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Animal Biotechnology for Livestock Production 1

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Sustainable agriculture is a rapidly growing field aiming at producing food and energy in a sustainable way for humans and their children. Sustainable agriculture is a discipline that addresses current issues such as climate change, increasing food and fuel prices, poor-nation starvation, rich-nation obesity, water pollution, soil erosion, fertility loss, pest control, and biodiversity depletion.

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Preface

Many developed countries are actually facing a ban of animal food products, promoted mainly by urban and vegetarian activists who have never experienced living in farms and who do not acknowledge that their modern way of life is largely the result of hard work of their elders with the help of farm animals. However, since the start of society, animal production has been an essential agricultural sector worldwide providing food, labor, aesthetics and social values, and even today many farmers would not survive without animals. This book entitled 'Animal Biotechnology for Livestock Production 1' is our first volume providing advanced knowledge on biotechnological methods to improve the livestock production, with focus on animal reproduction, health, diagnosis and nutrition. Chapter 1 presents on artificial insemination in cattle, with focus on physiology aspects of the estrous cycle, estrus synchronization program, ovulation synchronization program for timed artificial insemination, strategies for improving fertility and use of sexed semen in artificial insemination. Chapter 2 reviews biotechnological applications for production of dromedary camels, with details on camel herd reproduction, reproduction control and artificial insemination. Sperm dilution, thawing, conservation, and insemination techniques are also discussed. Recent biotechnological applications for livestock production are summarized in Chap. 3, with emphasis on somatic cell nuclear transfer, artificial insemination, embryo transfer, embryonic stem cell technology and marker assisted selection.

Cattle production in France. Copyright 2021 Eric Lichtfouse

Chapter 4 reviews applications of stem cells in livestock, with emphasis on mesenchymal stem cells. Immunomodulatory, antimicrobial activity, migration and reparative functions of stem cells are detailed. Chapter 5 presents techniques for profiling proteins and metabolites associated with feed efficiency in dairy cattle. Recent findings on key metabolites and proteins of metabolic pathways are also disclosed. Chapter 6 focuses on processing, packaging, and safety of dairy products. Applications of biotechnologies in food diagnosis are also explained. Chapter 7 reviews 'on-farm point-of-care' diagnostic technologies in animals. This chapter covers various point-of-care and on-farm diagnostic technologies for monitoring animal health and disease with focus on molecular, electrochemical-biosensors diagnostics. Chapter 8 presents biotechnological applications in the poultry industry. This chapter covers the concepts and developments of biotechnologies for poultry production, breeding, feed and nutrition. This chapter also discusses applications in poultry vaccines, biologics, disease diagnosis and food processing.

We express our thanks to all authors who have contributed high quality chapters. Our special thanks are due to the Indian Council of Agricultural Research (ICAR), the Government of India and the Director of the ICAR National Dairy Research Institute (NDRI), Karnal, India for providing the institutional support. We would like to acknowledge Dr. Sudarshan Kumar, Scientist, ICAR-NDRI, Karnal, India for his help in choosing contributors and reviewers. We would like extend our thanks to the staff of Springer Nature, for their generous assistance, constant support, and patience in initializing and publication of this book. We acknowledge our thanks to

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Vinod Kumar Yata is an interdisciplinary researcher working at National Dairy Research Institute, Karnal, India. Previously, he worked as an Assistant professor at the Department of Biotechnology, Dr. B R Ambedkar National Institute of Technology Jalandhar, Punjab, India. He received his Ph.D. in Biotechnology from Indian Institute of Technology Guwahati. He specializes in interdisciplinary research which includes Nanotechnology, Microfluidics, Animal Biotechnology, Cancer biology and Bioinformatics. He has developed a microfluidic device for the separation of live and motile spermatozoa form cattle semen samples. He opened up a new avenue to prodrug enzyme therapy by introducing the nanocarriers for the delivery of non-mammalian prodrug activating enzymes. He elucidated the structural features and binding interactions of several bio molecules by in silico methods. He has published three books as an editor and one book as an author with Springer Nature publisher. He has published several research papers in peer reviewed international journals and presented papers in several international conferences.

Ashok Kumar Mohanty is a principal scientist at Animal Biotechnology Centre, ICAR-National Dairy Research Institute, Karnal, India. His group is involved in various basic and applied research related to animal production systems. His research group has made pioneering contributions in the field of Animal Biotechnology, with emphasis on Gene cloning, Expression and Functional characterization of Animal Proteins, Proteomics in Animal Production, Cell and Molecular Biology and Structural Biology of Proteins. His group has developed a Buffalo Mammary Epithelial cell line for the first time which can be used a model system to understand lactation biology in animal as well as human. His team has also developed a pregnancy diagnostic kit for the early detection of pregnancy cattle and buffalo. His group is also extensively involved in developing low cost technology for semen sexing in cattle. He has organized a number of national and international workshops and international conferences. He is a recipient of several awards which includes, DBT Overseas Associateship by Ministry of Science & Technology, Govt. of India., Jawaharlal Nehru Award (gold medal) by Indian Council of Agricultural Research (ICAR), New Delhi for outstanding postgraduate research in the field of Animal Biotechnology and Young Scientist Award sponsored by International union of Crystallography (IUCr) and Dept. of Science and Technology (DST), Govt. of India for attending IUCr congress at Geneva, Switzerland. He is the Fellow of National Academy of Dairy Sciences, India and executive member of proteomics society of India and associate fellow of National Academy of Veterinary Science, India. He has supervised more than 50 graduate, PhD students and post docs. He published more than 200 peer reviewed research and review papers. He has also authored 8 book chapters in the areas of animal and food biotechnology published by in national and international publishers.

