

APPLICATION OF NUTRIGENOMICS FOR MILK FAT IMPROVEMENT IN DAIRY CATTLE

S. Banupriya, C. Kathirvelan* and P. Patric Joshua

Assistant Professor, Veterinary College and Research Institute
Tamil Nadu Veterinary and Animal Sciences University
Namakkal – 637005, Tamil Nadu

E-mail: kadhirc@gmail.com (**Corresponding Author*)

Abstract: Nutrigenomics that is the study of interaction between dietary components and the genome, and the regulating changes in proteins and other metabolism. The development of nutrigenomic studies has brought about a number of new research tools. Bioinformatics are now making their ways to solve the intervening puzzle between nutrient and genes. Numerous dietary components can alter genetic events, and thereby influence health. In addition to the essential nutrients, such as carbohydrates, amino acids, fatty acids, calcium, zinc, selenium, and vitamin A, C and E, there is a variety of nonessential bioactive components that seem to significantly influence health.

Keywords: Nutrient, Genes, Milk fat, Biotechnology.

Introduction

Over the last decade, advances in the biochemical technologies available for examining functional genomics have provided a number of new molecular tools for evaluating responses to nutritional strategies. These tools are largely based on an understanding of the expression and control of specific genes and gene products and have lead to the development of the sciences associated with nutrigenomics bioactive food compounds can interact with genes affecting transcription factors, protein expression and metabolite production. The study of how genes and gene products interact with dietary chemicals to alter phenotype and conversely, how genes and their products metabolize nutrients is called Nutritional genomics or “Nutrigenomics” (Kaput et al., 2005).

Nutrient gene interaction

- Genes are turned on and off according to metabolic signals that the nucleus receives from internal factors, e.g. hormones, and external factors, e.g. nutrients, which are among the most influential of environmental stimuli.
- Numerous dietary components can alter genetic events, and thereby influence health. In addition to the essential nutrients, such as carbohydrates, amino acids, fatty acids, calcium,

*Received May 17, 2016 * Published June 2, 2016 * www.ijset.net*

zinc, selenium, and vitamin A, C and E, there is a variety of nonessential bioactive components that seem to significantly influence health.

- These essential and nonessential bioactive food components are known to modify a number of cellular processes associated with health and disease prevention, including carcinogen metabolism, hormonal balance, cell signaling, cell cycle control, apoptosis, and angiogenesis. Often bioactive food components will modify several processes simultaneously.
- The complex mixture of natural substances that supplies both energy and building blocks to develop and sustain organism nutrients has variety of biological activity:
 - Antioxidants (act as a free radical scavengers)
 - Nutritional hormone (potent signaling molecules)
 - Phytochemicals (modulator for animal health and production)
- The essential nutrients imbalance of macronutrients in sub optimal level or even toxic concentration of certain feeds may cause many diseases and disorders.

Nutritional genomics in ruminants

- Dietary manipulations and nutritional strategies are key tools for influencing ruminant production.
- Genetic predisposition and nutritional management requires reproductive performance and fertility in dairy cattle.
- This is particularly important during the transition period and early lactation, when the animal is particularly sensitive to nutritional imbalances.
- Nutritional restriction due to intake of poor quality feeds, expression of specific genes associated with protein turnover, cytoskeletal remodeling, and metabolic homeostasis was clearly influenced by diet.
- Many of these changes in expression could be predicted from observed changes in animal growth and physiology during normal nutrient restriction.
- The Entophyte-infected tall fescue on gene expression in luteal tissue of heifers by using rat microarray. Revealed following changes in cell are, Specific differential expression of genes associated with neural functions, Transport function, Cell cycle regulation, Programmed cell death. This clearly indicated that nutrients act on transcriptional level (gene expression) heifers. (Jones *et al.*, 2004).

Nutrigenomics in ruminants for improved milk fat

1. Multiple conjugated linoleic acid isomers have been observed to reduce milk fat synthesis in the cow, but most mechanistic research has focused on trans-10, cis-12 conjugated linoleic acid.
2. Diet-induced milk fat depression is a reduction in milk fat caused by specific bioactive fatty acids produced during ruminal biohydrogenation under some dietary conditions.
3. Whole-animal metabolism, including glucose and insulin signalling, are not modified during diet-induced milk fat depression.
4. During milk fat depression, mammary lipid synthesis capacity is decreased due to a coordinated down-regulation of lipid synthesis enzymes.
5. SREBP1 and S14 are down-regulated in mammary tissue during milk fat depression, but their direct interaction with bioactive fatty acids of ruminal bio hydrogenation has not been delineated.
6. Results demonstrate the value of both the dairy cow and mouse as models to investigate the role of bioactive fatty acids in the regulation of milk fat synthesis during lactation.
7. The mechanistic understanding of the regulation of milk fat synthesis gained from investigations of diet-induced milk fat depression has had a substantial impact on dairy management and nutrition strategies.
8. The study of milk fat synthesis and its regulation by unique bioactive fatty acids is one of the most complete and successful examples of nutrigenomics in present-day animal science research (Bauman *et al.*, 2011).

These changes in gene expression can be used outward phenotypic characteristic of selenium deficiencies. Several selenium sources on gene expression intestinal tract of mice using a basic 23,000 element murine microarray. This is revealed in genes influenced by selenium supplementation. 100 of these can be directly associated with reproductive function. Direct effect of dietary selenium on gene expression in key reproductive tissue yet to be examined from these data can be used to identify candidate genes that are clearly regulated by various selenium supplementations.

Conclusion

Nutrigenomics is a rapidly emerging science still in its beginning stages. It is uncertain whether the tools to study protein expression and metabolite production have been developed

to the point as to enable efficient and reliable measurements. Nutrigenomics approaches will enhance researchers' abilities to maintain animal health, optimize animal performance and improve milk and meat quality. Also once such research has been achieved, it will need to be integrated together in order to produce results and dietary recommendations. All of these technologies are still in the process of development.

References

- [1] Bauman, D.E., Harvatine, K.J. and lock, A.L. (2011). Nutrigenomics, rumen derived bioactive fatty acids and the regulation of milk fat synthesis. *annu Rev Nutr.*, **31**:299-319.
- [2] Jones, K.L., King, S.S. and Iqbal, M.J. (2004). Endophyte-infected tall fescue diet alters gene expression in heifer luteal tissue as revealed by interspecies microarray analysis. *Mol. Reprod. Dev.*, **67**: 154–161.
- [3] Kaput, J., Ordovas, J.M. and Ferguson, L. (2005). The case for strategic international alliances to harness nutritional genomics for public and personal health. *Brit J Nutr.*, **94**:623-32.
- [4] Kore, K.B., Pathak. and Gadekar, Y.P. (2008). Nutrigenomics: Emerging face molecular nutrition to improve animal health and production. *Vet. wor.*, **9**:285-286.