

Nutrigenomics Approaches to Fine-Tune Metabolism and Milk Production: Is This the Future of Ruminant Nutrition?

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Ruminant nutrition is highly sophisticated. Immense research and application efforts have culminated in great successes. Today, we can satisfy with a relative high precision the nutritional needs of high producing dairy cows. Highly efficient genetic selection and improvement in overall management has resulted in a national average of ca. 10,000 kg of milk per year in USA. The 2012 USDA annual report indicated an average of 9,842 kg milk produced in one year (or ca. 32 kg/day), with a recent reported record of more than 32,000 kg/year (ca. 90 kg/day!). Dairy cows with a so sophisticated genetic makeup able to deliver extremely high milk yield require a more refined management, including feeding strategies that increase the precision in satisfying all requirements and account for the dynamic physiological adaptation of the animal to lactation and reproduction. This is evident by the increased importance of metabolic-related health problems and a continual decrease in fertility in high-yielding dairy cows. These problems can be addressed by improving overall nutritional management [1], including a strategy to use nutrients that can improve the metabolic adaptation of animals to lactation. As the genetic potential of dairy cows continues to improve, the advances in research for a more accurate feeding strategy are of utmost importance. In addition, there is an urgent need for research to improve efficiency of animal food production in an environmental sustainable way to feed the growing World human population. Not to mention, it is becoming increasingly evident that the quality of the food consumed by humans affects their health and consumers are playing important roles in World food markets.

With respect to research, we are now in a post-genomics era with the advent of systems biology. Today we have the opportunity to study in a holistic way the effect of any condition on the whole organism considering a large amount of molecular information (e.g., whole transcriptome, proteomics, metabolomics, and data from other omics-related technologies). We also have increasing availability of bioinformatics tools to biologically decipher such a large amount of data.

Dietary nutrients alter gene expression either directly or indirectly; thus, affecting protein expression and metabolic and/or signaling status of cells, tissues, organs, and the entire organism. The concept that food components affects biological functions by interacting with transcriptome has revolutionized the field of nutrition in monogastrics [2], but has the potential to affect also the field of ruminant nutrition, and, in the case of dairy cows, to affect efficiency and quality of milk production.

All the above strongly prompt for a new approach to feed dairy animals by taking advantage of the capacity of nutritional molecules to affect the whole biology of the organism. In addition to satisfying the nutritional requirements of the animals, the diet can also modify their biology by altering gene expression. The ration formulation can then be used to “fine-tune” the transcriptome (and, as consequence, the whole biology) of the animal to improve its efficiency in production and fertility as well as its overall well-being. The fine-tuning approach can also be utilized to improve milk quality. To achieve this fine-tuning approach, research is needed to understand the molecular effects of

nutritional molecules using systems biology approaches; i.e., systems nutrigenomics.

Nutrigenomics is defined as the study of “the genome-wide influences of nutrition” [3] and how this “affects the balance between health and disease by altering the expression and/or structure of an individual’s genetic makeup” [4]. Nutrigenomics in dairy cows is a relatively new area of research [5]. Among all nutritional factors able to affect cell biology by changing gene expression, dietary energy, fatty acids, and amino acids have the strongest potential.

Dietary energy has a powerful and broad effect on the transcriptome [6]. Despite the potential benefit on the metabolism of dairy animals that can be achieved using dietary energy [7], the effect on the transcriptome is broad and is distributed in multiple tissues (thus on the organismal metabolism). Study of the transcriptomics effects of amino acids in ruminants is a new area of investigation. However, recent data seem to support a nutrigenomics effect of amino acids on milk protein synthesis [8]. Transcriptomics effects for fatty acids, particularly long-chain fatty acids (LCFA), have been more widely studied. The effect of *trans10,cis12*-conjugated linoleic acid (*t10,c12*-CLA) on depressing milk fat synthesis (by decreasing the activity and expression of the nuclear receptor sterol regulatory element binding transcription factor 1, or SREBP1, that controls expression of key lipogenic genes) is the first and the most well-known nutrigenomics effect of LCFA on milk production [9]. However, even though this allows explaining milk fat depression in dairy cows, the practical application for milk synthesis fine tuning is quite limited. To date, the ability to increase milk fat synthesis through nutrigenomics still remains to be determined.