Eric Lichtfouse is a professor of environmental sciences and scientific writing at Aix Marseille University and Xi'an Jiaotong University. He has invented carbon-13 dating, a molecular-level method allowing to study the dynamics of organic compounds in temporal pools of complex environmental media. He has discovered temporal pools of individual substances in complex media such as soils. He is Chief Editor and founder of the journal Environmental Chemistry Letters, and the book series Sustainable Agriculture Reviews and Environmental Chemistry for a Sustainable World. He is the author of the book Scientific Writing for Impact Factor Journals, which includes an innovative writing tool: the micro-article. He has awards in analytical chemistry and scientific editing.

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Chapter 5
Metabolomics and Proteomics Signatures in Feed-Efficient Beef and Dairy Cattle

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Abstract Feed accounts for 40–60% of total expenses of beef and dairy cattle production costs. Therefore, feed-efficient cattle have a great potential to reduce production costs without compromising meat or milk production levels, resulting in a greater profit margin for producers. Many approaches for measuring feed efficiency are available with residual feed intake being one of the most common. The residual feed intake is defined as the difference between actual dry matter intake and expected dry matter intake based on animal size and production level. Therefore, compared with a least-efficient animal, the most-efficient animal would have a negative resid-

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ual feed intake coefficient value, indicating that it consumed less dry matter intake while maintaining the same level of production. Recent studies have focused on investigating changes in key metabolites and proteins that would shift metabolic pathways to support better feed efficiency. Recent reports highlighted that in most-efficient cattle metabolic pathways associated with energy, vitamins, and amino acid metabolism in rumen and skeletal muscle are upregulated to provide extra energy, thus, allowing for a similar level of production despite lower dry matter intake. Other studies demonstrated that most-efficient cattle reduce protein turnover in skeletal muscle including upregulation of key protein synthesis pathways, such as mechanistic target of rapamycin signaling, and the downregulation of key proteins in protein degradation such as ubiquitin-proteasome pathway, resulting in greater protein deposition in muscle. In this chapter, we discuss applications of novel comprehensive techniques for protein and metabolite profiling in rumen, intestine, blood, liver, and skeletal muscle to elucidate adaptive biological functions that support better feed efficiency in beef and dairy cattle.

Keywords RFI · Cow · Calves · Metabolomics · Proteomics · Rumen · Blood · Liver · Muscles · Hindgut

5.1 Introduction

Feed costs in the beef and dairy cattle industry are the most expensive inputs, and represent on average 40–60% of total expenses (Montaño-Bermudez et al. 1990). Therefore, enhancing feed efficiency would dramatically decrease overall costs, raise producer profitability, and increase animal protein availability for consumers (Clemmons et al. 2020). Hence, discovering robust biomarkers for selecting the most-efficient beef and dairy cattle is crucial.

Residual feed intake (RFI) is a commonly-used measurement of feed efficiency in beef and dairy cattle (Li et al. 2020; Zhang et al. 2020). The RFI is defined as the divergence of predicted dry matter intake (DMI) for maintenance and meat or milk production from the actual DMI after adjusting DMI for the level of production through a linear regression model (Xi et al. 2016). The predicted DMI is calculated as a function of changes in body weight (BW) and production level (Potts et al. 2017). The regression model defines which animal is below (negative) or above (positive) the predicted DMI (Durunna et al. 2011). The fact that RFI is a trait independent of body size and production level renders it a reliable measurement of feed efficiency (Gomes et al. 2012). Most-efficient (M-eff) cattle, i.e. with the favorable negative RFI coefficient, utilize less DMI than predicted to cover both maintenance and production requirements (Potts et al. 2017). Therefore, M-eff cattle are biologically- and economically-efficient compared with their least-efficient (L-eff)

counterparts having an undesirable positive RFI coefficient (Gomes et al. 2012; Lawrence et al. 2013). Despite the proven value of the RFI, the underlying biology associated with this trait is still not well known, hence, supporting the use of modern technologies in an effort to uncover putative biomarkers.

Metabolomics profiling provides a novel approach for rapidly-identifying M-eff animals. These techniques focus on detecting, identifying, and quantifying available free metabolites in a given biological sample (Fontanesi 2016). The origin of these metabolites could be either endogenous (i.e. derived from the animal) or xenobiotic (i.e. metabolites from plants or microbes) (Fontanesi 2016). Metabolites are intermediates or products of metabolic pathways (Clemmons et al. 2020) involved in energy, protein, and vitamin metabolism, all of which are of particular interest for feed efficiency divergence in cattle (Nafikov and Beitz 2007; Ferrell and Jenkins 1984). Liquid chromatography-mass spectrometry (LC-MS) techniques have been used to detect differences in ruminal, intestinal and circulating metabolite abundance between beef and dairy cattle divergent in RFI (Clemmons et al. 2017; Elolimy et al. 2020), with several metabolites identified as having a key contribution to better feed efficiency (summarized in Table 5.1). These alterations in metabolome profiles between M-eff and L-eff cattle could be used as predictive biomarkers for feed efficiency (Clemmons et al. 2019b; Artegoitia et al. 2017; Novais et al. 2019).

