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# Knowledge and Perception of Undergraduate Students towards Nutrigenomics for Personalized Nutrition in Federal University of Agriculture, Abeokuta, Ogun State

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## CERTIFICATION

This is to certify that this project work was carried out by **ADEMILUYI, DARE DAMILOLA** and is approved in partial fulfillment of the requirement for the award of B.Sc. Degree in Nutrition and Dietetics of the Department of Nutrition and Dietetics, College of Food Science and Human Ecology, Federal University of Agriculture Abeokuta, Ogun State, Nigeria under my supervision.

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**PROF. (MRS) I. O. OLAYIWOLA** **DATE**

**(Supervisor)**

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## DEDICATION

I dedicate this work to the Almighty God and my dearest parents **Mr. and Mrs. ADEMILUYI** who through their advice, love, care and financial assistance have made me be where I am today, I pray that the good Lord will continue to keep and guide them for me, Amen.

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All praise to God, The Almighty; who kept me this far, under whose guidance my education got to this level. The success of this program was made a reality by several people who constantly sowed productive seeds into my life and watered the seeds, giving it an avenue for growth, in terms of hospitable environments.

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I especially acknowledge all who we have indeed walked and worked together as colleagues, I say a big thanks to you. May God keep you all in his love and my prayer is that God will continue to bless and keep you people for me. Amen. Remain rapturous in Jesus name.

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## ABSTRACT

**Nutrigenomics is a scientific study of the molecular interaction between genes and nutrients. Personalized Nutrition is the practice of adapting the diet to meet specific nutritional needs or prevent chronic disease in individuals or genetic subgroups based on the results of genetic testing. Few studies have examined how college students perceive the possibility of targeted recommendations based on their genetic make-up. Multiple companies are now offering personalized dietary advice based on the results of genetic testing. College students, who are educated and more familiar with new technology, may provide valuable information about perceptions toward nutrigenomic technology while it is still in its early stages of development. The purpose of this study was to examine the knowledge and perception of undergraduate students towards nutrigenomics for personalized nutrition. Participants in this study were students from the Federal University of Agriculture, Abeokuta Ogun state who completed a paper survey questionnaire administered. A multistage sampling technique was used to select 400 respondents for the study. Analyses of results were completed using the Statistical Package for Social Sciences (SPSS) version 24. Independent sample t-tests were conducted comparing the mean scores of genetics knowledge and nutrigenomics perception among gender groups, and groups who may either be familiar with nutrigenomics for personalized nutrition therapy or not. Pearson correlation coefficients were calculated for the relationship between genetics knowledge scores and perception of nutrigenomics scores. ANOVA were be used to determine whether there are differences in genetics knowledge and perceptions toward nutrigenomics among groups of different class levels and different colleges.Participants ranged from 18 to 35 years old with a mean age of 21.17 years (n= 305). Study reveal that more than half (61.3%) of the respondents were females, most of them were between the ages of 18 and 23 years accounting for 81%.Based on survey results, a negative correlation was found, $r$ (398) = -0.037, $p \leq 0.461$, indicating a non-significant negative linear relationship between positive perceptions toward nutrigenomic testing and higher genetics knowledge scores. About 63% reported some familiarity with nutrigenomic testing. There was a significant effect for students who indicated participation in a college-level genetics course, ($p$ = 0.04)..However, due to multiple barriers, and especially excessive cost to consumers, public support of "omics" technology is unclear.Awareness about nutrigenomics for personalized nutrition should be done through mass media to inform the public about this field because majority of Nigerians are not aware that this field even exists.**

***Keywords***:- *Nutrigenomics, Personalized Nutrition, Knowledge, Perception.*

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# CHAPTER ONE

# INTRODUCTION

Nutrition is an important environmental factor that has profound implications for human development and health. Chronic exposure to certain dietary patterns, such as imbalanced energy or lack of essential nutrients leads to metabolic stress. This type of stress is closely related to the occurrence and progression of various chronic non-communicable diseases and aging. Metabolic stress affects the regulation of gene expression, leads to cellular and physiological changes, but rarely causes acute and harmful damage, such as Mutations of the genome (Sales *et al.,* 2014; Park *et al.,* 2017; Wilkins, 2017). Nutrigenomics is an emerging science that seeks to understand how dietary components and metabolites affect gene expression and interact with the genome. This omics science creates a link between factors relating to food and its genetic response. Understanding the interactions between genes and nutrients is important to learn how to regulate metabolic processes that contribute to age-related disease risk factors such as obesity, cardiovascular disease and inflammation(Park *et al.,* 2017).

The new science of nutrigenomics teaches us what certain foods tell our genes. What we eat directly determines the genetic messages our bodies receive. These messages, in turn, control all of the molecules that make up our metabolism: the molecules that tell the body to burn or store calories. In turn, being able to learn this language and control the messages and instructions it gives during body processes and metabolism can radically change how foods interact with the body, lose weight and optimize your health (Neeha & Kinth, 2014).

Food has been one of the most vital environmental factors for humans. Human history has evolved through genetic adaptations to diet consumed and this have sculpted the human genetic profile and influenced a variant of human traits. Local adaptations to regionally specific dietary components might have been one critical shaping force of the human genome, driving population differentiation and laying the genetic basis for human diversity. Genomic adaptations to environmental factors through the increasing frequency of advantageous mutations in the human population usually take hundreds of generations (thousands of years), whereas societal, cultural, and dietary transformations in human society are ever-accelerating (Ye & Gu, 2011). Food consumption patterns and the environment predisposition have been the two main factors that are affecting the broad spectrum of human health or a cause of illness to an individual. Studies in the nutritional area have increased the understanding of how to maintain healthy a group of individuals that live in different dietary conditions (Gibney& Walsh, 2013).

Maladaptation of the lagging genome to rapid dietary shifts may underlie a wide range of so-called civilization diseases, such as diabetes, obesity, cardiovascular diseases, and cancers. Comprehensive measures have been inputted into the examination of human diet and it genomic adaptations with the aim of explicate the basis of complex disorders through genetic profiling and modifying techniques and strategies of disease management through personalized medicine and nutrition(Ye & Gu, 2011). A paradigm shift in nutritional sciences is underway. “Nutrigenomics is the study of the relationship between gene expression and nutrition, proposes that disease can be prevented and reversed by drastically altering the nutritional environment”. Basic premises include people are genetically predisposed to develop some type of chronic illness, expression of these genes is largely influenced by the environment, food is a large part of this environment that affects gene expression, and whole-food, plant-based, nutritionally dense diets positively influence gene expression and the incidence of disease. “Nutrigenomics has given rise to "nutritional medicine" or "nutritional therapy," a system of healing based on the belief that food, in its whole and natural form, provides the substance needed to obtain and maintain a vibrant state of health”(Koithan, 2017).

The Human Genome Project of the 1990s, which sequenced all of the DNA in the human genome, kick-started the science of nutrigenomics. By 2007, scientists had discovered numerous interrelationships between genes, diet and disease (Neeha and Kinth, 2014; Sales et al., 2014). Nutrigenomics brings new

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terminology, novel experimental techniques and a fundamentally new approach to nutrition research, such as: High-throughput technologies that allow the global study of gene expression in a cell or organism. Nutrigenomics would require a combined effort from people in genetics and the public health, food science and culinary industries. It is very easy to prepare great tasting food. Put in some lard or butter and it will taste good. The challenge is to take out the fat and create healthy, but also great-tasting foods." Therefore, a shift in public health is urgently needed, and with the rising prevalence of obesity and chronic diseases such as type 2 diabetes, nutrigenomics could be prove to be the panacea of the future (Neeha&Kinth, 2014).

Genetic variation underlies the enormous range of phenotypic diversity and disease susceptibility in human populations. It is estimated that any two (2) individuals differ in 1-3% of their genome. Each person is estimated to carry around 250-300 genes with loss-of-function variants, 50-100 of which are involved in inherited diseases. With the rapid advancement of sequencing technologies, particularly the advent of next-generation and next-generation sequencing platforms, extensive efforts have been expended to unravel human genetic variations and understand their general characteristics, powers to shape their pattern, and most importantly, their clinical consequences. Ye and Gu (2011) claimed that genome-wide association studies have been successful in linking some genetic variations to complex traits and common diseases. This happens to be truth as majority of researches emphasis on the linking if genetic variant to some complex health disorder. Despite the difficulties in explaining all of the genetic implications, it still promises to elucidate the genetic architecture of human health, provide interesting hypotheses and suggest potential directions for medical research (Ye &Gu, 2011).

Interestingly, dietary and nutritional effects can be passed on to the next generation. The effects of diet on the body are also mediated by epigenetic mechanisms. Epigenetic mechanisms can mediate between nutrient availability and phenotype throughout life; However, little is known about how diet plays a role in longevity and aging via epigenetic mechanisms. This project aims to raise awareness of the growing evidence and use diverse data to make a valid proposal and enlightenment on the numerous dietary factors such as calorie restriction, nutrient intake/utilization and metabolism and polyphenols with other bioactive compounds that Epigenetic markers may influence influencing nutritional therapy for personalized nutrition (Park et al., 2017).

