, and calpstatin were assessed. Total RNA and elongation factor-2 were used as indicators of protein synthesis. Additional studies to evaluate the effect of compensatory growth response on muscle protein turnover and tenderness have shown that barrows and female pigs demonstrate compensatory growth, but tenderness is only improved in the meat of the female pigs (Andersen et al., 2005). Compensatory growth has also been used to increase meat tenderness in cattle (Allingham et al., 1998).

Byrne et al. (2005) similarly looked at nutritional plane differences to identify differential gene expression. As an extension of work initially reported by Reverter et al. (2003), 3 planes of nutrition were used to achieve 3 different growth rates in Bos indicus cattle. A cDNA gene expression array was used to evaluate gene expression in LM and subcutaneous fat. Twenty-eight genes were found to be upregulated when animals fed low- or medium-growth diets were compared with animals fed a high-growth diet, and 29 genes were found to be downregulated (Byrne et al., 2005). The genes that were upregulated were associated with protein turnover, cytoskeleton structure, and metabolic homeostasis, whereas the downregulated genes were associated with extracellular matrix structure and cytoskeleton structure.

Rectus abdominis and semitendinosus muscles were assessed for activity differences of enzymes involved in glycolytic and oxidative muscle metabolism in Charolais steers fed maize-silage compared with steers grazed on pasture to identify genes that could serve as indicators of grass-fed cattle (Cassar-Malek et al., 2009). Gene expression profiling in both muscles was done using macroarrays consisting of a cDNA bovine collection from bovine muscle, embryo, and mammary glands. Of the 212 transcripts that were differentially expressed, 149 were assigned to known genes. These genes were functionally associated with protein metabolism and modification, signal transduction, cell cycle, developmental processes, and muscle contraction. Selenoprotein W was found to be downregulated in steers grazed on pasture, and it was suggested that it may be a potential marker for grass-fed cattle.

**DNA Damage**

Damage to DNA is recognized as a cause of disease, accelerated aging, and infertility (Ames, 2006; Fenech, 2008). Damage of DNA may result from a suboptimal intake of vitamins and minerals, just as DNA damage results from other environmental exposures such as radiation and other carcinogens (Fenech, 2010). Vitamins and minerals serve as cofactors for enzymes or serve as part of the structure for proteins involved in DNA synthesis or repair and maintenance of genome integrity. Fenech (2010) reviewed the roles of vitamins B6, B12, C, and E, antioxidant polyphenols, folate, riboflavin, niacin, zinc, iron, magnesium, manganese, calcium, and selenium for the role and effect of their deficiency or excess on genomic stability in humans. These micronutrients are involved in a range of genomic stability functions, from cleavage and rejoining of DNA, maintenance of telomere length, antioxidant metabolism, and cofactors for DNA polymerases involved in nucleotide excision repair, to excision repair and base excision repair (Fenech, 2010). A deficiency of micronutrients can result when ruminants are exposed to adverse climatic conditions that increase the need for micronutrients (Aurousseau et al., 2006). The lack or excess of these micronutrients can result in DNA damage, although the apparent beneficial effects of vitamin E, retinol, folic acid, preformed nicotinic acid, and calcium were still increasing at a greater intake in humans (Fenech, 2001; Wald et al., 2001; Ashfield-Watt et al., 2002; van Oort et al., 2003). Studies are needed that investigate the role of these micronutrients on dietary requirements, health and fertility in cattle, and the interaction of these micronutrients to produce beneficial or harmful effects.

**Epigenetics**

The epigenome is heritable and modifiable by diet through methylation, histone modifications, noncoding small RNA, and chromatin-associated proteins. Dietary restriction of methyl donor molecules, such as folic acid, methionine, vitamin B12, and choline, can have direct effects on the epigenome through hypomethylation of the DNA to turn genes on or off. These effects are of particular importance during critical times of reprogramming of the epigenome. During early embryogenesis, the epigenetic slate is mostly wiped clean and then re-established during key times in the life of animal (Gluckman et al., 2009). Embryogenesis, gestation, puberty, and old
age are pivotal times for establishing epigenetic changes (Jirtle and Skinner, 2007).