The study of protein profiles in a biosample collected at a certain physiological state is called "proteome" (Reinhardt et al. 2012).Proteomics data provide a wealth of information that gene expression analysis could not. Therefore, proteomics analyses provide a better understanding of the biological functions in cattle. Few studies in recent years have applied proteomic approaches to unmask alterations in protein profiles in blood and skeletal muscle associated with RFI divergence that would help our understanding of the biology behind this trait (summarized in Table 5.2).

5.2 Metabolomic Signature in Feed-Efficient Cattle

In a recent study, Clemmons et al. (2020) used DionexUltiMate 3000 ultra-high performance liquid chromatography (UHPLC) system with an Exactive Plus Orbitrap MS to identify the metabolic signature in ruminal fluid between M-eff and L-eff beef steers. Authors used 50 purebred Angus steers at the age of 7 months and 264 ± 2.7 kg of BWfed individually using the GrowSafe System for 70 days to evaluate RFI divergent groups. At day 70 of the trial, the authors selected the extreme M-eff (n = 14) and the top L-eff (n = 15) steers. Rumimal fluid samples were collected on day 70 of the study using stomach tubing. Results revealed 8 DEM between M-eff and L-eff steers, with M-eff steers having greater succinate. In the rumen, bacteria such as *Selenomasruminantium* metabolize succinate in the presence of several bacterial enzymes and coenzyme A (CoA) to propionate (Wirth et al. 2018), a vital volatile fatty acid (VFA) used in the liver for gluconeogenesis (Wirth et al. 2018). Therefore, the greater ruminal succinate in M-eff group indicates a better capacity for hepatic gluconeogenesis to maintain similar meat

Table 5.1 Metabolomics studies in residual feed intake (RFI) divergent beef and dairy cattle

Breed type	Breed name	Sex	Age (months)	Average body weight (kg)	Sample type	Approach and platform	Changes in M-eff	References
Beef	Angus	Steers	7	264	Rumen fluid	Untargeted meabolomics (UHPLC-MS)	↑ succinate ↑ Uracil ↑ Thymine ↑ Hypoxanthine ↑ Pyridoxic acid ↑ Citraconate ↑ Xylose	Clemmons et al. (2020)
Beef	Nellore	Bulls	16-20	376	Blood (serum)	Untargeted meabolomics (LC-MS)	↓ Retinal ↓ Progesterone ↓ Stearic acid ↓ Vomifoliol, 2,3 ↓ Dihydroflavone ↓ Limonoate ↓ Phytanic acid	Novais et al. (2019)
Beef	Angus	Steers	7	264	Blood (serum)	Untargeted meabolomics (LC-MS)	↑ Pantothenate	Clemmons et al. (2019a, b)
Beef	Nellore	Cows	36	484	Blood	Targeted metabolites (enzymatic kits)	↑ Cholesterol	Broleze et al. (2020)
Beef	Nellore	Bulls	7	207	Blood (serum)	Targeted metabolites (enzymatic kits)	↓ Cortisol	Bonilha et al. (2017)
Dairy	Holstein	Heifers	At birth	43	Feces	Untargeted meabolomics (LC-MS)	↑ Cholesterol ester ↑ Biotin ↑ L-Tryptophan	Elolimy et al. (2020)
Dairy	Holstein	Cows	584	Lactating	Blood (serum)	Targeted metabolites (enzymatic kits)	↑ NPY ↓ Leptin ↓ NEFA	Xi et al. (2016)
Dairy	Murrah buffalo	Calves	4-6	70	Blood (plasma)	Targeted metabolites (enzymatic kits)	↑ IGF-1 ↑ Triiodothyronine T3 ↓ Thyroxin	Sharma et al. (2016)

Table 5.2 Proteomics studies in residual feed intake (RFI) divergent beef and dairy cattle

Breed type	Breed name	Sex	Age (months)	Average body weight (kg)	Sample type	Approach and platform	Changes in M-eff	References
Beef	Red Angus	Steers and heifers	Finishing stage	836	Ruminal epithelium	Targeted proteins (western blot)	↑ p-EEF2K ↑ p-EEF2K:EEF2K ↑ p-EIF2A:EIF2A ↓ UBA1 ↓ NEDD4 ↓ STUB1 ↓ MDM2	Elolimy et al. (2019)
Beef	Nellore	Bulls	7	239	Skeletal muscles	2D-PAGE	↑ HSPB1 ↓ 14-3-3 epsilon	Carvalho et al. (2019)
Beef	Nellore	Bulls	24-26	557	Liver	2D-PAGE	↓ HBB ↓ Aldehyde dehydrogenase ↓ Aspartate aminotransferase ↓ Glycine amidinotransferase	Baldassini et al. (2018)

production levels relative to L-eff animals. In support of this notion, Myer et al. (2015) reported that M-eff cattle had more succinate- and propionate-producing bacteria in the rumen such as *Succiniclasticum spp*. Similarly, M-eff steers had a greater concentrations of pantothenate in the serum, a precursor of CoA (Clemmons et al. 2017). These results indicate greater hepatic energy production in in M-eff steers, which likely contribute to maintain growth in M-eff steers despite lower DMI (Fan et al. 2015).