*A. Statement of Problem*

Experts believe that nutrigenomics has great potential to reduce the incidence and impact of complex diseases, including non-communicable diseases, which currently account for almost two-thirds of deaths worldwide (Bauer et al., 2014). Many scientists predict that new developments will soon emerge that will promote the health and well-being of the general public, genetic subgroups, and individuals based on their genetic makeup (Fenech, Foundation, El-Sohemy, Cahill, & Ferguson, 2011). However, public support for genomics technology, particularly by emerging adults, will have an impact on the successful implementation of personalized nutritional care, and it remains uncertain whether enough groundwork has been established to justify the use of nutrigenomics in nutrition (Gudde, 2009; Wilkins , 2017). Many barriers need to be addressed for nutrigenomics to have a positive impact on global health. For example, most Americans are unaware that nutrigenomics technologies exist, although several companies now offer these tests (San-Cristobal, Milagro, Martínez&Uk, 2013). Another issue is the complexity of the field, which requires extensive knowledge of nutrition, genetics and biochemistry, making it difficult to understand even for highly educated individuals (Keith, 2013). It was also noted that there are concern whether the aim of matching certain nutrients to individual genotypic data is achievable, or not, perhaps it might even be a burden to the society. Some professionals believe that claims cannot yet be scientifically proven and raise significant ethical dilemmas, including concerns about cost, privacy, and misuse of genetic information (Pavlidis et al., 2015).

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Given the depth of knowledge required to understand nutrigenomic processes, perhaps college students who are better educated (Ryan & Bauman, 2016), are more exposed to new scientific and technological advances (Johnson et al., 2013), and engage in a at a more influential stage in their lives may find these concepts particularly appealing. As the youngest population of educated adults, the college population is perhaps a good starting point for assessing basic knowledge and perceptions related to nutrigenomics. A concerted effort by the scientific community is required to strictly follow the guidelines for experimental design, analysis and data storage for nutrition research. This strategy will help to create a solid database useful for clinicians and dieticians (Shamim et al., 2017).

*B. Justification of the Study*

This study will increase public support for nutrigenomics technology, particularly among emerging adults, which will be necessary for the successful implementation of this technology and the achievement of the highly desirable goal of personalized nutritional delivery (Pavlidis et al., 2015). Because the study of nutrigenomics requires a solid foundation in nutrition, genetics, and biochemistry, this field is often difficult to understand and appreciate, even for highly educated individuals. Therefore, this study will provide students and other healthcare professionals with an awareness of nutrigenomic technology and its application in nutritional therapy (Ferguson et al., 2016). Given the depth of knowledge required to understand nutrigenomics processes, college students who are better educated (Ryan & Bauman, 2016) and more exposed to new scientific and technological advances (Johnson et al., 2013) might these concepts find attractive, making them a critical group of potential future consumers.

The students also form a very diverse and influential population, coming from a wide range of cultural and seriocomic backgrounds. Therefore, examining the knowledge and perceptions of university students could help researchers and healthcare providers strategize, identify future opportunities, and address potential challenges in this rapidly evolving scientific field.

*C. Objectives of the Study*

a) Broad objective

To assess the knowledge and perception of undergraduate students towards nutrigenomics for personalized nutrition therapy in Federal University of Agriculture, Abeokuta, Ogun State

b) Specifics objective

The specific objectives of this study are to;

- assess the socio-demographic characteristics of the respondents,
- examine the awareness and perception of university students toward Nutrigenomics for Personalized Nutrition,
- evaluate various factors influencing the awareness about Nutrigenomics for personal nutrition and
- evaluate the effect of the knowledge of genetics among respondents towards the understanding of nutrigenomics.

*D. Operational definitions*

Awareness: having knowledge that something exists or being familiar with a subject at present based on information or experience; Nutrigenomics awareness measured through survey questions (Al-shammari, 2013).

Knowledge: facts, information, and skills acquired through experience or education; genetics knowledge measured through a series of survey questions (Al-shammari, 2013)

Perception: a way of regarding, understanding, or interpreting something; a mental impression; perceptions toward nutrigenomics measured through a series of survey questions (Al-shammari, 2013).

Nutrigenomics Test: a genetic test that examines an individual's genome, allowing for personalization of their nutrition care (Wilkins, 2017).

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Personalized Nutrition Care: the practice of adapting the diet to meet specific nutritional needs or prevent chronic disease in individuals or genetic subgroups based on the results of genetic testing

Nutrigenomics: The scientific study of the molecular interaction between genes and nutrients (Neeha & Kinth, 2014).

Nutrigenetics: The scientific study of the relationships between genes, diet, and health outcomes (Neeha & Kinth, 2014).

Metabolomics: Investigates the metabolome that consists of all of non-proteinaceous, small molecules present in a biological system. Changes in the metabolome content reflect the biological responses to external stimuli (nutrients among others), which involves altered gene expression and protein production/ activity associated with metabolic pathways (Oleaga *et al.*, 2012).

Proteomics: Analyses all the proteins in a biological system, their interactions and their functional states although effectively, usually only the most abundant subset of 300 or so proteins is relatively easily analyzed(Oleaga *et al.*, 2012).

Epigenetics: Investigates the genome modifications that are copied from a generation to another but not implying changes in DNA sequencing (Sales *et al.*, 2014).

Transcriptomics: Investigates gene expression changes at the mRNA level in response to different stimuli. Utilizes a variety of technologies, most commonly microarrays and next-generation sequencing (Sales *et al.*, 2014).

Risk: Exposure to the chance of injury, loss, or undesirable outcome.

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# CHAPTER TWO

# LITERATURE REVIEW

*A. Background of the Study*

Science as related to geneticinformation, knowledge and gene metabolic pole are emerging in an accelerated pace. New technologies and scientific discoveries deepen our understanding of how nutrients and dietary patterns affect the maintenance of health and the development of disease. Many omics approaches such as transcriptomics, proteomics and metabolomics will help us to understand the interactions between nutrients and the genome (Academy, 2014).

Nutrigenetics and nutrigenomics are defined as the science of the effect of genetic variation on the dietary response, or the role of nutrients and bioactive food compounds in gene expression (Fenech et al., 2011). The use of this genomic information along with high-throughput omic technologies enables the acquisition of new insights aimed at gaining a better understanding of the interactions between nutrients and genes by genotype, with the ultimate goal of providing personalized nutritional strategies for optimal health and disease develop prevention (Trujillo et al., 2006; Academy, 2014).

Three key factors underpin nutrigenetics and nutrigenomics as an important science. First, there is massive variant in the inherited genome that range between ethnic groups and individuals, have a considerable effect on nutrient bioavailability and metabolism. Second, people vary greatly in their food/nutrient availability and choices, based on cultural, economic, geographic, and taste perception differences. Third, malnutrition (deficiency or excess) itself can affect gene expression and genome stability; The latter leads to mutations at the gene sequence or chromosomal level that can cause abnormal gene dosage and gene expression, leading to unfavorable phenotypes during the different life stages (Fenech et al., 2011).

Genotyping alone is not enough to personalize nutrition for improved health.1 Understanding and manipulating how nutrition affects an individual's phenotype requires technologies that can detect the processes from the transcription and synthesis of proteins influenced by the genetic blueprint the identification of metabolites that tell us what happened, both abnormal and normal. As new scientific discoveries and technologies continue to inform the science of nutritional genomics, translating these scientific discoveries into practical clinical application requires gathering the same rigorous evidence that forms the backbone of dietary practice (Academy, 2014; Fenech et al., 2011) .

Dietary changes throughout human history have been suggested to play an important role in human evolution. Genetic variations caused by dietary adaptations during human evolution could have important health implications in today's society. The advancement of sequencing technologies and the rapid accumulation of genomic information present an unprecedented opportunity to comprehensively characterize genetic variations in human populations and to unravel the genetic basis of human evolution. A number of selection detection methods based on different theoretical models and exploiting different aspects of selection signatures have been developed (Ye &Gu, 2011). The use of these method at species and population levels have led to the identification of Human-specific selection events that distinguish humans from non-human primates and local adaptation events that contribute to human diversity. Examination of candidate genes has revealed paradigms of adaptation to specific dietary components, and genome-wide selection scans have confirmed the prevalence of dietary selection events and provided many more candidates awaiting further investigation. Understanding the role of nutrition in human evolution is fundamental to the development of evidence-based, genome-informed nutritional practices in the age of personal genomics (Ye &Gu, 2011).

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Nutrigenetics and nutrigenomics hold promise for better nutritional advice for the general public, genetic subgroups, and individuals (Fenech et al., 2011; Ye &Gu, 2011). In the future, the integration of nutrition and genomics may lead to increased use of personalized diets to prevent or delay the onset of disease and to optimize and maintain human health. The aim of this chapter is to provide an overview of this novel approach to nutrition (Fenech et al., 2011). In addition, we will also include the most relevant results from our research on the nutrigenomic effects of food polyphenols on cancer cells. In addition to essential nutrients such as calcium, zinc, selenium or vitamins, there are a variety of classes of non-essential nutrients and bioactive components such as polyphenols that appear to have a significant impact on health (Trujillo E et al., 2006). These bioactive components are known to modify multiple cellular processes associated with health and disease prevention, including carcinogen metabolism, hormone balance, cell signaling, cell cycle control, apoptosis, and angiogenesis. Our studies focus on highlighting the molecular mechanisms underlying the chemopreventive effects of these bioactive food compounds (Ye &Gu, 2011).