Development appears to be a particularly sensitive time for epigenetic changes. In humans, the nutritional status of the mother during the periconceptual period affects the offspring later in life without changes in birth weight (Painter et al., 2005; Heijmans et al., 2008). Intrauterine growth retardation in livestock due to epigenetic effects has been investigated and reviewed (Wu et al., 2006). The implications for epigenetic changes due to periconceptual nutrition of dams should be considered when raising both replacements and livestock that are destined for the feedlot. Cloned cattle exhibit epigenetic reprogramming that results in generalized hypomethylation, which has been suggested to be the cause for greater rates of embryo morbidity and mortality in cloned cattle (Smith et al., 2010). Dietary restriction can also have effects on carcass quality. In ewes on restricted diets, their lambs had fewer numbers of muscle fibers than lambs of ewes that were unrestricted (Quigley et al., 2005). Du et al. (2010) reviewed the literature on fetal programming in beef cattle and identified similar opportunities.

Lack of DNA methylation at cytosine-purine-guanine (CpG) islands near coding sequences and in repetitive DNA enhances transcription through chromatin remodeling. The cytosine-guanine-rich areas that constitute CpG islands often serve as promoters for nearby genes. The methylation of the CpG islands commonly results in repressed transcription (Simmons, 2011).

A second type of epigenetic regulation involves the presence or absence of methylation, acetylation, and phosphorylation of lysine residues on the N-termini of histones H3 and H4. This type of epigenetic regulation also influences gene expression and repair of DNA damage (Reik, 2007; Fenech et al., 2011; Zheng et al., 2011). Histone acetylation and gene regulation has been studied recently by using histone deacetylase inhibitors. Dietary factors, such as diallyl disulfide, sulforaphen, and butyrate, have the ability to inhibit genome-wide type I and type II histone deacetylase inhibitor enzymes, resulting in high levels of H3 and H4 acetylation (Dashwood and Ho, 2007). When random histone deacetylase inhibition is induced, approximately 8% of genes evaluated were differentially expressed (Li and Li, 2006). The investigation of butyrate on bovine kidney cells identified that IGF-2, transforming growth factor β-1, tumor protein 53, transcription factor E2F4, and cell division cycle 2 (CDC2) were key genes involved in the regulation of gene networks affected by hyperacetylation of this short-chain VFA (Li et al., 2007). Further studies are needed to understand how butyrate, an important nutrient component in cattle, affects gene expression. Other changes in gene expression may be due to transposon activation and insertion of transposons into promoters of housekeeping genes (Fenech, 2005; Sharma et al., 2010).

Two techniques that have been instrumental in epigenetic studies are RNA-sequencing (RNA-seq) and chromatin immunoprecipitation followed by sequencing (ChIP-seq). The use of these techniques provides an integrated approach to epigenomics, transcriptomics, proteomics, and genomics (Hawkins et al., 2010). Sequencing cDNA after reverse transcribing RNA transcripts can be accomplished with RNA-seq. This process generates millions of short sequencing reads that are then aligned to a sequenced genome to identify the genes from which they came. Chromatin immunoprecipitation and next generation sequencing to identify the DNA binding sites of proteins is possible using procedures like ChIP-seq. This technique also generates millions of short sequence reads (i.e., 30 to 50 bp) that must then be aligned to a sequenced genome. The ChIP-seq procedure is useful in developing a comprehensive list of loci that share a binding site or epigenetic modification.

The RNA-seq employs next-generation sequencing to provide greater coverage of the gene transcripts being expressed in a tissue as it overcomes the limitation of identifying transcripts that are only complementary to hybridization probes designed for expression arrays [for a review of RNA-seq, see Gilad et al. (2009)]. Because it is impractical to design probes that cover all of the exons of all genes, it is difficult to investigate the role of alternatively spliced transcripts with microarrays. With RNA-seq, alternatively spliced transcripts are captured and may be cataloged. The use of RNA-seq also has the advantage of identifying transcripts that align to DNA sequences that are not yet annotated and that would most likely not be included on an expression array. The use of RNA-seq may also facilitate comparisons across studies more easily than the use of microarrays because it does not rely on hybridization intensities that can vary across studies (Gilad et al., 2009).

There are also disadvantages of RNA-seq. One disadvantage is the cost. However, with advances in sequencing technology, these costs will continue to decrease and make this technology more in line with the costs of microarrays. A second disadvantage of RNA-seq is the tremendous amount of data that must be analyzed and the availability of a genome in which it can be aligned. For species yet to be sequenced, this lack of a suitable genome sequence may prove a major hurdle. Another disadvantage of RNA-seq compared with microarray technology is that genes with longer transcripts are more likely to be over-represented compared with very short transcripts (Oshlack and Wakefield, 2009).