Clemmons et al. (2020) also reported that M-eff steers had more abundant nucleic acids and nucleic acid derivatives in the rumen including uracil, thymine, and hypoxanthine, indicating an increased production of microbial protein in M-eff steers (Leng and Nolan 1984). Additionally, Clemmons et al. (2020) highlighted that M-eff steers had greater pyridoxic acid, a byproduct of vitamin B6 catabolism (Linkswiler and Reynolds 1950), suggesting better protein and muscle accretion in the M-eff group (Clemmons et al. 2020). Other key metabolites associated with carbohydrate metabolism such as citraconate was more abundant in ruminal fluid in M-eff steers (Clemmons et al. 2020). Citraconate is a metabolite generated through TCA cycle activity suggesting higher energy production took place in the rumen of M-eff steers (Clemmons et al. 2020). Collectively, data indicate that M-eff cattle have greater capacity for energy production in the rumen and liver to maintain similar growth performance despite lower DMI.

A recent study useduntargeted metabolomics via liquid chromatography-mass spectrometry (LC-MS) to uncover differencs in serum metabolomic profiles between young M-eff and L-eff Nellore bulls (Novais et al. 2019). In this study, serum samples from 98 Nellore bulls at 16–20 months of age and 376 ± 29 kg BW were collected 21 days before the start of a 70 day RFI evaluation period (Novais et al. 2019). Authors detected 7808 DEM between M-eff and L-eff groups (Novais et al. 2019). Seven metabolites had lower concentrations in the M-eff group including retinal, progesterone, stearic acid, vomifoliol, 2,3 dihydroflavone, limonoate and phytanic acid (Novais et al. 2019). Retinal is involved in the retinol pathway, previously reported to be downregulated in feed-efficient beef cattle (de Almeida Santana et al. 2016). Similarly, progesterone (a key metabolite in steroid hormone biosynthesis) was suppressed in the liver of M-eff Jersey cows (Salleh et al. 2017). Interestingly, this study revealed metabolites exclusively produced by bacteria or plants inclduing vomifoliol, 2,3 dihydroflavone, limonoate and phytanic acid that were lower in the M-eff group (Novais et al. 2019), likely due to lower DMI.

Clemmons et al. (2019a) conducted a study to discover differences in serum metabolome between M-eff and L-eff beef cattle. In this study, they used LC-MS analysis for untargeted metabolomics of serum samples collected from M-eff (n = 14) and L-eff (n = 15) weaned Angus steers at 7 months old and 264 ± 2.7 kg of BW. The GrowSafe system was used to monitor individual DMI for each steer during the 70-day RFI trial (Clemmons et al. 2019a). Weekly, 9 mL of blood samples were collected via venipuncture from the coccygeal vein to separate serum. Results indicated that pantothenate was greater in the M-eff group (Clemmons et al. 2019a). Pantothenate, a substrate for CoA synthesis, is produced by ruminal bacteria such as Flavobacteriiathen absorbed via ruminal epithelium to reach the

circulation (Clemmons et al. 2019a). Interestingly, Clemmons et al. (2019a)reported that Flavobacteriia were more abundant in M-eff steers, a result that is in line with previous studies revealing a better capacity for energy production from lower DMI in M-eff cattle.

Using commercial enzymatic kits, Broleze et al. (2020) evaluated differences in targeted metabolites in blood between M-Eff and L-eff beef cows. In this study, DMI of 53 primiparous Nellore beef cows at 36.8 ± 1.23 months of age and 484 ± 40.9 kg of BW was monitored individually using the GrowSafe System for 168 days between 22 and 190 days in milk (DIM; early-tomid-lactation stage) to calculate RFI coefficients for each cow (Broleze et al. 2020). Blood samples were collected from all animals for analysis of glucose, cholesterol, triglycerides, andß-hydroxybutyrate (Broleze et al. 2020). Cholesterol was the only metabolite that differed in concentrationse, being greater in M-eff beef cows (204 mg/dL vs. 192 mg/dL) (Broleze et al. 2020). Because another study reported increased plasma cholesterol in feed-restricted dairy cows (Gross et al. 2015), authors suggested that lower DMI in M-eff cows (consumed 11.5% DMI) partly explaind the response observed (Broleze et al. 2020). In another study, Bonilha et al. (2017) used commercial enzymatic kits to evaluate differences in specific serum metabolites including insulin, non-esterified fatty acids (NEFA), insulin-like growth factor I (IGF-I), and cortisol between M-eff (n = 13) and L-eff (n = 12) Nellore bulls at 210 days of age and 207 kg BW monitored for individual DMI for 70 days. Cortisol, a biomarker of stress, was lower in M-eff bulls indicating a lower degree of systemic stresss (Bonilha et al. 2017) and providing support to previous studies reporting lower circulating cortisol in M-eff cattle (Gomes et al. 2013; Richardson et al. 2004).

