

# **Section I**

## **Introduction**

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# 1

## Nutrigenomics and Proteomics in Health and Disease: An Overview

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Association between diet and chronic diseases has long been recognized through epidemiological studies. Modern molecular nutrition focuses on health promotion, disease risk reduction, and performance improvement through diet and lifestyle considerations (Kussmann and Blum 2007; Ronteltap et al. 2008). New genomic, proteomic, and metabolomic techniques are now enabling us to find out more about the basis of these associations through examination of the functional interactions of food with the genome at the molecular, cellular, and systemic levels (Corthésy-Theulaz et al. 2005; Kato 2008; Mariman 2006). The human genome is estimated to encode over 30,000 genes and to be responsible for generating more than 100,000 functionally distinct proteins. While traditional nutrition research has dealt with providing nutrients to nourish populations, nowadays it focuses on improving health of individuals through diet. Modern nutritional research is aiming at health promotion and disease risk reduction and on performance improvement (Trujillo et al. 2006). Nutrigenetics questions as to how individual genetic disposition, manifesting as single nucleotide polymorphisms, copy-number polymorphisms, and epigenetic phenomena, affects susceptibility to diet. Nutrigenomics addresses the inverse relationship; that is, how diet influences gene transcription, protein expression, and metabolism. Metabolomics is a diagnostic tool for metabolic classification of individuals. A major methodological challenge and first prerequisite of nutrigenomics is integrating genomics (gene analysis), transcriptomics (gene expression analysis), proteomics (protein expression analysis), and metabolomics (metabolite profiling) to define a “healthy” phenotype (Kussmann et al. 2006; Milner 2004). The long-term deliverable of nutrigenomics is personalized nutrition for maintenance of indi-

vidual health and prevention of disease (Fay et al. 2008; Kaput 2008; Ronteltap et al. 2008). “Nutrigenomics” may offer a new approach for understanding the beneficial effects of dietary compounds on the development of severe polygenic diseases, such as cardiovascular disease, diabetes, and hypertension (Keusch 2006).

This book aims to compile current science-based nutrigenomics and proteomics in food and health. The book comprises four sections: (I) Introduction, (II) Genomics and Proteomics in Health and Diseases, (III) Food Factors–Gene Interactions, and (IV) Advanced Analytical Techniques for Nutrigenomics and Proteomics.

Chapter 1 summarizes aims and scope as well as overall highlights of this book. Chapter 2 consists of introductory *omics* in nutrition and health research. Nutrigenomics contains the three omics disciplines gene, protein, and metabolite profiling (transcriptomics, proteomics, and metabolomics) as applied to the field of nutrition and health. Furthermore, nutrigenomics forms the scientific basis for developing nutrition adapted to the specific needs of (rather large) consumer groups, be they healthy, at risk, or diseased. The three omics platforms are introduced in this chapter that also describes their application in nutritional research. Microarray-based gene expression analysis is the most mature genome-wide profiling platform. Consequently, transcriptomics in nutritional studies is widely applied when it comes to basic and preclinical research in either cell culture systems or animal models. Proteomics has evolved as an analog to genomics, from identifying all proteins present in a given sample at a given time to a global molecular analysis platform addressing functional aspects of biological systems. Comparing such variations in the proteome enables the discovery of key proteins and