Food is one of the most important environmental factors for humans. Genetic adaptations to the diets consumed throughout human history have shaped the human genome and influenced a variety of human traits. Local adaptations to regionally specific dietary components may have been a key formative force of the human genome, driving population differentiation and laying the genetic basis for human diversity. Genomic adaptations to environmental factors through the increasing frequency of beneficial mutations in human populations typically take hundreds of generations (thousands of years) while societal, cultural, and dietary changes in human society are accelerating (Ye &Gu, 2011). Food intake and the environment are the two main factors that affect an individual's health or illness. Studies in the field of nutrition have increased understanding of how a group of individuals living under different dietary conditions can remain healthy (Gibney& Walsh, 2013).

*B. Overview of Nutrigenetics and Nutrigenomics Nutrigenetics*

The term nutritional genomics is often used as an umbrella term for two main areas of research: nutrigenomics and nutrigenetics. However, it is important to note the difference between the terms nutrigenomics and nutrigenetics because while these terms are closely related, they are not interchangeable. Nutrigenomics focuses on the effects of nutrients on genes, proteins, and metabolic processes, while nutrigetics involves determining the impact of individual genetic variations on the diet-disease interaction (Oleaga et al., 2012). For example, nutrigenomics researchers study the role of nutrients in gene expression, and nutrigetics researchers determine how genetic polymorphisms (mutations) affect the response to nutrients (Oleaga et al., 2012).

In addition, other terms such as epigenetics, transcriptomics, proteomics or metabolomics appear when reviewing scientific literature. They all describe processes, new tools or situations in this emerging field of nutrition. The ultimate goal is to (i) reconcile the nutriome (i.e., the combination of nutrient intakes) with the current genome status (i.e., inherited and acquired genome) so that genome maintenance, gene expression, metabolism, and cell function can proceed normally and homeostatically sustainably, and ( ii) better interpretation of data from epidemiological and clinical intervention studies on the health effects of dietary factors, which can help revise recommendations for personalized nutrition (Fenech et al., 2011; Oleaga et al., 2012).

The basic hypotheses underpinning the science of nutrigenetics and nutrigenomics are as follows:

Diet can affect health by directly affecting the expression of genes in critical metabolic pathways and/or indirectly by affecting the occurrence of genetic mutations at the base sequence or chromosome level, which in turn leads to changes in gene dosage and gene expression.

The health effects of nutrients and nutriomes (nutrient combinations) depend on inherited genetic variants that alter the uptake and metabolism of nutrients and/or the molecular interaction of enzymes with their nutrient cofactor and thus the activity of biochemical reactions.

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Better health outcomes can be achieved when nutritional requirements are individually tailored for each individual, taking into account both his/her inherited and acquired genetic characteristics according to life stage, dietary preferences and health status (Fenech et al., 2011).

Nutritional genomics is a relatively new and very fast-moving field of research, linking molecular biology, genetics and nutrition (Fenech et al., 2011; Oleaga et al., 2012). It provides a genetic understanding of how diet, nutrients, or other dietary components affect the balance between health and disease by altering the expression and/or structure of an individual's genetic makeup. The conceptual basis for this new branch of genome research builds on the following premises (Oleaga et al., 2012)

a) Nutrigenetics

It is important to note the difference between the terms nutrigenomics and nutrigenetics because, while these terms are closely related, they are not interchangeable. Nutrigenetics specifically studies the modifying effects of heredity (or acquired mutations in cancer) in nutrition-related genes on micronutrient intake and metabolism, as well as dietary effects on health (Fenech et al., 2011). Nutrigenetics focuses on the effects of genetic variation on binomial diet/disease, or dietary requirements and recommended intakes for individuals and populations. To achieve its goals, the methodology used in nutrigenetics involves the identification and characterization of genetic variants associated with specific nutrients or food components or responsible for a differential response to specific nutrients or food components (Academy, 2014; Fenech et al., 2011 ; Oleaga et al., 2012) We live in a time when it is becoming increasingly affordable to have one's genome analyzed to provide information about a wide range of critical mutations (e.g. variants) in critical genes involved in nutrient metabolism and signaling pathways that require micronutrients as cofactors (Oleaga et al., 2012). Gender itself is a critical genetic variation affecting micronutrient requirements for health maintenance (Fenech et al., 2011). The main challenge is to determine whether it is possible to make good use of this information to provide reliable and predictable personalized nutritional recommendations for specific health outcomes.

These variations, commonly referred to as polymorphisms, include single-nucleotide polymorphisms (SNPs), differences in copy numbers, inserts, deletions, duplications, and rearrangements or reorganizations. SNPs are undoubtedly the most common, as they occur every 1,000 base pairs. These differences can determine an individual's susceptibility to a disease related to diet or one or more dietary components, as well as affect the individual's response to dietary changes. There is some parallelism between nutrigenetics and pharmacogenetics, although it is more difficult to conclude in the field of nutrition, as there are important differences between drugs and food components, such as chemical purity, number of therapeutic targets, and duration of exposure, among others (Fenech et al ., 2011; Oleaga et al., 2012; National Institutes of Health (NIH), 2012).

An important new aspect of nutrient-gene interaction studies with the potential for intra- and transgenerational effects is epigenetics (Fenech et al., 2011). Epigenetics refers to the processes that regulate how and when certain genes are turned on and off, while epigenomics refers to the analysis of epigenetic changes in a cell or a whole organism. Epigenetic processes have a powerful impact on normal growth and development, and this process is deregulated in diseases such as cancer (Riscuta, 2016; Sales et al., 2014). Diet alone or through interaction with other environmental factors can cause epigenetic changes that turn certain genes on or off. The epigenetic silencing of genes that would normally protect against disease could make people more vulnerable to developing that disease later in life. The heritable and diet-modifiable epigenome is the global epigenetic pattern determined by global and gene-specific DNA methylation, histone modifications, and chromatin-associated proteins that control the expression of housekeeping genes and repress the expression of parasitic DNA such as transposons (Fenech et al., 2011).

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One of the best-described examples of the action of SNPs is the relationship between folic acid and the gene encoding MTHFR (5,10-methylenetetrahydrofolate reductase) (Riscuta, 2016). MTHFR plays a role in providing 5-methylenetetrahydrofolate, which is required for remethylation of homocysteine to methionine. Methionine is essential for many metabolic pathways, including the production of neurotransmitters and the regulation of gene expression. Folic acid is essential for the efficient functioning of this MTHFR. There is a common polymorphism in the gene for MTHFR that results in two protein forms: the wild-type (C), which functions normally, and the thermally labile version (T), which has significantly reduced activity. People with two copies of the wild-type gene (CC) or one copy of each (CT) appear to have normal folate metabolism. Those with two copies of the unstable version (TT) and low in folate accumulate homocysteine and have lower methionine, increasing their risk of vascular disease and premature cognitive decline (Jacques et al., 2002; Sales et al., 2014; Riscuta, 2016). For example, in people with low folic acid intake, TT homozygotes have higher serum homocysteine levels compared to other genotypes, which would lead to an increased risk of cardiovascular disease.

Lack of methylation due to deficiency of methyl donors (eg, folate, vitamin B12, choline, and methionine) or inhibition of DNA methyltransferases during life results in transposon activation and promoter silencing when the activated transposons insert adjacent to a housekeeping gene promoter] . As a consequence of these stochastically occurring glitches, there is an inexorable shift toward global DNA hypomethylation and silencing of tumor suppressor genes with aging, resulting in changes in genotype (due to chromosomal missegregation), gene expression profile, cellular phenotype, and an increased risk of cancer (Park et al., 2017).

b) Nutrigenomics

Nutrigenomics is the application of genomics in the field of nutritional research that allows associations between specific nutrients and genetic factors, e.g. how food or food ingredients affect gene expression. Nutrigenomics allows for a better understanding of how diet affects metabolic pathways and how this process dies down in diet-related diseases (Neeha&Kinth, 2014). It is an attempt to study the genome-wide influences of diet and aims to identify the genes that influence diet-related disease risk at the genome-wide level and to understand the mechanisms underlying these genetic predispositions (Shamim et al., 2017). Nutrigenomics will also identify the genes involved in physiological responses to nutrition and the genes in which small changes, called polymorphisms, can have significant consequences for nutrition and the influence of environmental factors on gene expression.

The field of nutrigenomics spans multiple disciplines and includes dietary effects on genome stability (DNA damage at the molecular and chromosomal levels), epigenome alterations (DNA methylation), RNA and micro-RNA expression (transcriptomics), protein expression (proteomics), and metabolite alterations (metabolomics), all of which can be examined individually or in an integrated manner in order to diagnose the state of health and/or the course of the disease. Of these biomarkers, however, only DNA damage is a clear biomarker of an underlying pathology that can be mitigated by promoting apoptosis of genetically aberrant cells or by reducing the rate of accumulation of DNA damage. Changes at the epigenome, transcriptome, proteome, and metabolome levels may reflect easily modifiable homeostatic responses to altered dietary exposure and alone may not be sufficient to indicate definite irreversible pathology at the genomic level (Fenech et al., 2011; Oleaga et al., 2012 ;Neeha and Kinth, 2014; Park et al., 2017).