In a recent study, Elolimy et al. (2020) detected shifts in hindgut metabolomics profiles between M-eff and L-eff dairy preweaned calves. In this study, DMI in 26 neonatal Holstein heifer calves was individually monitored from birth to weaning at 42 days of age. Calves were retrospectively classified into two groups: M-eff (n = 13) and L-eff (n = 13) heifers based on individual RFI coefficient (Elolimy et al. 2020). Fecal samples were collected every two weeks throughout the study to perform untargeted metabolomics using an LC-MS approach (Elolimy et al. 2020). At birth, M-eff calves had an enrichment of metabolites belonging to energy-producing pathways including pyruvate metabolism, gluconeogenesis, TCA cycle, and biotin suggesting a greater availability of energy for growth and development during the preweaning period (Akram 2014; Vailati-Riboni et al. 2016; Elolimy et al. 2020). Furthermore, the M-eff group upregulated vitamin (biotin metabolism), fatty acid (arachidonic acid metabolism), and amino acid (alanine metabolism) related pathways that would likely enhance gut function and development (Elolimy et al. 2020; León-Del-Río 2019). During the preweaning period, Elolimy et al. (2020) demonstrated that M-eff calves had greater supply of B vitamins in the hindgut including vitamins B6, B7 (biotin) and B9 (folate). Vitamin B6 is essential for metabolism of fatty acids, amino acids, and glucose (Rodriguez-Melendez and Zempleni 2003). Vitamin B7 is important for mucosal immune responses (Jenkins et al. 2017). M-eff calves also had greater capacity for metabolism of amino acids

such as tyrosine, tryptophan, and phenylalanine (Elolimy et al. 2020) likely contributing to the similar growth achieved (Elolimy et al. 2020).

Another study measured the concentrations of leptin, prolactin, neuropeptide Y (NPY), insulin-like growth factor 1 (IGF-1), ghrelin, insulin, β-hydroxybutyrate, glucose, NEFA and growth hormone (GH) in serum between M-eff and L-eff dairy cows (Xi et al. 2016). The authors selected 29 lactating Holstein cows from a total of 84 based on their RFI coefficients to end up with two groups including M-eff (n = 15) and L-eff (n = 14) dairy cows (Xi et al. 2016). Blood samples were collected from all 29 cows through jugular venipuncture on day 1, 25 and 50 during the feeding period (Xi et al. 2016). The authors reported no differences in serum prolactin, IGF-1, ghrelin, insulin, β-hydroxybutyrate, glucose and GH (Xi et al. 2016). However, M-eff cows had greater concentration of NPY and lower leptin and NEFA (Xi et al. 2016) indicating lower propensity for fat mobilization, suggesting that M-eff cows likely had sufficient energy supply and experienced a lesser degree of negative energy balance.

Sharma et al. (2016) calculated RFI coefficients for 18 growing male Murrah buffalo calves at 4–6 months old and 70 ± 1.0 kg of BW after 99 days of a feeding trail, resulting in M-eff (n = 7) and L-eff calves (n = 11). Blood samples were collected at the start and end of the feeding trial by venipuncture of the anterior *vena cava* to evaluate plasma content of IGF-1, GH, creatinine, insulin, albumin, hydroxyproline, triio-dothyronine (T3), thyroxin (T4), and total protein using commercial kits (Sharma et al. 2016). No differences in plasma concentrations of creatinine insulin, albumin, hydroxysproline and total protein were detected (Sharma et al. 2016). However, M-eff calves had greater plasma IGF-1, and T3, but lower T4 (Sharma et al. 2016).

Overall, the above findings of alterations in several metabolites associated with better feed efficiency in beef and dairy cattle provide a list of robust biomarkers that could be studied in the future for their potential as physiological indicators predictive of feed-efficient cattle.

5.3 Proteomics Signature in Feed-Efficient Cattle

Elolimy et al. (2019) investigated changes in ruminal epithelium protein abundance between M-eff (n = 6) and L-eff (n = 6) Red Angus heifers and steers using the western blot approach. In this study, Elolimy et al. (2019) evaluated 29 proteins involved in protein synthesis (MTOR signaling) and degradation (ubiquitin-proteasome pathways) in ruminal epithelium collected after slaughter at the end of 70 days of a feeding trail. The M-eff group had greater abundance of proteins crucial for cellular protein synthesis such as phosphorylated eukaryotic elongation factor 2 kinase (p-EEF2K), phosphorylated eukaryotic elongation factor 2 kinase:total eukaryotic elongation factor 2 kinase (p-EEF2K:EEF2K, and phosphorylated eukaryotic translation initiation factor 2A:total eukaryotic translation initiation factor 2A (p-EIF2A:EIF2A)(Elolimy et al. 2019). On the other hand, M-eff cattle had

lower abundance of proteins involved in protein degradation pathways such as total ubiquitin like modifier activating enzyme 1 (UBA1), total neural precursor cell expressed, developmentally downregulated 4, E3 ubiquitin protein ligase (NEDD4), total STIP1 homology and U-box containing protein 1 (STUB1), and total MDM2 proto-oncogene (MDM2) (Elolimy et al. 2019). No differences were detected in plasma insulin and ruminal epithelium insulin signaling proteins (Elolimy et al. 2019). These data indicated that M-eff beef cattle have a greater rate of protein synthesis relative to protein degradation in ruminal epithelium. These changes likely result in better growth of ruminal epithelium to absorb more VFA produced from the anaerobic microbial fermentation of plant fiber in M-eff beef cattle.