the identification of modulated pathways involved, for example, in specific nutrition-related processes. Over the last two decades, proteomics has developed into an established technology for biomarker discovery, clinical applications, disease profiling and diagnostics, and the study of protein interactions and of the dynamics of signaling pathways. Metabolites represent the endpoints of metabolism and can provide information on the molecular events associated with the adaptations of the body to increased or decreased fluxes of nutrients through metabolic pathways. Metabolomics in nutrition addresses the challenge of characterizing food-related metabolic modulations. Moreover, individual metabolites such as cholesterol, glucose, and homocysteine are considered as markers for health or disease status. Nutrigenomics and nutrigenetics are key science platforms to promote health and prevent disease through nutrition that better meets the requirements and constraints of consumer groups with specific health conditions and particular lifestyles. Section II comprises three chapters on the impact of nutrigenomic and proteomic interventions on health and diseases. Chapter 3 deals with personalized nutrition and medicine. The concept of personalizing nutrition and medicine—and therefore healthcare—emerged from the human genome and haplotype projects. The results of these large-scale, international initiatives offered the hope that nutrition and medicine could be tailored to the individual. The significant advances in understanding complex biological processes relied on reductionistic approaches: hold all variables but one constant. While this strategy was successful for certain monogenic phenotypes, understanding complex systems requires analytical approaches that incorporate rather than avoid complexity. The key challenge for personalizing healthcare then is not the complexity of the data sets, but acquiring those data sets in a manner to reduce noise and increase true signals. This might best be accomplished by preselecting phenotypes based on quantitative data, or alternatively, preselecting genotypes that maximize differences in allele frequencies of candidate genes involved in nutrient metabolism or other physiological traits. The integrative whole system analyses of the data sets and new visualization methods such as shown with network analysis tools provide a path not only to perform these complex experiments, but also to develop biological insight into the outcomes. The development of nutrigenomics and genetics and the application of this knowledge will provide strategies for maintaining health and improving medical treatment of chronic diseases.

Chapters 4 and 5 discuss obesity and nuclear receptors and inflammatory genes involved in obesity-

induced inflammatory responses and pathologies. Obesity is the state of excessive formation of adipose tissues. Recent research has clarified the differentiation of adipocytes, the level of subsequent fat accumulation, and the secretion of the biologically active adipocytokines by adipocytes). In particular, it has been clarified that adipocytokines secreted by adipocytes play a significant role in the pathogenesis of diseases such as diabetes and cardiovascular diseases and are closely associated with the pathogenesis and exacerbation of ailments arising from obesity. This chapter discusses obesity and the metabolic syndrome and then describes the nuclear receptors that are most important in adipocyte differentiation and the mechanism underlying the expression of function of adipocytes affecting obesity from the viewpoint of nutrigenomics. Obesity is also a low-grade systemic chronic inflammatory condition, characterized by abnormal cytokine production, increased acute phase proteins, and other inflammatory mediators. Obesity-induced inflammation consists of a set of inflammatory immune components and inflammatory signaling pathways similar to those involved in classical inflammation, such as inflammatory cells like macrophages, inflammatory mediators like cytokines and chemokines, as well as inflammatory signaling molecules. Obesity-induced inflammation is considered to serve as the potential mechanism linking obesity to obesity-related pathologies such as insulin resistance, type 2 diabetes, fatty liver disease, atherosclerosis, some immune disorders, and several types of cancer. Chapter 5 specifically focuses on obesity-induced inflammatory components, linking to obesity-related pathologies. Adipose tissue-derived inflammatory genes/proteins such as adipocytokines and signaling molecules and the inflammatory cross-talk within adipose tissue cells through adipocytokine. Allergies affect almost 20% of the population in the developed world and allergies can be life-threatening. Individuals may be allergic to a variety of natural or synthetic molecules, such as foods, drugs, chemicals, dust, pollen, and metals. Genomic and proteomic methods are powerful techniques for the identification, characterization, and in vitro diagnosis of allergies. Chapter 6 describes molecular mechanisms of allergy and gene interactions and susceptibility to allergic responses. It also reports on recent therapeutic approaches for allergies using recombinant DNA techniques.

Section II includes various food factors–gene interactions and their impact in health and diseases. This section consists of 16 chapters that cover lipids, proteins/peptides/amino acids, carotenoids, phytochemicals, and probiotics. Chapters 7 and 8 deal with the beneficial effects of conjugated linoleic