Using the current genomic tools, which include transcriptomics, proteomics, and metabolomics, there are two approaches to nutrigenomics research. The first would identify genes, proteins, or metabolites that are affected by diet (nutrients or bioactive compounds) and determine what mechanisms are involved in this interaction, and consequently figure out the regulatory pathways through which diet induces these changes . The second approach looks for early biomarkers (genes,

proteins or metabolites) associated with specific dietary components or the whole diet (García-Cañas et al., 2012). These biomarkers could serve as "warning signals" of changes in homeostasis and have health implications (Afacan, N.J., Fjell CD., 2012; Fenech et al., 2011; Oleaga et al., 2012).

There are numerous examples (De Vrieze et al., 2009; Wittwer et al., 2011; Afacan, N.J., Fjell CD., 2012) that illustrate the interaction between dietary components and the genome, from mammalian cells in culture to studies in the human genome. However, most usages are still descriptive. As an example of a typical nutrigenomic research approach, we outline our research, the main objective of which is to investigate the mechanisms underlying the potential chemo-preventive effects of a particular type of well-known food compound, polyphenols. Polyphenols are the most common antioxidants found in food. Their main food sources are fruits and plant-based beverages such as fruit juices, tea, coffee, and red wine. Vegetables, grains, cocoa, chocolate, and dried legumes also contribute to the overall intake of polyphenols. Their total food intake could be as high as 1g/day, which is much higher than any other class of phytochemicals and known antioxidants (Oleaga et al., 2012).

*C. Experiments and technologies used in the study of nutrigenomic*

The biological effects of nutrients and bioactives compounds in food depend on a range of physiological processes including absorption, transport, biotransformation, uptake, binding, storage and excretion, as well as on cellular mechanisms of action such as binding to nuclear receptors or the regulation of transcription factors. Each of these processes can involve multiple genes with common polymorphisms that could alter their function and ultimately the physiological response to a food compound. Research on diet-gene interactions has also examined how genes influence food preferences by influencing sensory, reward, or homeostatic energy pathways (Garcia-Bailo et al., 2009). Establishing a genetic basis for food likes or dislikes could lead to the development of novel food products that target specific genotypes or ethnic populations, and could explain some of the inconsistencies between studies linking foods to chronic disease risk (Fenechet al. , 2011).

Genetic variation throughout the human genome is recognized as increasingly complex. Single nucleotide polymorphisms (SNPs) are the most common form of sequence variation in the human genome, with over 10 million SNPs reported in public databases (Thorisson GA, 2003; Park et al., 2017), but copy number variants appear to be much more widespread than previously thought and could represent a major source of genetic variation. Nucleotide repeats, insertions, and deletions are other types of variations that could also change a person's response to the diet. Genetic polymorphisms are usually found in at least 1% of the population, although common polymorphisms can occur in up to 40-50% of the population. Genetic polymorphisms can either have no effect or have significant effects on the structure or function of the gene product. Various experimental approaches can be used to identify genetic variants that modify the effects of dietary factors or affect food preferences. A candidate gene approach is the most common method, in which a gene is selected based on its known or putative function (Fenech et al., 2011).

Depending on the number of SNPs in the gene and whether some of them have known functional effects, analyzes are performed using single SNPs or combinations of SNPs, such as B. haplotypes performed. Recent studies have begun using genome-wide scans to identify previously unknown genetic variants that might alter a feeding response. Understanding the genetic basis for individual variability in response to bioactive foods will provide a more accurate measure of exposure of target tissues of interest to these compounds and their metabolites, and allow for a better understanding of human health implications and disease risk. Identifying relevant interactions between diet and genes will not only benefit individuals seeking personalized nutritional advice, but will also help improve public health recommendations by providing sound scientific evidence linking specific dietary components to diverse health outcomes (Bull C, 2008).

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A variety of studies have clearly shown that nutrients alter the expression of genetic information at the level of gene regulation, signal transduction, and through changes in chromatin structure and protein function. Diet can affect gene expression levels by affecting transcription factors or causing epigenetic changes such as methylation DNA. Global changes in gene expression profiles could represent molecular 'signatures' reflecting exposure to specific nutrients (RM, 2008). Peripheral blood mononuclear cells can be used as a source of mRNA and serve as a surrogate for changes in target tissues of interest. Metabolomics and proteomics are increasingly used to identify biomarkers of exposure and to discriminate between individuals with different dietary habits. The type of information generated could one day be incorporated into existing biobanks to relate diseases to possible dietary exposures when such information can no longer be reliably collected or assessed. However, there remain some challenges related to sample handling and processing as well as data interpretation that need to be overcome (Scalbert et al., 2009; Fenech et al., 2011).

Among the experimental study designs, epidemiological studies are of particular interest as they examine the effects of dietary exposure and genetic variants in humans. Limitations of nutritional epidemiology studies include inaccuracies associated with estimating nutrient intakes. But even if the exact intake levels were known, the biological "dose" will vary widely from person to person because genetic variability affects either the absorption, biotransformation, metabolism, distribution, or elimination of a nutrient or bioactive food (El -Sohemy et al., 2007; Fenech et al., 2011). The incorporation of genetic polymorphisms into nutritional epidemiology studies has helped address several limitations inherent in such studies. These include recall bias in case-control studies and residual confounding in observational studies in general. An example of how nutrigenomics has been used to clarify the role of specific dietary factors comes from a study on coffee and heart disease (Cornelis MC, El-Sohemy A, Kabagambe EK, 2006).

Several studies had examined this association and concluded that coffee either increases risk, has no effect, or reduces risk (Neeha&Kinth, 2014; Ordovas JM, 2004). Although coffee is a fairly complex beverage containing a large number of bioactive compounds, it is an important source of caffeine in several populations, and there have been concerns that caffeine may be particularly harmful to the cardiovascular system. Caffeinated coffee has been found to increase heart attack risk in people who carry a version of a gene that makes them "slow" caffeine metabolizers, but has no effect in people who are "fast" caffeine metabolizers (Cornelis MC, 2007). The insights gained through the application of genomic information in nutrition research will not only provide a more rational basis for personalized dietary advice, but also improve the quality of evidence for population-based dietary recommendations.

Discoveries in the field of nutrigenomics should be translated into more effective nutritional strategies to improve overall health by identifying unique targets for prevention. Several large-scale international initiatives in nutrigenomics are currently underway, with new programs being developed to fill the existing gaps and complement existing initiatives (Kaput, 2007; Wilkins, 2017). Sequencing an individual's genome has sparked interest in the field of personalized medicine (Ferguson et al., 2016), but replication and validation of nutrigenetic studies must remain a priority before personalized nutrition is considered a worthwhile approach to improving human health can.

*D. Precision Nutrition: The Road to Tailored Dietary Advice*

One of the ultimate goals in the promising field of precision nutrition is the development of tailored nutritional recommendations to treat or prevent metabolic disorders (Betts, J.A.; Gonzalez, 2016). More specifically, the pursuit of precise nutrition in order to develop more comprehensive and dynamic nutritional recommendations based on changing, interacting parameters in a person's internal and external environments throughout life. To that end, precision nutrition approaches incorporate factors other than genetics, such as: B. Dietary habits, dietary behaviors, physical activity, the microbiota and the metabolome (Toro-mart et al., 2017).

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Translating the growing knowledge from basic nutritional research into meaningful and clinically relevant nutritional advice is one of the central challenges in clinical nutrition today. From nutrigenomics to deep phenotyping, many factors need to be considered when developing personalized and unbiased nutritional solutions for individuals or population subgroups. Likewise, a concerted effort between basic scientists, clinical scientists and health professionals is required to create a comprehensive framework that will enable the implementation of these new findings at the population level. In a world marked by an overwhelming increase in the prevalence of obesity and associated metabolic diseases such as type 2 diabetes and cardiovascular disease, tailored dietary regulation represents a promising approach to both prevention and treatment of metabolic disease syndrome.

With the mapping of the human genome completed, a cumulative number of association studies were conducted to identify the genetic factors that might explain the inter-individual variability in metabolic response to specific diets. In this sense, while numerous genes and polymorphisms have already been identified as relevant factors in this heterogeneous response to nutrient intake (McMahon et al., 2014; Toro-mart et al., 2017), there is also currently clinical evidence supporting these statistics Associations weakly support providing a comprehensive framework for personalized nutritional interventions in most cases (Ahmadi, K.R.; Andrew, 2014).

Although most of the knowledge on this topic is still relatively far from reaching its full expected potential in terms of translation and application of this knowledge to precision nutrition (Özdemir, V.; Kolker, 2016), some of it has been successfully developed in the public domain as well as in the private sector. On the one hand, hypolactasia diagnostics (Toro-mart et al., 2017), celiac disease exclusion (Ludvigsson et al., 2014) or phenylketonuria screening (Toro-mart et al., 2017) have made it possible to implement a tailor-made nutritional advice on the basis of the genetic makeup, d. H. Avoidance of products containing lactose, gluten and phenylalanine in persons at risk. In the private sector, many companies already offer genetic testing to adjust diets based on individual responses to specific nutrients. This is the case, for example, with genetic tests based on the specific metabolism of caffeine (slow or rapid metabolisers) (Cornelis et al., 2007), the propensity to gain weight from saturated fat intake (Corella et al., 2009; Corella et al., 2011) or the increased risk of high blood pressure from high salt consumption (Toro-mart et al., 2017), among others. Together, these dietary recommendations based solely on genetic background represent a simple approach to the concept of personalized nutrition. Although the concept of precision nutrition is quite similar and sometimes interchangeable, the latter refers to a conceptual framework that covers a broader range of individual characteristics that contribute to an effective and dynamic approach to nutrition (Betts, J.A.; Gonzalez, 2016). While gene-based personalized nutrition is already being successfully implemented based on numerous research studies like the ones mentioned above, given its complexity, precision nutrition may still lack sufficient evidence for full implementation (Toro-mart et al., 2017).