Carvalho et al. (2019) employed a proteomics approach to unmask differences in key proteins associated with energy metabolism in skeletal muscle of RFI divergent beef cattle. Daily DMI was recorded for 129 young Nellore bulls at 7 months old and 239 ± 30.1 kg of BW during 98 days of RFI evaluation period (Carvalho et al. 2019). At the end of the study, Carvalho et al. (2019) selected 9 bulls for M-eff group and another 9 bulls for L-eff group. After slaughter, longissimus muscle was sampled for protein profiling using a two-dimensional electrophoresis (2D-PAGE) with mass spectrometry (ESI-MS) (Carvalho et al. 2019). Heat shock protein beta 1 (HSPB1), a key protein for cellular development and differentiation (Zhang et al. 2014; Carvalho et al. 2014) and inhibitor of protein degradation in muscle fibers, was greater in the M-eff group (Carvalho et al. 2019) suggesting greater protein synthesis. Therefore, this adaptation likely contributed to better feed efficiency in M-eff cattle through decrease protein turnover in skeletal muscle.

Another proteomics study conducted by Baldassini et al. (2018) used 2D-PAGE and ESI-MS techniques to profile hepatic proteins in RIF divergent Nellore bulls. In this study, Baldassini et al. (2018) used 18 Nellore bulls at 24–26 months of age during the finishing period (M-eff = 9 and L-eff = 9). After slaughter, liver samples were collected from the 18 animals for protein extraction and proteomic profiling (Baldassini et al. 2018). Results indicated that hemoglobin subunit beta protein (HBB) was downregulated in the M-eff group (Baldassini et al. 2018) likely from lower numbers of red blood cells since hemoglobin binds to oxygen to form oxyhemoglobin inside the red blood cells (Hsia 1998). The data indicated a need to determine blood hemoglobin concentrations between M-eff and L-eff groups in future studies. Baldassini et al. (2018) reported that the M-eff group had lower abundance of oxidative stress-associated proteins such as aldehyde dehydrogenase, aspartate aminotransferase, and glycine amidino transferase proteins, highlighting a lower degree of hepatic oxidative stress and less reactive oxygen species (ROS) content in liver of feed-efficient cattle.

Davis et al. (2016) investigated differences in oxygen uptake by mitochondria in muscle and respiratory chain proteins between M-eff and L-eff beef cattle. They calculated RFI coefficients in 92 Hereford-crossbreed steers in63-day feeding period using the individual feed intake system. The top 10 M-eff and top 8 L-eff steers based on RFI coefficient ranking were used for subsequent analysis. Mitochondrial complex I (CI), II (CII), and III (CIII) protein concentration in M-eff and L-eff groups was assessed using bicinchoninic acid colorimetric procedures.

Lymphocytes were isolated from blood samples collected via jugular venipuncture from both groups (Davis et al. 2016). Results indicated that M-eff steers did not differ in CI, CII, and CIII protein concentration. Therefore, mitochondrial proteins do not seem to play a key role in the RFI divergence between M-eff and L-eff steers.

5.4 Conclusions

Comprehensive metabolome and proteome studies revealed associations between RFI divergent cattle and shifts in metabolome/proteome profiles that might explain the biology behind superior feed efficiency in cattle. Overall, M-eff cattle are characterized by metabolite and protein profiles that would provide extra energy and nutrients to help maintain similar levels of production despite a lower DMI. Further studies are warranted to expand our understanding of the biological contribution of key metabolites and proteins to RFI divergence in cattle at different production stages. Additionally, the relationship between metabolome/proteome profiling among different tissue in the same individual animals such as rumen, blood, skeletal muscles and milk should be examined in order to provide a more holistic overview into feed-efficient cattle.

References

Akram M (2014) Citric acid cycle and role of its intermediates in metabolism. Cell Biochem Biophys 68(3):475–478. https://doi.org/10.1007/s12013-013-9750-1

Artegoitia VM, Foote AP, Lewis RM, Freetly HC (2017) Rumen fluid metabolomics analysis associated with feed efficiency on crossbred steers. Sci Rep 7(1):2864. https://doi.org/10.1038/s41598-017-02856-0

Baldassini WA, Bonilha SFM, Branco RH, Vieira JCS, Padilha PM, Lanna DPD (2018) Proteomic investigation of liver from beef cattle (Bos indicus) divergently ranked on residual feed intake. Mol Biol Rep 45(6):2765–2773. https://doi.org/10.1007/s11033-018-4341-2

Bonilha SFM, Branco RH, Mercadante MEZ, Dos Santos Goncalves Cyrillo JN, Monteiro FM, Ribeiro EG (2017) Digestion and metabolism of low and high residual feed intake Nellore bulls. Tropl Anim Health Prod 49(3):529–535. https://doi.org/10.1007/s11250-017-1224-9

Broleze DF, Souza LL, Zorzetto MF, Savegnago RP, Negrao JA, Bonilha SFM, Mercadante MEZ (2020) Feed efficiency and maternal productivity of Bos indicus beef cows. PLoS One 15(6):e0233926. https://doi.org/10.1371/journal.pone.0233926

Carvalho ME, Gasparin G, Poleti MD, Rosa AF, Balieiro JCC, Labate CA, Nassu RT, Tullio RR, LCdA R, Mourão GB, Coutinho LL (2014) Heat shock and structural proteins associated with meat tenderness in Nellore beef cattle, a Bos indicus breed. Meat Sci 96(3):1318–1324. https://doi.org/10.1016/j.meatsci.2013.11.014

Carvalho EB, Gionbelli MP, Rodrigues RTS, Bonilha SFM, Newbold CJ, Guimaraes SEF, Silva W, Verardo LL, Silva FF, Detmann E, Duarte MS (2019) Differentially expressed mRNAs, proteins and miRNAs associated to energy metabolism in skeletal muscle of beef cattle identified for low and high residual feed intake. BMC Genomics 20(1):501. https://doi.org/10.1186/s12864-019-5890-z