acid (CLA) and regulation of gene transcription by fatty acids. CLA has been shown to exert various physiological functions, other than antimutagenicity, such as anticarcinogenic and antiobesity (reduction of body fat mass) activities, prevention of atherosclerosis, enhancement of immune function, and suppression of blood pressure, despite the fact that physiological properties of CLA are still limited. The physiological effects of CLA are also described along with potential health benefits of conjugated linolenic acid. Dietary fat is an important macronutrient required for the growth and development of all organisms. Excessive levels of dietary fat or imbalance in its composition (saturated versus unsaturated fat) have been related to the onset or development of several chronic diseases such as coronary artery disease, obesity, and type 2 diabetes as well as certain types of cancer. The biological functions of lipids are mainly carried out by fatty acids and/or derived signaling molecules such as ceramides, diacylglycerols, eicosanoids, and coenzyme A thioesters (acyl-CoA). The last two decades have provided evidence that major (glucose, fatty acids, amino acids) or minor (iron, vitamin, etc.) dietary constituents regulate gene expression in a hormone-independent manner. The molecular mechanisms by which fatty acids and/or their metabolites control the transcription of genes involved in their own metabolism or in carbohydrate metabolism are also described. These effects are mediated either by direct binding on transcription factors such as PPARs, LXR, HNF-4, RXR, etc. (each belonging to the nuclear receptor superfamily) or alternatively through modifications in nuclear abundance and/or activity of numerous transcription factors such as SREBP-1c, ChREBP, and NF- $\kappa$ B.

Chapter 9 focuses on amino acid biological functions as nonnutrient. Although amino acids are widely known as the building blocks of proteins, their functions in living organisms are vast as they can interact with the endocrine, neuronal, and immune systems to influence the balance between health and disease. These systems, particularly in diseased states, affect the amino acid availability and may induce pathways to alter protein synthesis. The underlying mechanism of the regulation of the biological functions is partially due to amino acid control of gene expression. This chapter reviews the importance of amino acid balance and the consequences of amino acid imbalance at the genetic level. Health and disease implications through amino acid deficiency and supplementation was explored. Many amino acid studies have reported health benefits during diseased states, such as cancer, inflammatory disorders, diabetes, gastrointestinal disorders, and muscular wasting diseases. Understanding the mechanism of amino

acid control of genes, both singly and in unison, may provide its involvement in disease progression and prevention. Many researchers have reported that food proteins and their peptides express a variety of functions in the body, including a reduction of blood pressure, antimicrobial activity, antioxidative, anti-inflammatory, antisatiety, anticancer, antiobesity, anti-allergy, modulation of immune cell functions, and regulation of nerve functions. Bioactive peptides are peptide sequences present in the intact protein that under normal circumstances do not have biological properties, but when they are released as peptides *in vitro* or *in vivo*, they exert biological activities. There is increasing commercial interest in the production of bioactive peptides from various sources such as egg, milk, cereal, and fish proteins. Chapter 10 summarizes recent advances of food-derived bioactive peptides—gene interactions and their mechanisms of actions. Although their properties and physiological effects have not been completely explored, bioactive peptides can broadly be divided into two categories: (1) peptides that exert their effects by direct physical interaction with another molecule, and (2) peptides that interfere with gene expression. Bioactive peptides that alter gene expression can do so by (1) epigenetic modification of the proteins that attach to the DNA, (2) alteration of the cell's primary signaling ligand to indirectly influence transcription factor activity, and (3) interference with cell signaling and gene expression via direct binding of peptide ligand to receptor. Understanding the behavior of dietary proteins and peptides in the intestine is also important for designing functional foods with physiological functions.

Carotenoids represent a large group of isoprenoid structures with many different structural characteristics and biological activities. To date, a wide range of carotenoids have been isolated, identified, and quantified from the extracts of fruits and vegetables commonly consumed in the world. The best known biological function of carotenoids is their established role as pro-vitamin A. Chapter 11 describes the nutrigenomic study on the anti-obesity effect of allenic carotenoids from seaweeds and vegetables, with special reference to their regulations on relative gene and protein expressions. Fucoxanthin and neoxanthin are the major carotenoids present in chloroplasts of brown seaweeds and higher plants, respectively. Fucoxanthin is the most abundant of all carotenoids, accounting for >10% of the estimated total natural production of carotenoids. The key for success of fucoxanthin will be induction of uncoupling protein 1 in white adipose tissue (WAT) and downregulation of adipokines such as TNF $\alpha$ . The regulatory effect of fucoxanthin on PPAR $\gamma$  and  $\gamma_3$ -AR in WAT is

correlated with its antiobesity and antidiabetic effects. Furthermore, the relationship between carotenoid structure and suppressive effect on the differentiation of 3T3-L1 adipose cells shows that carotenoids containing an allene bond and an additional hydroxyl substituent on the side group may show the characteristic antiobesity activity.