*E. Personalized Nutrition*

The influence of nutrition on nutritional and health status is rapidly increasing. This trend has led to increasing diversity in knowledge and perspective towards food in high-income countries (HICs). Consumers are overwhelmed by the information provided by literature of all kinds, as well as the content made available via social media. Food companies, restaurants and retailers have diversified their portfolios and adapted to the new demands for vegetarian, vegan and organic food, and for foods that take account of food intolerances and health-related trends (Arnold, 2017). The lack of an existing proposed or unified definition that is commonly accepted for “personalized nutrition” in the view point of this latest nutrition science discovery, has led to confusion about what personalized nutrition means, from the perspectives of information generated through technology, development of industries that produce foods, ingredients through technology, and dietary recommendations that make do with information gathered from this technology. This discovery offers a great benefit to the society at large, that engage in the use of its principle. This in turn offers huge opportunity to help practitioners and users to improvetheir adherence and compliance with dietary regime and guidelines, causing a radical change in the view point of nutrition

recommendations, dietary management and delivery from population-based to individualized nutrition therapy. The collaborative and holistic approach of this, can also serve as a guide for companies or organizations that target individualized nutrition delivery to individuals or society as a whole (Sean, 2020).

Personalized nutrition at its acme should not only be limited to management and prevention of disease, but also be effective and efficient in limiting the prevalence of disease or reducing the period of disease manifestationas compared to general nutritional recommendations. Inasmuch the genetic profile is identified, the condition can be properly managed or better still, treated by an individualized nutrition intervention, so that it will be useful in the selection of nutrients according to their composition in the nutrients that defend the genetic profile (Tania and Mona, 2020).

The comprehensive goal of discovery in nutritional science is to improveand preserve health using phenotypic, medical, nutritional,genetic profile and other relevant/germane clinical finding and knowledge about individuals, so as to deliver precise and improve healthy dietary advice and other nutritional services. Personalized nutrition is also useful to patients and to healthy people who may or may not have directly necessitate genetic susceptibilities to specific diseases. This science can be useful in numerous facets, but just to mention but few: (a) for the dietary management of people with certaindiseases; (b) who is in need of special assistance or support through individualized medical nutritional therapy, such as prenatal care for women or geriatric nutritional support in old age; (c) for the innovation and initiation of a well improved nutritional care plan for effective control of nutritional diseases that is of public health importance. Overall principle of personalized nutrition at the grassroots aims to maximize the importance and reducing the negative effects of dietary changes for individual nutritional support. Nevertheless, this focus on the individual may have diminish impact on the populations at large. To have a comprehensive and massive impact, there must be a massive deployment on a larger scale and in such a manner in which it will reduces (rather than widen) health disparities. Some people may also wish to use individualized nutrition approach to achieve personal ambitions thatare in little way related to health, for instance, to deal with preferences for, and dislikes of, specific foods, to attempt to achieve a desired body size or shape, or for competitive sports or fashion modelling (Pickering and Kiely, 2018).

*F. Current Use of Genetic Testing for Personalized Nutrition*

Nearly 1,000 genes have been associated with human disease and 97% of these can result in monogenetic diseases such as celiac disease, phenylketonuria, and galactosemia. A monogenetic disease is a disease resulting from a single defective gene on the autosomes and although they are relatively rare, they affect millions of people worldwide (Mutch *et al.,* 2005; World Health Organization, 2017). Typically, these conditions are diagnosed at birth or in early adulthood, although Celiac's Disease can be diagnosed at any stage of life. Genetic testing and personalized nutrition are currently being used to diagnose and treat these diseases, which can be classified into three main categories including dominant, recessive, and X-linked. The nature of monogenic diseases depends on the specific functions that are typically performed by the affected gene. Recessive diseases are autosomal diseases where two copies of an abnormal gene are passed down from both parents. A monogenetic dominant disease differs in that they involve damage to only one gene copy. X-linked diseases are those that are caused by mutations on the X-chromosome and can be inherited when one copy of the gene is inherited from a parent who has the disorder (World Health Organization, 2017).

Unlike monogenetic conditions, chronic diseases that are reaching epidemic proportions across the globe often arise from dysfunctional biological networks (polygenetic) and no single mutated genes. For this reason, dietary interventions to prevent chronic diseases are complex, requiring knowledge of how a complex mixture of nutrients (diet) will interact to change biological functions (Wilkins, 2017). However, to use genetic blueprints (genotypes) for dietary prevention of disease, the mechanisms driving the connection between diet and the outward expression of our genes (phenotype) must be identified first. An important aim of nutrigenomics research is to study genome-wide influences of diet, specifically focusing on the role of metabolic stress in the creation of metabolic syndrome, inflammation, insulin resistance, and chronic

diseases such as obesity, diabetes, heart disease, and some types of cancer (Afman & Müller, 2006; Wilkins, 2017).

a) Celiac Disease
Celiac disease is a chronic inflammatory condition of the small intestine with known heritable characteristics and is characterized by permanent intolerance to gluten/gliadin. Genetic variants in HLA-DQ genes indicate a high level of risk and probability for the development of Celiac Disease (Ludvigsson *et al*., 2014). It is also known that Celiac's Disease runs in families, with twins having a 75% concurrence of disease development (Wilkins, 2017). This condition requires strict avoidance of gluten (Ludvigsson *et al.*, 2014) to limit the inflammatory reaction, which directly affects intestinal cell structure and function by altering gene expression (Pavlidis *et al*., 2015). Studies have indicated that certain dietary components including long-chain omega-3 fatty acids, plant flavonoids, and carotenoids may act through a variety of mechanisms including decreasing inflammatory mediators through cell signaling and genetic expression, therefore reducing the production of damaging oxidants(Ferretti *et al*., 2012; Wilkins, 2017) Nutrition therapy for celiac disease includes these food parts due to their role in preserving the intestinal barrier and protecting against toxicity (Pavlidis *et al.*, 2015).

b) Phenylketonuria (PKU)
PKU is an inborn error of metabolism, characterized by the defective phenylalanine hydroxylase (PAH) enzyme and is inherited as an autosomal recessive trait (Mutch *et al.*, 2005; Wilkins, 2017). The human phenylalanine hydroxylase gene includes two sections of polymorphic sites and this genetic variation has been reported to decrease the enzyme's activity (Wilkins, 2017). Individuals with PKU must avoid foods high in protein and phenylalanine to prevent buildup of excess phenylalanine in the blood, which can lead to serious neurological damage (Sweeney *et al.*, 2011).

c) Galactosemia
Galactosemia is a rare recessive disorder affecting the galactose-1-phosphate uridyltransferase enzyme (GALT) (Mutch *et al.*, 2005). Without proper functioning of this enzyme, there is a failed conversion of galactose to glucose leading to an accumulation of galactose in the blood. Elevated serum galactose can cause mental retardation if left untreated(Mahan, & Escott-Stump, 2008). A galactose-restricted diet is the main treatment for individuals with Galactosemia(Wilkins, 2017)

*G. Personalized Nutrition and Chronic Disease Prevention*

Companies such as GenoVive, Nutrigenomix, Habit's, and Arivale are currently using direct to consumer genetic testing to create personalized nutrition plans for their clients(Nutrigenomix, 2013; GenoVive *et al*., 2015; Pioneer, 2015; Habit, 2016). Advertising an approach that is centered on the notion that health depends not only on an individual's diet but also on the way their body responds to what they eat, these companies help clients develop an approach to nutrition that is based on their unique genetic blueprint. According to Dr. Alan Greene, M.D. Chief Officer at Habit: "The value of personalized nutrition is already a foundational truth based on science: The official dietary recommendations of the National Academy of Sciences, the Institute of Medicine, and the USDA Food and Nutrition Board, which are based on extensive review of available science, recognize that optimal intakes vary by age, gender, and life stage" (Habit, 2016).

Personalized nutrition companies use their client's blood, biometrics, and/or genetics as distinct data points concerning other factors such as lifestyle, physical activity, dietary patterns, stress levels, and sleep patterns. Next, the companies determine the best dietary choices for each client's genotype to optimize bodily functions for that individual. Some companies, such as Arivale, also use microbiome tests to explore the diversity of gut bacteria. Decision tree logic, algorithms, and analysis of SNPs are all techniques used to create personalized dietary recommendations (Habit, 2016; Pioneer, 2015).

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Among Nutrigenomic companies, some of the most commonly tested genes include MTHFR, VDR, and FTO. The MTHFR gene codes for the enzyme, methylenetetrahydrofolatereductase, which catalyzes the conversion of 5,10 methylenetetrahydrofolate to 5-methyltetrahydrofolate, a co-substrate for remethylation of homocysteine to methionine (Janson & Tischler, 2012). This enzyme is also responsible for the conversion of folate from its inactive form to its active form. Individuals with the A allele for the MTHFR gene variant are shown to have lower activity of the MTHFR enzyme, which can lead to increased levels of homocysteine and elevated cardiovascular disease risk (Crider *et al.,* 2011). Nutrigenomic companies have the opportunity to pinpoint individuals who are at increased risk for high homocysteine by testing for this genetic variation.