Chromatin immunoprecipitation (ChIP) is a technique used to identify DNA binding of proteins in vivo (Park, 2009). Chromatin immunoprecipitation followed by sequencing is a technique for genome-wide profil-
The gastrointestinal tract is home to numerous commensal bacteria that constitute the gastrointestinal microbiome. The interaction of the host, the gastrointestinal microbiome, and the diet is responsible for not only the efficient utilization of feed but also their ability to effectively respond to pathogens. The gastrointestinal microbiome has been studied in many mammalian species, and the ability of the microbiota to adapt to different diets is similar across mammalian lineages (Muegge et al., 2011). The microbiome species were not specific to mammalian phylogeny alone but aligned based on the functional repertoire of the species and their diet (Ley et al., 2008; Muegge et al., 2011). This indicates that the microbiomes may consist of different species but the functions required within the gastrointestinal tract are collectively similar. Herbivores were characterized by fecal microbiomes that provided enzymes necessary for biosynthetic reactions involved in AA metabolism (Muegge et al., 2011). In contrast, the fecal microbiomes of carnivores were more involved in AA degradation. The microbes present in humans have been estimated to consist of 100 trillion cells and encode 100-fold more unique genes than are found in the human genome (Ley et al., 2006). Of the microbes that live within mammals, the majority of them reside within the gastrointestinal tract (Qin et al., 2010).

The establishment of a functional microbiome is important to the immune function of the host. Colonization of mice with a cocktail of 46 strains of gram-positive Clostridium early in life resulted in resistance to dextran sodium sulfate-mediated colitis and systemic IgE responses in adult mice (Atarashi et al., 2011). If these mice were treated with antibiotics that targeted gram-negative or gram-positive bacteria, only those mice not treated with a gram-positive antibiotic showed the positive effects of resistance to colitis. The 46 strains of Clostridium have also been shown to affect the accumulation of cluster of differentiation 8 intraepithelial lymphocytes in the colon (Umesaki et al., 1999). Taken together, these data indicate that exposure to Clostridium helps modulate the immune system through the intestinal flora by promoting anti-inflammatory immune responses by expanding and activating T cells (Barnes and Powrie, 2011).

Clarke et al. (2010) reported a role for microbiota in mice in the development of the immune system of the gastrointestinal tract. By promoting the development of the innate immune system, the microbes facilitated killing Streptococcus pneumoniae and Staphylococcus aureus by bone-marrow-derived neutrophils. This process occurred through the pattern recognition receptor, nucleotide-binding oligomerization domain-containing protein-1 (Nod1). Administration of Nod1 ligands was sufficient to prime neutrophil function after removal of microbes. Neutrophils are one of the primary defenses against extracellular pathogens. Cattle with an insufficient neutrophil response to extracellular pathogens are at risk for a wide range of infectious and inflammatory disease. Results of this study are in keeping with...
others in mice that have shown that the microbiota are central in fighting disease progression in arthritis, central nervous system inflammation, diabetes, intestinal inflammation, and obesity (Cerf-Bensussan and Gaboriau-Routhiau, 2010). The role of microbiota in susceptibility to inflammatory diseases is underway in cattle and should provide insight into their role in the innate immune system in ruminants.

**SUMMARY AND CONCLUSIONS**

Nutrigenetics is a field that is ripe with promise brought about by the new genomic resources available to the cattle community. The availability of genome-wide assays that interrogate hundreds of thousands of DNA variants will facilitate the understanding of how genomic variation affects the interaction of diet with the physiological response of the animal. Nutrigenomics approaches this interaction by evaluating how the effects of specific diets, nutritional restriction, or excess nutrients influence DNA damage, the epigenome, and gastrointestinal microbiota. New resources to identify the factors affecting these processes will enhance the work that is critical to unravel these interactions in cattle.

The 2 fields of nutrigenomics and nutrigenetics share the objective to elucidate the interaction between diet and the genome to optimize animal health. Although the approaches to delineate these interactions are different, much will be gained by both approaches. The merging fields of nutrigenetics and nutrigenomics is an opportunity for nutritionists, geneticists, molecular biologists, and computational biologists to collaborate to gather a more complete picture of the dietary requirements of cattle and how genomic variation affect these requirements. The merging of these disciplines will require nutritionists to learn more about genetics and geneticists to better understand the complexities of metabolism, but as these disciplines better appreciate each other’s expertise, a better trained cohort of multidisciplinary experts will result.

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