Chapter 12 deals with the control of systemic inflammation and chronic diseases by the use of turmeric and curcumenoids. Numerous plant-derived, but also microbially derived, substances, often referred to as chemopreventive agents, have documented anti-inflammatory effects and are believed to reduce the rate of aging and prevent degenerative malfunctions of organs and also development of acute and chronic diseases. Among these are various curcumenoids, the active ingredients in turmeric and curry-containing foods, and thousands more of hitherto little or totally unexplored substances. This chapter focuses on documented experimental and clinical effects of supplementation of turmeric, various curcumenoids, and pure curcumin. The Food and Drug Administration (FDA) has approved a health claim for soy-based food products for health benefits primarily based on epidemiological data indicating that high soy consumption is associated with a lower risk of cardiovascular diseases. Soy isoflavones also show a beneficial role in obesity, diabetes, coronary artery disease, and osteoporosis in postmenopausal women. Soy isoflavones have been shown to inhibit carcinogenesis and cancer cell growth in vivo and in vitro. It has also been found that soy isoflavones lower total cholesterol and low-density lipoprotein cholesterol, suggesting the effect of isoflavones on cardiovascular disease risk reduction. Chapter 13 presents gene expression and proteomic profiling by soy isoflavones. It has been found that soy isoflavones regulate the expression of genes that are related to estrogen regulation, organ differentiation, and fat and bone metabolism in normal cells. Soy isoflavones also inhibit the growth of cancer cells through the modulation of genes, which control cell proliferation, cell cycle, apoptosis, oncogenesis, transcription regulation, and cell signal transduction system. In this chapter, current evidence on the molecular effects of soy isoflavones as documented by nutrigenomic and nutripoteomic research is provided.

Over the last two decades more than five thousand peer-reviewed articles and tens of thousands of news articles have provided evidence for enhanced health benefits of tea consumption. At present, multiple evidences have proven the involvement of tea beverages in health promotion that are directly linked to its polyphenol content. Green tea has firmly es-

tablished its powerful strength in reducing oxidative stress, suppressing cancer-related risks, cardiovascular disease, neuronal damage, and hepatic disorders, among others. Epidemiological and clinical studies have also proven that individuals consuming tea or many form of tea polyphenols benefit from a lower incidence of cancers and other lifestyle-related diseases such as diabetes, obesity, and cardiovascular disease, among others. However, the question that is duly continued to be answered is how green tea polyphenols exert their health beneficial effect? Chapter 14 explores how green tea polyphenols modulate genome functions for protective health benefits. Is it a simple site-specific activity or alteration of a pathway that ultimately lead to altered activity of one or more secondary molecules required to maintain normal cell function or enhancing the meaningful roles of the molecules to maintain cell machinery systems? This chapter reviews how green tea polyphenols modulate genome function, gene repair, protecting genes, and exerting the roles considered auspicious, that even remained unknown until a decade ago. This chapter also lists the latest evidences in accordance with the enhanced philological functions. Reactive oxygen species are generated ubiquitously in aerobic organisms. When these cytotoxic agents overwhelm endogenous antioxidant defense systems, serious oxidative stress and damage occur as reflected by the oxidative modification of macromolecules such as lipid, protein, and DNA. Thus, it is critical that cells maintain optimal antioxidant defenses in order to reduce oxidative damage. Dietary supplementation and therapeutic use of antioxidants are emerging measures to prevent and treat oxidative stress-induced diseases. Chapter 15 describes oat avenanthramides as novel antioxidants. Oat (*Avena sativa*), although consumed in considerably lower quantities worldwide than wheat and rice, has a highly edible quality and contains high nutritional value compared to other minor grains. Over the past decade, interest of restoring oat as a natural antioxidant additive in food has been on the rise. Other than tocopherols, tocotrienols, and flavonoids, oat contains a unique group of approximately 40 different types of polyphenolic compounds called avenanthramides (AVA) that consist of an anthranilic acid derivative and a hydroxycinnamic acid derivative linked by an amide bond similar to those found in peptides. There is strong evidence that AVA are potent inhibitors of cell proliferation and inflammatory processes, especially in the endothelial cells and smooth muscle cells of blood vessels. These effects have been shown to be mediated by its inhibition of proinflammatory cytokine production and signaling. AVA have also been reported