The VDR gene codes for the vitamin D3 receptor (Haussler et al., 2008) and plays an important role in the metabolism of calcium and phosphorus. The VDR gene influences intestinal calcium absorption, bone cell growth, bone density, and may play a role in other chronic conditions such as type 2 diabetes and cardiovascular disease (Mahan &Escott-Stump, 2008). Nutrigenomic companies have the opportunity to identify individuals who are at an increased risk for low vitamin D levels. Companies may recommend supplementation based on which VDR gene variants are found for each individual.

The FTO gene has been linked to appetite regulation and the A-allele for the variant is associated with increased risk for obesity (Wilkins, 2017). It is believed that individuals with high impact FTO variants may benefit from decreased total dietary fat consumption or modified fat consumption, depending on their current diet and lifestyle (Kilpeläinen, *etal.*, 2012). These individuals are also informed of the high importance of physical activity because the effect of the FTO gene is significantly less in physically active individuals (Wilkins, 2017).

After completing genetic tests, behavioral science is utilized to provide additional support through one-on-one coaching. Registered dietitians, physicians, and other health care providers employ counseling techniques to keep clients focused, prioritize goals, and motivate sustainable long-term behavior change (Habit, 2016; Pioneer, 2015). While it is becoming increasingly recognized that not all people respond to diet equally, research in the developing field of nutrigenomics is lacking and the Academy of Nutrition and Dietetics (AND) does not recommend nutrigenetic testing as a means of providing personalized nutrition recommendations because it does not have enough evidence-based research to support its effectiveness (San-cristobal et al., 2013).

The position of AND requests that commercialized tests become more transparent to consumers, reporting data about the analytical techniques used and providing the number and names of SNPs. Also, AND expresses concerns with the application of personalized nutrition care, based on the fact that many health care professionals lack the knowledge to translate genetic results into common language, therefore presenting a risk for misunderstandings and misuse of genetic information among patients (San-cristobal et al., 2013; Wilkins, 2017). Furthermore, the cost for enrollment in these programs can range from $1,800 to $3,500 per year, (GenoVive, 2015; Pioneer, 2015). Consumers must pay these fees in full because they are not covered under current insurance plans, putting nutrigenomic testing out of reach for individuals who cannot afford these expenses.

### *H. Prevention of Chronic Disease Using Personalized Nutrition*

Nutrigenomic knowledge has the potential to provide improved methods for the prevention of some of the most prevalent and deadly chronic diseases. For example, multiple nutrigenomic and nutrigenetic studies have indicated that complex interactions may explain differences observed in obese phenotypes, which vary within and across populations. Genes play an important role in body weight homeostasis through multiple mechanisms including appetite, physical activity, adipocyte differentiation, insulin signaling, mitochondrial function, lipid turnover, thermogenesis, and energy efficiency (Joffe & Houghton, 2016). In one study, personalized calorie-controlled diets were created using 24 variants in 19 genes involved in metabolism. Weight loss and weight maintenance between 50 individuals on the tailored diets were compared to weight

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loss and weight maintenance in individuals on generic diets. Results showed that the group receiving the personalized dietary advice performed better during the weight-loss period, and were more able to maintain their weight over the following year (Fenech et al., 2011). Since there is strong evidence of a correlation between the development of obesity and other chronic conditions, interventions like these could lead to the prevention of other diet-related diseases.

*I. Knowledge and Awareness of Nutrigenomics*

Studies have indicated that there may be limited awareness and a lack of general knowledge about current nutrigenomic processes (Lapham *et al*., 2000; Goddard *et al.*, 2009; Morin, 2009) and no studies have tested these factors across college-students. In a study of Canadian consumers and physicians, findings indicate that members of the public are unfamiliar with the term "nutrigenomics," however others were able to provide a simple definition. Even though the knowledge was limited among these participants, this did not deter many from appreciating the potential value of better information linking nutrition and one's genetic profile (Wilkins, 2017). In a population-based survey on direct-to-consumer nutrigenomic testing in Michigan, Oregon, and Utah, awareness of genetic testing was highest in Oregon (24.4%) and lowest in Michigan (7.6%) indicating significant differences in awareness among different states. Nationally, 14% of respondents indicated awareness of nutrigenomic tests. It was estimated that only about 1% of the total population had used a genetic test. Other predictors of awareness in this study were higher income and increasing age, except among those 65 years or older(Goddard *et al.*, 2009; Wilkins, 2017).

In another study, conducted by SynovateInc, 5,250 consumers responded to the Health-Styles survey and 14% of respondents were aware of direct-to-consumer genetic tests. Education and age less than 55 years were significant independent predictors of awareness (Goddard *et al.*, 2009). In a study examining the genetic knowledge of patients with chronic disease from the Netherlands, half to three-fourths of respondents reported having little knowledge about genetics and older respondents reported significantly less knowledge. Individuals that were younger and better educated were more likely to be aware of the nutrigenomics tests in all three of these studies (Wilkins, 2017). Since college students typically are younger and more educated than the overall U.S. population, a survey to determine their awareness, knowledge, and interest in nutrigenomic testing may prove useful.

Knowledge of nutrigenomics is also limited among dietitians and physicians, indicating a need for training in this area. Health-Styles survey data revealed that 44% of physicians are aware of nutrigenomic tests but only 44% have ever had patients ask about such tests, and 74% had never discussed results of a nutrigenomic test with a patient (Wilkins, 2017). In a national survey of 390 dietitians, a mean knowledge score of 41% demonstrated generally low levels of knowledge in genetics and diet-gene interactions. In dietitians, higher reported confidence was associated with higher knowledge scores (Whelan, K., McCarthy, S., & Pufulete, 2008). The Human Genome Education Model Project, a collaborative project of Georgetown University Medical Center and the Alliance of Genetic Support Groups communicated similar findings. Surveys were sent to 3,600 health professionals including dietitians, occupational therapists, physical therapists, speech-language-hearing specialists, and social workers. Almost 80% of respondents reported taking no formal courses in genetics and 80% had heard little to nothing about the Human Genome Project (Lapham *et al.*, 2000; Wilkins, 2017). Two-thirds of these health care professionals reported interest in continuing education in genetics. This study along with others presents the need for a solid foundation in genetics to apply nutritional genomics to the treatment and prevention of chronic disease in the future (Lapham *et al*., 2000; Wilkins, 2017).

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*J. Barriers and Considerations Related to Nutrigenomics*

Nutrigenomics is an emerging science with high expectations, but there are major concerns about whether the goal of matching foods to individual genotypes is within reach. Whether or not nutrigenomic foods and personalized diets flourish in the world's market depends on multiple hurdles being overcome. Some consider the use of nutrigenomics for personalized nutrition to be controversial, and possibly unethical (San-cristobal *et al.,* 2013; Pavlidis *et al.,* 2015). Others are not convinced that enough research has been done to support the nutrition claims being made by companies who offer genetic testing, and therefore do not trust the validity of these recommendations (Fenech *et al.,* 2011). Moreover, many individuals are unaware of the existence of nutrigenomic technology or lack enough knowledge to understand and appreciate its importance in health promotion (Fenech *et al.,* 2011). These barriers need to be understood and addressed to promote the successful implementation of nutrigenomic technology and the adoption of personalized nutrition (Wilkins, 2017).

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# CHAPTER THREE

# METHODOLOGY

*A. Study Design*

The purpose of this cross-sectional survey research study is to access the knowledge and perception of undergraduate students towards nutrigenomics for personalized nutrition therapy at the Federal University of Agriculture, Abeokuta. Independent variables included gender, age, current academic standing, college major, awareness of nutrigenomics and nutrigenetics, and current or past enrolment in college-level genetics or nutrition courses. Dependent variables were genetics knowledge and perception of college students toward nutritional genomics for personalized nutrition.

*B. Study population*

The study population included undergraduate students of the Federal University of Agriculture, Abeokuta. Participants in the study are full-time students and it involved only undergraduate students enrolled at the Federal University of Agriculture, Abeokuta, Ogun State for the 2018/2019 section.

a) Inclusion criteria
The full-time undergraduate students attending the University who agreed to participate in the study and signed the consent form.

b) Exclusion criteria
The undergraduate students excluded from the study were those who were under the age of 18 years old was excluded from the study.

*C. Sample size determination*

The sample size ($n$ = 400) was determined using the Fischer formula ($n$ =N/1+N*$e^2$) (Ajay & Micah, 2014) as the population from which the sample size was drawn is more than 1250.

*D. Sampling technique and procedure*

The study applied a multistage sampling method.

a) Stage 1: Selection of colleges
In the first stage, the colleges in the university under the study area were identified and listed out. Colleges were selected using the simple random technique. Eventually, Four (4) colleges are selected at random.

b) Stage 2: Selection of departments
This stage involves listing of various departments under individual colleges selected at random. Two departments each were randomly selected from each college using a simple random sampling technique, which in turn giving a total of eight (8) departments. These colleges are

c) Stage 3: Stratified respondents into Strata
This stage involved the collation of the number of students in the levels that meet up with the inclusive criteria. Selected departments are being stratified into strata (level) using a stratified sampling technique. These departments are (1) Food Science and Technology (2) Nutrition and dietetics (3) Pure and Applied Botany (4) Biochemistry (5) Plant Breeding and Seed Technology (6) Plant Physiology and Crop Production (7) Animal Breeding and Genetics and (8) Animal Nutrition.

d) Stage 4: Selection of respondents
This stage involved the selection of respondents using a simple random sampling method.
The full-time undergraduate students attending the University who agreed to participate in the study and signed the consent form.The undergraduate students excluded from the study were those who were

under the age of 18 years old was excluded from the study. Fifty (50) respondents (undergraduate students) are selected from each selected department by a simple random sampling method.

