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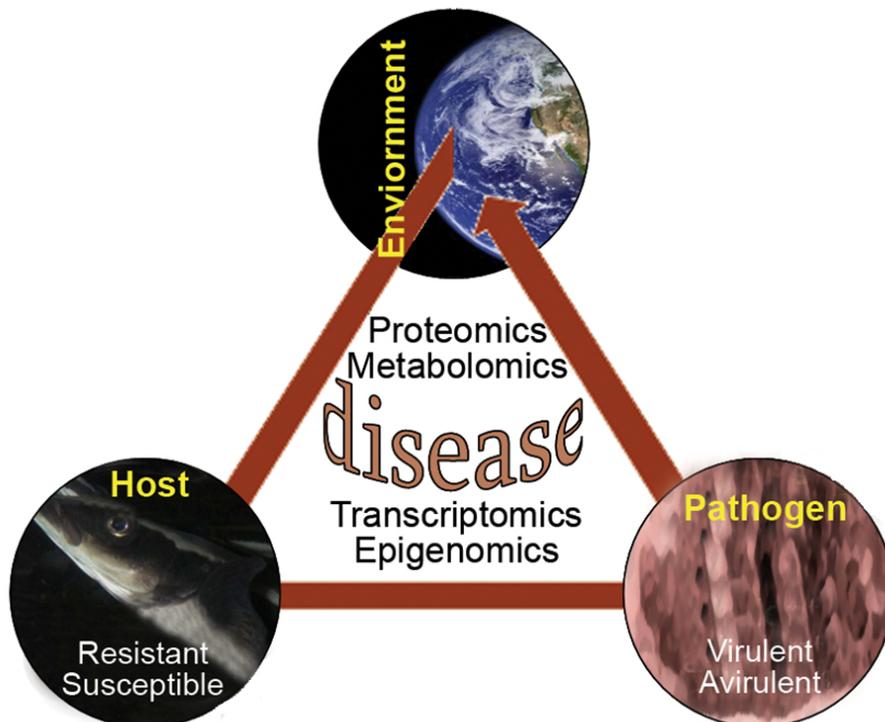
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Nutrition and genes research at Virginia Tech

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Scientists can develop elite feeds with positive effects on production economics and animal welfare



Nutrigenomic research centers on how dietary ingredients influence gene expression and health. Application of various “-omic” technologies can lead to better understanding of the interactions within the “disease triangle” that exists among hosts, pathogens, and the environment.

Good nutrition promotes good health, while dietary imbalances can lead to illness. Some people and populations are more prone to nutritionally driven ailments than others, and many nutrition-related illnesses have a genetic basis.

Nutrients modify gene expression by altering normal metabolic processes. Clinical nutritionists are using novel approaches to better understand disease processes. Key weapons in the nutrition arsenal include a growing number of molecular techniques that enable the dissection of interrelationships among diet, health, and disease processes. A central figure in the nutritional armory is a subdiscipline of functional genomics, termed nutritional genomics or “nutrigenomics.”

Nutrigenomics

Nutrigenomics is the study of how foods affect genes and how individual differences in genetic makeup affect the ways in which animals respond to nutrients with regard to health. Enhanced understanding of how dietary chemicals impact human and animal health will improve our ability to develop methods to prevent and cure many nutrition-related ailments.

Nutrigenomics uses a number of “-omic” disciplines, including transcriptomics, proteomics, metabolomics, and epigenomics. The huge data sets generated by this research rely heavily on the field of bioinformatics, which has developed new methods to acquire, store, share, analyze, present, and manage the information. These techniques provide powerful means to monitor numerous and sometimes negligible genomic changes.

Genomics and aquaculture

Functional genomics – the combination of genomics, proteomics, genotyping, transcriptomics, and metabolomics – has expanded rapidly over the last decade, but research on important aquaculture species is still relatively uncommon. Transcriptomics studies using microarrays represent important components of nutrigenomic research, since they highlight the impacts of different treatments on the activation or silencing of specific genes.

Certain affected genes may offer commercial benefits such as enhancement of immune function or stress resistance, and thus may be targeted via nutritional intervention to increase the performance or welfare of the cultured animal. Microarray technologies have examined treatment effects on abalone, shrimp, zebrafish, fugu, medaka, puffer fish, rainbow trout, Atlantic salmon, gilthead sea bream, sea bass, and catfish.

Due to the commercial availability of zebrafish microarrays, research at the Virginia Tech Aquaculture Center has concentrated on this species. Three entities cooperate in the program: the College of Natural Resources Department of Fisheries and Wildlife Sciences, the Virginia Bioinformatics Institute Core Laboratory Facility, and the Virginia-Maryland Regional College of Veterinary Medicine Department of Large Animal Clinical Sciences.