Clemmons BA, Mihelic RI, Beckford RC, Powers JB, Melchior EA, McFarlane ZD, Cope ER, Embree MM, Mulliniks JT, Campagna SR, Voy BH, Myer PR (2017) Serum metabolites associated with feed efficiency in black angus steers. Metabolomics 13(12):147. https://doi.org/10.1007/s11306-017-1282-z

Clemmons BA, Martino C, Powers JB, Campagna SR, Voy BH, Donohoe DR, Gaffney J, Embree MM, Myer PR (2019a) Rumen Bacteria and serum metabolites predictive of feed efficiency phenotypes in beef cattle. Sci Rep 9(1):19265. https://doi.org/10.1038/s41598-019-55978-y

Clemmons BA, Martino C, Schneider LG, Lefler J, Embree MM, Myer PR (2019b) Temporal stability of the ruminal bacterial communities in beef steers. Sci Rep 9(1):9522. https://doi.org/10.1038/s41598-019-45995-2

Clemmons BA, Powers JB, Campagna SR, Seay TB, Embree MM, Myer PR (2020) Rumen fluid metabolomics of beef steers differing in feed efficiency. Metabolomics 16(2):23. https://doi.org/10.1007/s11306-020-1643-x

Davis MP, Brooks MA, Kerley MS (2016) Relationship between residual feed intake and lymphocyte mitochondrial complex protein concentration and ratio in crossbred steers. J Anim Sci 94(4):1587–1591. https://doi.org/10.2527/jas.2015-9843

de Almeida Santana MH, Junior GA, Cesar AS, Freua MC, da Costa GR, da Luz ESS, Leme PR, Fukumasu H, Carvalho ME, Ventura RV, Coutinho LL, Kadarmideen HN, Ferraz JB (2016) Copy number variations and genome-wide associations reveal putative genes and metabolic pathways involved with the feed conversion ratio in beef cattle. J Appl Genet 57(4):495–504. https://doi.org/10.1007/s13353-016-0344-7

Durunna ON, Mujibi FD, Goonewardene L, Okine EK, Basarab JA, Wang Z, Moore SS (2011) Feed efficiency differences and reranking in beef steers fed grower and finisher diets. J Anim Sci 89(1):158–167. https://doi.org/10.2527/jas.2009-2514

Elolimy AA, Abdel-Hamied E, Hu L, McCann JC, Shike DW, Loor JJ (2019) Rapid communication: residual feed intake in beef cattle is associated with differences in protein turnover and nutrient transporters in ruminal epithelium. J Anim Sci 97(5):2181–2187. https://doi.org/10.1093/jas/skz080

Elolimy A, Alharthi A, Zeineldin M, Parys C, Loor JJ (2020) Residual feed intake divergence during the preweaning period is associated with unique hindgut microbiome and metabolome profiles in neonatal Holstein heifer calves. J Animal Sci & Biotechnol 11:13. https://doi.org/10.1186/s40104-019-0406-x

Fan H, Wu Y, Zhou X, Xia J, Zhang W, Song Y, Liu F, Chen Y, Zhang L, Gao X, Gao H, Li J (2015) Pathway-based genome-wide association studies for two meat production traits in Simmental cattle. Sci Rep 5:18389. https://doi.org/10.1038/srep18389

Ferrell CL, Jenkins TG (1984) Energy utilization by mature, nonpregnant, nonlactating cows of different types. J Anim Sci 58(1):234–243. https://doi.org/10.2527/jas1984.581234x

Fontanesi L (2016) Metabolomics and livestock genomics: insights into a phenotyping frontier and its applications in animal breeding. Anim Front 6(1):73–79. https://doi.org/10.2527/af.2016-0011

Gomes RC, Sainz RD, Silva SL, César MC, Bonin MN, Leme PR (2012) Feedlot performance, feed efficiency reranking, carcass traits, body composition, energy requirements, meat quality and calpain system activity in Nellore steers with low and high residual feed intake. Livest Sci 150(1):265–273. https://doi.org/10.1016/j.livsci.2012.09.012

Gomes RC, Sainz RD, Leme PR (2013) Protein metabolism, feed energy partitioning, behavior patterns and plasma cortisol in Nellore steers with high and low residual feed intake. Rev Bras Zootec 42:44–50

Gross JJ, Kessler EC, Albrecht C, Bruckmaier RM (2015) Response of the cholesterol metabolism to a negative energy balance in dairy cows depends on the lactational stage. PLoS One 10(6):e0121956. https://doi.org/10.1371/journal.pone.0121956

Hsia CC (1998) Respiratory function of hemoglobin. N Engl J Med 338(4):239–247. https://doi.org/10.1056/nejm199801223380407

Jenkins TP, Rathnayaka Y, Perera PK, Peachey LE, Nolan MJ, Krause L, Rajakaruna RS, Cantacessi C (2017) Infections by human gastrointestinal helminths are associated with changes in faecal microbiota diversity and composition. PLoS One 12(9):e0184719. https://doi.org/10.1371/journal.pone.0184719