*E. Method of Data collection*

Data were collected using a well-structured questionnaire. The survey questionnaires were be sent out to a total of 400 participants in a printed format and the questionnaire was designed to be interviewer-administered type.

a) Instrument used for data collection
The survey questionnaire was adapted from the questionnaire (Wilkins, 2017) and modified to reflect the demographics of the survey area and comprised four main sections including 1) general demographics, 2) perceptions related to nutrigenomics for personalized nutrition, 3) factors affecting consciousness to knowledge of nutrigenomics and 4) general knowledge of genetics. The survey questionnaire consists of a total of 30 questions.

b) Part I: General Demographics
Part I of the survey included six general demographic questions including age, ethnicity, weight, height, class ranking, and participation in college-level nutrition or genetics courses. Participants who did not meet the criteria of being 18 years or older, were unable to complete the survey. Participants who did not agree to the terms of consent were also unable to complete the survey. Descriptive statistics was used to calculate means, standard deviations, frequencies, and percentages for analysis of data collected from Part I.

c) Part II: Perceptions of Nutrigenomics for Personalized/Individualized Nutrition
Survey was used to assessed the perception or attitudes of respondents to nutrigenomics through a series of 22 questions. These questions require participants to consider possible merit and demerit aspects of the use or implementation of nutrigenomics for Individualized nutrition. The outlook or view of higher institution students were evaluated using a five-point Likert-style scale (Wilkins, 2017). Items in this part of the questionnaire were either positive/supportive or negative/opposing. Negative questions were reverse scored and an average score were determined for each item in this section. Higher scores in this section were indicating greater positive attitudes to nutrigenomics for individualized nutrition. More negative scores were indicating that respondent's perceived risks, or negative aspects of nutrigenomics, to outweigh benefits (positive aspects).

d) Part III: Factors influencing the awareness towards the knowledge of Nutritional genomics
Part III of the survey assessed the degree of common factors either encouraged or discouraged the respondents' tendency to be aware of nutrigenomics for individualized nutrition care. Respondents were presented with a list of 12 common factors and were asked to indicate how much influence these had upon their attitude toward the knowledge of nutrigenomics. Parameters in this section of the survey was measured using a five-point Likert-type scale, ranging from (1) to (5) indicating different degree of awareness. Space was provided for participants to enter any other factors that are not listed in this section.

e) Part IV: General Genetic Knowledge
This portion of the survey assessed college students' general genetic knowledge. The questions in this section of the survey were measured using a true-false quiz. Genetic knowledge was assessed based on responses to a 19-question assessment in which participants could choose between 1) true, 2) false, or 3) not white. Participants were instructed not to "guess" the answers, but to choose "don't know" if they did not know the answer, felt comfortable answering it, or understood the question. The score for this portion of the survey was measured using a continuous scale. The general genetics knowledge score was assessed by identifying the correct answer with a score of one. Incorrect answers were scored as zero. "Don't know" answers were also coded as zero. The total knowledge value was

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calculated from the sum of the correct answers. The mean score was determined by averaging the percentage of correct answers for each participant.

*F. Data Analysis*

Analysis of the results was completed using the Statistical Package for Social Sciences (SPSS) version 25. Descriptive statistics (mean, standard deviation, frequency distribution, and percentages) were used to analyze demographics including age, gender, class rank (levels), and history of attending college-level nutrition or genetics courses. The independent variables are gender, age, field of study, current academic status, knowledge of nutrigenomics, and current or previous enrollment in college-level genetics or nutrition courses. Dependent variables include general genetic knowledge and conceptions of nutritional genomics for personalized nutritional therapy.

Independent sample t-tests was be conducted comparing the mean scores of genetics knowledge and nutrigenomics perception among gender groups, and groups who may either be familiar with nutrigenomics for personalized nutrition therapy or not. Familiarity with nutrigenomics was determined by asking participants if they had ever read or heard about nutrigenomics. Similarly, t-tests were also use to see whether university students who took nutrition and/or genetics course scored differently on the genetics knowledge and nutrigenomics perception assessments.

A Pearson correlation coefficient was calculated for the relationship between genetics knowledge scores and perception of nutrigenomics scores. ANOVA was used to determine whether there are differences in genetics knowledge and perceptions toward nutrigenomics among groups of different class levels and different majors (1) Animal Nutrition 2) Biochemistry 3) Animal Breeding and Genetic 4) Plant Breeding and Seed Technology, and 5) Nutrition and Dietetics & Others). A significance of $P \leq 0.05$ is set for all t-test and ANOVA measurements (Omage & Omuemu, 2018).

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# CHAPTER FOUR

# RESULT AND DISCUSSION

## *A. Results*

a) The socio-demographic characteristics of the respondents.

The socio-economic and demographic characteristics of the respondents analyzed in this study include age, sex, level, and department. The demographic data of participants are highlighted in Table 1. Participants ranged from 18 to 35 years old with a mean age of 21.17 years (n= 305). Analyses of results obtained from this study in Table 1 reveal that more than half (61.3%) of the respondents were females, most of them were between the ages of 18 and 23 years accounting for 81% (n=305). Approximately 51% of students in this study reported participation in a college-level nutrition course and 70% reported participation in a college-level genetics course. Departmental participation in the study shows that NTD has the highest percentage (19%); followed by PPCP and PBST (having 13.5 and 13% respectively) and AGB and FST accounting for 25% altogether.

| Variables | Frequency | Percentage (%) |
|---|---|---|
| Gender | | |
| Male | 155 | 38.7 |
| Female | 245 | 61.3 |
| Total | 400 | 100.0 |
| Mean $\pm$ SD - 21.17 $\pm$ 2.70 | | |
| Age | | |
| 18-23 | 247 | 81.0 |
| 24-29 | 56 | 18.4 |
| 30-35 | 2 | 7 |
| Total | 305 | 100.0 |
| Level | | |
| 100 | 68 | 17.0 |
| 200 | 114 | 28.5 |
| 300 | 84 | 21.0 |
| 400 | 58 | 14.5 |
| 500 | 76 | 19.0 |
| Total | 400 | 100.0 |
| Department | | |
| COLANIM | 88 | 22.0 |
| COLPLANT | 106 | 26.5 |
| COLFHEC | 127 | 31.8 |
| COLBIOS | 79 | 19.8 |
| Total | 400 | 100.0 |

Table 1: Socio-Demographic Characteristics of the respondents

b) Knowledge of genetics among undergraduate towards the understanding of nutrigenomics.

This section of the survey assessed the general genetic knowledge of college students with a series of true or false questions. Table 2 displays the results of this knowledge assessment. As a result of missing data that result from an incomplete response to some questions, valid percent was used. On average, participants answered approximately 56% (n =223) of questions correctly in this section. A Pearson correlation coefficient was calculated for the relationship between participants' genetics knowledge and their perceptions toward nutrigenomic testing. Based on survey results, a negative correlation was found, $r$ (398) = -0.037, $p \leq 0.461$, indicating a non-significant negative linear

relationship between positive perceptions toward nutrigenomic testing and higher genetics knowledge scores.

An independent sample t-test (Table 3) was used to compare the mean knowledge scores between participants who indicated participation in college-level nutrition and/or genetics course and those who did not. There was no significant effect for students who indicated participation in a college-level nutrition course, (p. 0.098), with those who indicated participation having similar scores on the genetics knowledge assessment. Students who participated in a nutrition course had a mean score of 11.02 $\pm$ 4.07 while those that do not participate have a mean score of 11.69 $\pm$ 3.69. However, students who indicated participation in a college-level genetics course also scored significantly lower on the genetics knowledge assessment, (p. 0.571), with a mean score of 11.25 $\pm$ 3.81. There was no significant effect for students who indicated participation in a college-level genetics course.

Another independent sample t-test was conducted comparing the mean genetics knowledge scores of participants who indicated some familiarity with nutrigenomic testing and those who indicated no familiarity. Based on the results of this test, participants who reported awareness of nutrigenomic testing scored slightly higher on the genetics knowledge assessment than participants who indicated no awareness at a mean of 11.44 $\pm$ 3.83 but not enough to show a significant (p. 0.630).

A one-way ANOVA (Table 4) was conducted comparing the genetics knowledge scores of students based on their class standing. A significant difference in genetics knowledge was found among class ranks, (p =0 .002). Tukey post-hoc test revealed no significant difference seen between the 100level, 200level, and 300level students, (p. 0.05), however, 500level and 400level students scored significantly lower on the genetics knowledge test than the 100level, 200level, students (p =0.002) and 300level students (p $\geq$ 0.003) respectively.