to modulate endogenous antioxidant defense such as increasing plasma glutathione level and upregulating tissue superoxide dismutase activity, the mechanisms of which remain to be elucidated. Chapter 16 reviews cancer-preventive effects and molecular actions of anthocyanins. Anthocyanins are naturally occurring polyphenolic compounds that confer an intense color to many fruits and vegetables. A few population-based investigations have highlighted the potency of anthocyanins or anthocyanin-containing mixtures on cancer prevention or cancer risk reduction. Studies on animal models have revealed that high intake of anthocyanins or anthocyanin-containing mixtures protects against tumorigenesis of colon, skin, and mammary glands. Extensive studies in cancer cell lines have shown the inhibitory effects of anthocyanins or anthocyanin-containing mixtures on the growth of cancer cells derived from malignant human tissues including vulva, stomach, colon, lung, breast, leukemia, uterus, mouth, and prostate. Recent molecular data have demonstrated that anthocyanins could modulate oncogenic cellular signaling transduction pathways (MAPK and EGFR), transcriptional factor activations (AP-1, NF- $\kappa$ B, p53), and downstream gene expressions (COX-2, iNOS, Bax). These molecular actions are involved in the processes of cell transformation, inflammation, and apoptosis, which provide molecular basis for the cancer-preventive effects of anthocyanins.

Chapter 17 deals with how food components activate capsaicin receptor, transient receptor potential vanilloid subtype 1 (TRPV1). Capsaicin is a pungent principle of hot pepper. Capsaicin exerts several biological activities such as causing burning sensation, stimulating primary afferent neurons conducting chemical pain or hotness, enhancing energy metabolism, showing protection against stomach mucosa, inducing apoptosis in some cancer cells, and so on. Many of them are exerted through capsaicin receptor activation. Because obesity is one of the serious factors on lifestyle-related diseases such as hypertension, stroke, diabetes, and hyperlipemia, this chapter focuses on the thermogenic action or body fat lowering effect of capsaicin. Thermogenic action of capsaicin is thought to be exhibited through activation of TRPV1. From the discovery of TRPV1 gene in 1997, food components activating TRPV1 have been vigorously investigated. There are lists of capsaicinoids of hot pepper, piperine of black pepper, eugenol of clove, ginsenosides of Asian ginseng, and evodiamine of *Evodia rutaecarpa*, among others. Capsiate inhibits accumulation of body fat in humans. Anthocyanins are the largest group of water-soluble pigments in the plant

kingdom. In the human diet, they are derived primarily from a wide variety of plant sources including crops, beans, fruits, vegetables, and red wine, and their effects are also diverse and important to health promotion. Chapter 18 focuses on blackcurrant (*Ribes nigrum* L.) anthocyanins because blackcurrant is rich in it and blackcurrant is consumed in many countries. This chapter provides a review of the newly discovered effects of anthocyanins including their antiobesity effect, antidiabetes effect, and vision improvement. Chapter 19 describes various biological activities of licorice. Licorice, the root of the leguminous *Glycyrrhiza* plant species, is one of the most useful and popular plants in both Asia and Europe, and the history of its consumption as a traditional medicine and food goes back to over 4,000 years to the era of ancient Mesopotamia and Egypt. Licorice contains triterpenes and phenolic constituents such as glycyrrhizin, a well-known typical active constituent of licorice, and the species-specific constituents glabridin, glycycomarin, and licochalcone A in *G. glabra*, *G. uralensis*, and *G. inflata*, respectively. In *G. glabra*, the species specific compound is glabridin. Various studies have shown the biological effects of glabridin, licorice, or its extracts. These include antioxidative, estrogen-like, anti-inflammatory and anti-*Helicobacter pylori* activities. Hydrophobic flavonoids from *G. glabra* are extracted and concentrated, and the resulting extract is referred to as licorice flavonoid oil (LFO). DNA microarray analysis suggests that the antiobesity effects of LFO are attributable to suppressed fatty acid synthesis and activated fatty acid catabolism in the liver. LFO has also received FDA approval as a new dietary ingredient in the United States in 2006. Therefore, further studies that elucidate the mechanism of LFO containing licorice hydrophobic flavonoids would contribute to the efficient application of LFO in the treatment of metabolic syndrome. Isopentyl diphosphate and its isomer dimethylallyl diphosphate are the universal five-carbon precursors of isoprenoids. Isoprenoids are contained in many herbal plants, and several isoprenoids have been shown to be available for pharmaceuticals, for example, artemisinin and taxol as malaria and cancer medicines, respectively. Various isoprenoids are contained in many plants not only for herbal use but also for dietary consumption. Chapter 20 reports on several bioactive isoprenoids, contained in herbal or dietary plants, which have possibilities to ameliorate metabolic disorders via activation of ligand-dependent transcription factors, that is, nuclear receptors. Chapter 21 reviews anti-inflammatory and anticarcinogenic potential of citrus coumarins and