In monogastrics, it has been well established that LCFA can affect expression of genes mainly by their capacity to directly or indirectly (i.e., through their metabolites) bind and activate (or inhibit) transcriptional factors. Among all the transcriptional factors able to bind and be activated by LCFA the peroxisome proliferator-activated receptors (PPARs) are, so far, the more potent. This knowledge in monogastrics let few dairy researchers to start investigating the role of PPARs in ruminants [10]. Data in dairy ruminants support a role of PPARs in ruminant physiology, particularly lipid metabolism including regulation of milk fat synthesis [10]. In addition, there is a strong agonistic effect of LCFA, particularly the saturated fatty acids, in

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activating PPARs in ruminants. A model involving activation of PPAR isotypes by LCFA in several major tissues at precise physiological stages has been proposed [10]. In order to test such a complex nutrigenomics model, a systems physiology approach, together with sophisticated molecular biology techniques, must be carried out. The technologies to undertake nutrigenomics studies with a systems biology approach are costly and the main limitation for most of the research in these areas is the lack of adequate funding. Despite the high cost, investments in nutrigenomics studies using systems physiology approaches in dairy ruminants have the potential for a very high payoff in production, fertility, and animal well-being.

We are at the frontier of the nutrigenomics era in ruminants. The need to improve nutrition in dairy cows is great, especially considering the real urgency of increasing production by maximizing the limited resources but minimizing the environmental impact. Nutrigenomics can provide the means to effectively face these challenges. Thus, systems nutrigenomics can play a pivotal role in shaping the future of ruminant nutrition.

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References

1. Trevisi E, Bionaz M, Piccioli-Cappelli F, Berton G (2006) The management of intensive dairy farms can be improved for better welfare and milk yield. *Livestock Science* 103: 231-236.
2. Mutch DM, Wahli W, Williamson G (2005) Nutrigenomics and nutrigenetics: the emerging faces of nutrition. *FASEB journal : official publication of the Federation of American Societies for Experimental Biology* 19: 1602-1616.
3. Muller M, Kersten S (2003) Nutrigenomics: goals and strategies. *Nature reviews Genetics* 4: 315-322.
4. Kaput J, Rodriguez RL (2004) Nutritional genomics: the next frontier in the postgenomic era. *Physiological genomics* 16: 166-177.
5. Loor JJ, Bionaz M, Drackley JK (2013) Systems Physiology in Dairy Cattle: Nutritional Genomics and Beyond. *Annual Review of Animal Biosciences* 1: 365-392.
6. Bionaz M, Loor JJ (2012) Ruminant metabolic systems biology: reconstruction and integration of transcriptome dynamics underlying functional responses of tissues to nutrition and physiological state. *Gene Regul Syst Bio* 6: 109-125.
7. Dann HM, Litherland NB, Underwood JP, Bionaz M, D'Angelo A, et al. (2006) Diets during far-off and close-up dry periods affect periparturient metabolism and lactation in multiparous cows. *J Dairy Sci* 89: 3563-3577.
8. Nan X, Bu D, Li X, Wang J, Wei H, et al. (2014) Ratio of Lysine to Methionine alters expression of genes involved in milk protein transcription and translation and mTOR phosphorylation in bovine mammary cells. *Physiol Genomics*.
9. Bauman DE, Harvatine KJ, Lock AL (2011) Nutrigenomics, rumen-derived bioactive fatty acids, and the regulation of milk fat synthesis. *Annu Rev Nutr* 31: 299-319.
10. Bionaz M, Chen S, Khan MJ, Loor JJ (2013) Functional Role of PPARs in Ruminants: Potential Targets for Fine-Tuning Metabolism during Growth and Lactation. *PPAR Res* 2013: 684159.