The center’s research examines the impacts of various dietary modifications on gene expression profiles in homologous (zebrafish) and heterologous (tilapia and cobia) species. Important components of this research were to present gene expression data and to illustrate their biological effects.

Nutrients change genes

Nutrition is a very important area of study for aquaculture. By increasing understanding of dietary manipulation effects on fish production, scientists can develop elite feeds with positive effects on production economics and animal welfare, and develop “designer fish” that target specific market demands. To date, significant progress has been made toward elucidating the potentially valuable effects of dietary minerals and immunostimulants on animal health and developmental processes.



Nutrigenomic research requires sophisticated analytical equipment. Here, gene chips are scanned to quantify the amount of target bound to the DNA probe on a microarray at the Virginia Bioinformatics Institute Core Laboratory Facility.

In their studies investigating dietary supplementation with organic selenium, a mannan oligosaccharide and organic protein source, the authors identified profound and similar impacts on gene expression in whole animal and intestinal samples from zebrafish and tilapia. The importance of these studies is several-fold.

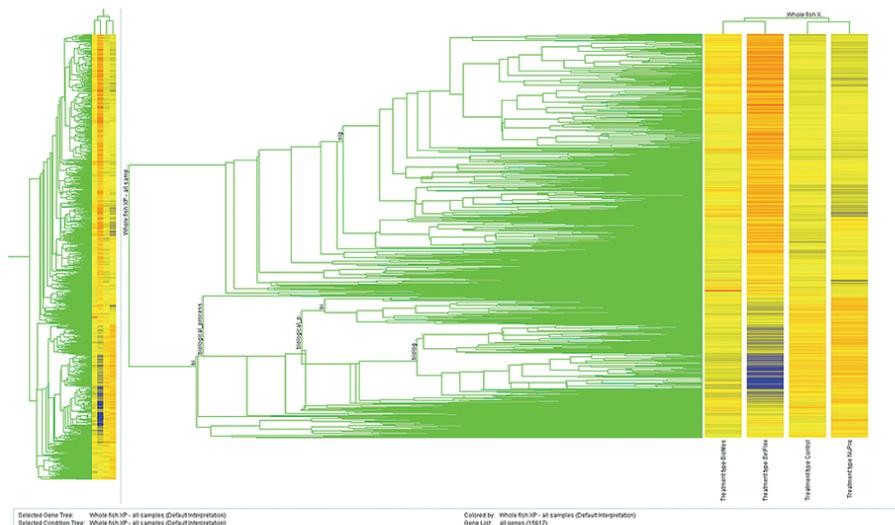
Firstly, because the identical treatments impacted specific genes and gene sets similarly, these results suggested that the zebrafish microarray can, with caution and validation, be applied to heterologous species. This could be a vital finding, since so few species-specific micro-arrays are commercially available. Moreover, producing said microarrays is prohibitively expensive. However, further validations of these observations must be undertaken.

Secondly, comparison of gene expression profiles from both whole animal and intestinal samples indicated that specific tissues or organs of interest must be targeted for analysis to avoid dilution artifacts. Thirdly, the results categorically illustrated genomewide affects of dietary manipulation.

For example, data analysis of fish fed organic selenium demonstrated that over 1,100 genes were upregulated, of which 30 percent were involved in enzymatic actions. The magnitude of response of specific genes was also much higher in zebrafish fed organic selenium, resulting in responses of sixfold or higher, up to a 14-fold increase in gene expression in one instance.

The current challenge is to identify the specific metabolic pathways affected by the genes in question. Some of these may provide characteristic signatures associated with a particular physiological status. In fact, a major issue requiring resolution is the current lack of availability of validated biomarkers that are specific, sensitive, predictable, and quantifiable.

Once microarrays reveal potential biomarkers, their applicability and value must be validated using other methods, such as quantitative reverse-transcriptase-polymerase chain reaction, Northern or Western blotting, or quantifying protein levels by enzyme-linked immunosorbent or similar assays.



This microarray gene tree illustrates the impact of four dietary treatments on changes in mRNA abundance in zebrafish. The varied colors highlight the degrees of difference among 15,000 genes, with red and blue representing high and low expression levels, respectively.

More arrays needed

Research at Virginia Tech Aquaculture Center employs transcriptomics technology to examine how to enhance the welfare of cultured fish and manipulate production for the benefit of producers, processors, and consumers. Yet nutrigenomics-related research regarding aquaculture remains at an early stage of development.

A critical requirement for advancing nutrigenomics in aquaculture will be to develop rigorously validated heterologous microarrays or species-specific gene chips. Alternatively, the production of miniarrays, wherein specific groups of genes involved in nutrition and immune function are represented, may provide a more rapid and cost-effective application of the technology.

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