polymethylated flavonoids. Citrus fruits are well known to contain an array of secondary metabolites in terms of their chemical structures and biological activities, which biosynthesize monoterpenes (*d*-limonene, etc.), triterpenes (limonoids), flavonoids (nobiletin, hesperidin, etc.), coumarins (auraptene, bergamottin, etc.), and carotenoids ( $\beta$ -carotene,  $\beta$ -cryptoxanthin, etc.). Ample evidence obtained from *in vitro* and *in vivo* experiments as well as epidemiological surveys indicates that frequent intake of citrus fruits is beneficial to human health. These citrus compounds are hydrophobic and thus tend to localize in gastrointestinal mucosa in rodents as compared to general polyphenols present. Thus, abundant data have revealed both auraptene and nobiletin to be highly promising citrus components with anti-inflammatory and anticancer activities, with notable action mechanisms and effects on metabolism. One of the distinct characteristics of citrus fruits, as compared with other foods, is the variety of active constituents in terms of chemical characteristics and bioactivities. Thus, combination studies using different types of citrus components for enhancing each efficacy are warranted, such as combining nobiletin (targeting COX-2 transcription) and auraptene (targeting COX-2 translation) to determine their additive or even synergistic effects.

Food and Agricultural Organization of the United Nations and the World Health Organization define *probiotics* as “live microorganisms which when administered in adequate amounts confer a health benefit on the host.” The majority of probiotics are strains of lactobacilli or bifidobacteria and they are administered in food products such as yogurt, milk drinks, and cheese, as well as capsules and tablets. The effect that beneficial microbes have on health maintenance is becoming more and more recognized, given the realization that so many organisms reside in the human body. The reintroduction of beneficial organisms (probiotics) to the host has mostly been via food and dietary supplement products, and thus relevant to nutrigenomics. Chapter 22 discusses some examples of how probiotic microbes and their proteinaceous and other by-products contribute to health. As more human and microbial genomic information emerges, it will become clearer under what conditions probiotic organisms interface with the host in an optimal way.

Section IV highlights recent advances in analytical techniques for nutrigenomic and proteomic research in food and health. Chapter 23 describes microarray as a powerful tool for studying the functions of food and its nutrients. Microarray is a high-throughput genomic tool. It can be used for profiling and monitoring the expression levels of tens and thousands