Lawrence P, Kenny DA, Earley B, McGee M (2013) Intake of conserved and grazed grass and performance traits in beef suckler cows differing in phenotypic residual feed intake. Livest Sci 152(2):154–166. https://doi.org/10.1016/j.livsci.2012.12.024

Leng RA, Nolan JV (1984) Nitrogen metabolism in the rumen. J Dairy Sci 67(5):1072–1089. https://doi.org/10.3168/jds.S0022-0302(84)81409-5

León-Del-Río A (2019) Biotin in metabolism, gene expression, and human disease. J Inherit Metab Dis 42(4):647–654. https://doi.org/10.1002/jimd.12073

Li B, VanRaden PM, Guduk E, O'Connell JR, Null DJ, Connor EE, VandeHaar MJ, Tempelman RJ, Weigel KA, Cole JB (2020) Genomic prediction of residual feed intake in US Holstein dairy cattle. J Dairy Sci 103(3):2477–2486. https://doi.org/10.3168/jds.2019-17332

Linkswiler H, Reynolds MS (1950) Urinary and fecal elimination of B6 and 4-pyridoxic acid on three levels of intake. J Nutr 41(4):523–532. https://doi.org/10.1093/jn/41.4.523

Montaño-Bermudez M, Nielsen MK, Deutscher GH (1990) Energy requirements for maintenance of crossbred beef cattle with different genetic potential for milk. J Anim Sci 68(8):2279–2288. https://doi.org/10.2527/1990.6882279x

Myer PR, Smith TP, Wells JE, Kuehn LA, Freetly HC (2015) Rumen microbiome from steers differing in feed efficiency. PLoS One 10(6):e0129174. https://doi.org/10.1371/journal.pone.0129174

Nafikov RA, Beitz DC (2007) Carbohydrate and lipid metabolism in farm animals. J Nutr 137(3):702–705. https://doi.org/10.1093/jn/137.3.702

Novais FJ, Pires PRL, Alexandre PA, Dromms RA, Iglesias AH, Ferraz JBS, Styczynski MP, Fukumasu H (2019) Identification of a metabolomic signature associated with feed efficiency in beef cattle. BMC Genomics 20(1):8. https://doi.org/10.1186/s12864-018-5406-2

Potts SB, Boerman JP, Lock AL, Allen MS, VandeHaar MJ (2017) Relationship between residual feed intake and digestibility for lactating Holstein cows fed high and low starch diets. J Dairy Sci 100(1):265–278. https://doi.org/10.3168/jds.2016-11079

Reinhardt TA, Lippolis JD, Nonnecke BJ, Sacco RE (2012) Bovine milk exosome proteome. J Proteomics 75(5):1486–1492. https://doi.org/10.1016/j.jprot.2011.11.017

Richardson EC, Herd RM, Archer JA, Arthur PF (2004) Metabolic differences in Angus steers divergently selected for residual feed intake. Aust J Exp Agric 44(5):441–452

Rodriguez-Melendez R, Zempleni J (2003) Regulation of gene expression by biotin (review). J Nutr Biochem 14(12):680–690. https://doi.org/10.1016/j.jnutbio.2003.07.001

Salleh MS, Mazzoni G, Höglund JK, Olijhoek DW, Lund P, Løvendahl P, Kadarmideen HN (2017) RNA-Seq transcriptomics and pathway analyses reveal potential regulatory genes and molecular mechanisms in high- and low-residual feed intake in Nordic dairy cattle. BMC Genomics 18(1):258. https://doi.org/10.1186/s12864-017-3622-9

Sharma VK, Kundu SS, Prusty S, Datt C, Kumar M (2016) Nutrient utilisation, growth performance and blood metabolites in Murrah buffalo calves (Bubalus bubalis) divergently selected for residual feed intake. Arch Anim Nutr 70(6):455–469. https://doi.org/10.1080/1745039X.2016.1233678

Vailati-Riboni M, Meier S, Burke CR, Kay JK, Mitchell MD, Walker CG, Crookenden MA, Heiser A, Rodriguez-Zas SL, Roche JR, Loor JJ (2016) Prepartum body condition score and plane of nutrition affect the hepatic transcriptome during the transition period in grazing dairy cows. BMC Genomics 17(1):854. https://doi.org/10.1186/s12864-016-3191-3

Wirth R, Kádár G, Kakuk B, Maróti G, Bagi Z, Szilágyi Á, Rákhely G, Horváth J, Kovács KL (2018) The planktonic core microbiome and core functions in the cattle rumen by next generation sequencing. Front Microbiol 9:2285. https://doi.org/10.3389/fmicb.2018.02285

Xi YM, Wu F, Zhao DQ, Yang Z, Li L, Han ZY, Wang GL (2016) Biological mechanisms related to differences in residual feed intake in dairy cows. Animal: Int J Animal Biosci 10(8):1311–1318. https://doi.org/10.1017/S1751731116000343

Zhang Q, Lee HG, Kang SK, Baik M, Choi YJ (2014) Heat-shock protein beta 1 regulates androgen-mediated bovine myogenesis. Biotechnol Lett 36(6):1225–1231. https://doi.org/10.1007/s10529-014-1489-2

Zhang Y, Li F, Chen Y, Wu H, Meng Q, Guan LL (2020) Metatranscriptomic profiling reveals the effect of breed on active rumen eukaryotic composition in beef cattle with varied feed efficiency. Front Microbiol 11:367. https://doi.org/10.3389/fmicb.2020.00367