of genes (entire genomes). It can also be used to determine the influence of food nutrients and/or bioactive compounds (food factors) on metabolic pathways and to understand how food nutrients and factors maintain homeostatic control of gene expression levels. Microarray technology is a “nutrigenomics” tool and can be used to investigate the levels of transcripts in particular. Typically, food is a complex and variable mixture of nutrients and other components. Most food factors are weak dietary signals and must be considered in the context of chronic exposure. Microarray analysis clearly indicates the effects exerted by food factors and nutrients on metabolic pathways via transcriptome modifications. Moreover, the results of microarray analysis suggest that food factors and nutrients influence the metabolome because alterations in the transcriptome cause changes in the metabolome. Therefore, microarray analysis is one of the most convenient tools for inferring the proteome and metabolome. This technology will enhance understanding of the manner in which food and nutrition influence metabolic pathways and how these factors maintain homeostasis under normal conditions or diet-related or non-diet-related disease conditions. Chapter 24 highlights challenges and current solutions in proteomic sample preparation. Proteomics is a discipline of relatively short history, but it holds great promise in elucidating biochemical information via quantitative determinations of the whole collection or representative proteins. One of the common objectives in proteomic studies is the discovery of biomarkers. Although biological systems are extremely complex, and the technology challenges are still many, hundreds and thousands of biomarker candidates are being discovered with advancements made in proteomic technologies. One of the major hurdles in proteomics is the identification of true biomarkers via analytical and clinical validation studies. This chapter reviews some critical aspects of biomarker determination using proteomic methods and some examples of new developments in the proteomic sample preparation techniques, particularly the “pressure cycling technology.” In the past few years, many high-throughput techniques have been developed and applied in biological studies. These techniques such as “next generation” genome sequencing, chip-on-chip, and microarray, among others, can be used to measure gene expression and gene regulatory elements in a genome-wide scale. Moreover, as these technologies become more affordable and accessible, they have become a driving force in modern biology. Traditionally, biologists described these relationships between a limited number

of genes or proteins using a descriptive language. With the huge amount of data produced by high-throughput techniques, biologists have to deal with thousands of biological relations in a single experiment. In this situation, the traditionally descriptive ways for biological relations are not sufficient to deal with the huge number of relations under study. The only way to deal with a large amount of relations is through mathematical representations and computations by researchers in biological sciences. Chapter 25 first introduces basic computational concepts and then illustrates the procedures and computational techniques for high-throughput data analysis, using examples from cancer research. Proteomics is central to nutrigenomics and has the potential to explain many of the physiological changes associated with nutritional stimuli. In proteomics, all proteins expressed in a cell or tissue are analyzed to identify the presence or absence of some key proteins that provide information about the early stages of disease or different conditions. However, a comprehensive analysis of peptides and small proteins of a biological system corresponding to the respective genomic information was missing in proteomics. Chapter 26 introduces the concept of peptidomics. The term *peptidomics* was first introduced as a subset of proteomics for the description of peptides as gene products in February 2000 at the ABRF conference “From Singular to Global Analysis of Biological Systems.” This was coined as a short version of “peptide proteomics” and was defined as the technology for comprehensive qualitative and quantitative description of peptides in a biological sample. Studies of peptidomics cover peptides with low-molecular-weight and small proteins (0.5–15 kDa), since peptides among the families of hormones, cytokines, and growth factors play a central role in many physiological processes. In addition, application of peptidomics knowledge to the nutrient effect may yield potential information about the diet-induced peptide changes and may act as good biomarkers. However, the field of peptidomics is relatively new and has potential to progress in future with the advent of high-throughput mass spectrometry-based technologies coupled with bioinformatics and genomic databases.

Completion of human genome project coupled with the advancement in “omic” technologies enabling researchers to analyze the complex interplay of metabolism, gene expression, and function, and more broadly, genetic diversity within and between human populations. Nutrition science has broadened to the new discipline of nutrigenomics, which allows an in-depth understanding of metabolism, health, and pathophysiology of disease that ultimately could be

used to prevent or treat diseases. The major goal of this book is to comprehensively understand the response of the body’s genes to diets and food factors through various omics technologies such as transcriptomics, proteomics, and metabolomics. This will contribute to the development of new preventive and therapeutic strategies for both pharmacological and nutritional interventions (Bauer et al. 2004; Mariman 2006; Milner 2007).

The editors have succeeded in bringing together many renowned international experts in nutrigenomics and proteomics in health and diseases. We are grateful to all the authors for their state-of-the-art compilation of recent rapid development in this field. We believe that this book certainly deserve a broad readership in the disciplines of nutrition, pharmacology, nutraceutical/functional foods, food science, biology, biochemistry, biotechnology, and life science. This book could also be used as a reference book by senior undergraduate and graduate students as well as nutraceutical and pharmaceutical industry.

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