A second one-way ANOVA was also conducted comparing genetics knowledge among students. Results from this test are displayed in Table 5. Departments were categorized into four main groups including; 1) College of Animal Science and Livestock Production 2) College of Food Science and Human Ecology 3) College of Biological Science and 4) College of Plant Science and Crop Production. A statistically significant difference was found among colleges at α0.05. While Tukey post-hoc revealed no significant difference in genetic knowledge scores among College of Animal Science and Livestock Production and College of Plant Science and Crop Production (*p*. 0.008), College of Biological Sciences scored significantly higher on the knowledge assessment than College of Animal Science and Livestock Production ($p \leq 0.001$). Also, the College of Biological Sciences scored significantly higher on the genetics knowledge test than all other majors ($p \leq 0.05$). On average, the College of Biological Sciences (n = 79) scored the highest on the genetics knowledge assessment, while the College of Animal Science and Livestock Production (n = 88) scored the lowest.

The general knowledge score was scored by identification of the correct answer as a score of 1. Incorrect answers were scored as a score of 0. The general knowledge score was scored by identification of the correct answer as a score of 1. Incorrect answers were scored as a score of 0. Total scores were calculated from the sum of correct responses.

| Item | Mean ± SD (n) | Correct % (n) | Incorrect % (n) | Don't know % (n) |
|---|---|---|---|---|
| *True or false* | | | | |
| A gene is a portion of DNA, which codes for protein, which leads to a trait. | 1.06 ± 0.46 (383) | 93.7 (359) | 2.6 (10) | 3.7 (14) |
| Males inherit two X-chromosomes at birth, one from their mother and one from their father. | 0.83 ± 1.48 (384) | 42.2 (162) | 48.4 (186) | 9.4 (36) |
| The human genome project has estimated that humans have between 20,000 and 25,000 genes. | 1.95 ± 1.16 (391) | 35.8 (140) | 11.3 (44) | 52.9 (207) |
| Genes contain chromosomes. | 0.45 ± 0.85 (396) | 21.7 (86) | 70.5 (279) | 7.8 (31) |
| A genotype is the genetic make-up of an organism. | 1.09 ± 0.56 (397) | 88.4 (351) | 4.8 (19) | 6.8 (27) |
| In humans, each cell normally contains 23 pairs of chromosomes, for a total of 46. | 1.12 ± 0.54 (396) | 90.7 (359) | 2.3 (9) | 7.1 (28) |
| A phenotype is a physical expression of alleles (brown eyes or blue eyes). | 1.20 ± 0.67 (397) | 85.4 (339) | 3.0 (12) | 11.6 (46) |
| A mutation occurs when the structure of a gene changes. | 1.21 ± 0.74 (396) | 81.3 (322) | 5.3 (21) | 13.4 (53) |
| Mutations always lead to negative health outcomes. | 1.00 ± 1.19 (392) | 29.1 (114) | 47.2 (185) | 23.7 (93) |
| An allele is the different forms of a gene, represented by letters. | 1.52 ± 1.02 (397) | 61.0 (242) | 8.8 (35) | 30.2 (120) |
| A dominant trait is a trait that is hidden in the F1 generation. | 1.14 ± 1.14 (392) | 41.3 (162) | 34.4 (135) | 24.2 (95) |
| Epigenetics is the study of changes in an organism's gene expression without a change in the genetic code. | 1.79 ± 1.22 (397) | 50.6 (201) | 7.6 (30) | 41.8 (166) |

Table 2: Genetic Knowledge Test Scores among Respondent

| Item | Mean ± SD (n) | Correct % (n) | Incorrect % (n) | Don't know % (n) |
|---|---|---|---|---|
| *True or false* | | | | |
| DNA repair is a collection of processes where a cell identifies and repairs DNA molecules that encode its genome. | 1.47 ± 0.90 (391) | 72.1 (282) | 2.8 (11) | 25.1 (98) |
| A point mutation is a type of mutation that causes a single nucleotide base substitution, insertion, or deletion. | 1.66 ± 1.04 (394) | 56.9 (224) | 6.9 (27) | 36.3 (143) |
| An example of a genotype that is heterozygous is AA. | 1.02 ± 1.04 (394) | 47.2 (186) | 34.5 (136) | 18.3 (72) |
| An example of a genotype that is homozygous is cc. | 1.40 ± 0.97 (397) | 65.2 (259) | 9.8 (39) | 24.9 (99) |
| Mutations can create variations in protein "switches" that control protein function. | 1.57 ± 0.97 (392) | 64.5 (253) | 4.6 (18) | 30.9 (121) |
| Mutations cannot be reversed through DNA repair. | 1.65 ± 1.24 (397) | 35.3 (140) | 21.4 (85) | 43.3 (172) |
| A recessive trait can be carried in a person's genes without appearing in their phenotype. | 1.34 ± 0.92 (397) | 69.3 (275) | 9.3 (37) | 21.4 (85) |
| RNA contains the genetic information which is encoded in gene preserve for generation to come. | 0.91 ± 1.24 (396) | 14.4 (57) | 60.1 (238) | 25.5 (101) |

Table 2 Cont'd: Genetic Knowledge Test Scores among Respondent

**Note.**Abbreviations.SD, standard deviation; n, number of members in the sample.

| College Course participation | Mean ± SD | (n)% | p-Value |
|---|---|---|---|
| **Nutrition** | | | |
| Yes | 11.02 ± 4.07 | (196) 50.8 | 0.652 |
| No | 11.69 ± 3.69 | (190) 49.2 | |
| **Genetic** | | | |
| Yes | 11.29 ± 3.81 | (272) 69.9 | 0.004 |
| No | 11.54 ± 4.45 | (117) 30.1 | |
| **Have you heard or read about these genetics fields?** | | | |
| Yes | 11.44 ± 3.831 | 242 | 0.081 |
| No | 11.23 ± 4.341 | 143 | |

Table 3: Differences in Genetics Knowledge Scores according to College Genetics and/or Nutrition Course Participation

*Show t-test statistical significance, where statistical significance was set at α-0.05.
Abbreviations: SD, standard deviation; n, number of members in the sample.

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| Level | Mean ± SD | n (%) |
|---|---|---|
| 100 | 12.43 ± 03.61 | 68 (17.0) |
| 200 | 11.50 ± 04.16 | 114 (28.5) |
| 300 | 11.70 ± 03.96[a] | 84 (21.0) |
| 400 | 11.11 ± 04.10[ab] | 58 (14.5) |
| 500 | 09.92 ± 03.74[a] | 76 (19.0) |
| Total | 11.33 ± 03.91 | 400 (100) |

Table 4: Differences in Genetics Knowledge Scores based on Departmental levels

a = statistically significant difference between 100L, 300L and 500L students, (p =0 .002); b = statistically significant difference between 100L and 400L students. Abbreviations.SD, standard deviation; n, number of members in the sample.

| Test Variable | Group Variable | p-Value | Test Variable (Mean ± SD) |
|---|---|---|---|
| **COLANIM** | COLPLANT | *0.008 | 09.88 ± 3.84[a] |
| | COLFHEC | 0.104 | |
| | COLBIOS | 0.000 | |
| **COLPLANT** | COLANIM | *0.008 | 11.66 ± 3.51[a] |
| | COLFHEC | 0.694 | |
| | COLBIOS | 0.102 | |
| **COLFHEC** | COLANIM | 0.104 | 11.10 ± 4.12[b] |
| | COLPLANT | 0.694 | |
| | COLBIOS | *0.004 | |
| **COLBIOS** | COLANIM | *0.000 | 12.99 ± 3.99[c] |
| | COLPLANT | 0.102 | |
| | COLFHEC | 0.004 | |

Table 5: Differences in Genetics Knowledge Scores according to Colleges

*. The mean difference is significant at the ≤ 0.05 level.

*Show t-test statistical significance, where statistical significance was set at p. 0.05.
a = statistically significant difference between COLANIM and COLPLANT, (p ≤ 0.002); b = statistically significant difference between COLFHEC and COLBIOS, (p. 0.004); and c = statistically significant difference between COLANIM and COLBIOS (p.≥ 0.001). Abbreviations: **SD**, standard deviation; **N**, number of members in the sample.

c) Awareness and Perception of Respondent toward Nutrigenomics for Personalized Nutrition.
When students were asked if they were familiar with genetic testing for personalized nutrition, only about 63% reported some familiarity with nutrigenomic testing. The remaining 37% of participants indicated they had never heard or read about this field. Results from assessment of perceptions regarding genetic testing for personalized nutrition are displayed in Table 6. On a modified 5-point Likert style scale, ranging from (1) 'strongly disagree' to (5) 'strongly agree' with (3) indicating 'neither agree nor disagree', participants most strongly agreed with the statement, "Knowledge nutrigenomics for personalized nutrition will lead to the prevention of some diseases," with a mean response of 3.58 ± 0.48 (n=396). Students showed most concern with the cost and availability of nutrigenomic tests and knowledge, and about 49% of participants agreed with the statement, "Nutrigenomic testing would cost too much and would only be available to the rich."

Independent sample t-tests were conducted comparing mean perception scores based on gender and between participants who indicated some familiarity with nutrigenomic testing and those who indicated no familiarity. There was no significant difference in perception of nutrigenomics between

genders ($p \geq 0.05$); however, participants who indicate participate in the genetic level course had a significantly more positive perception towards nutrigenomics than participants who indicated no awareness, ($p$. 0.04).

Independent sample t-tests (Table 7) were also used to compare the mean perception scores between participants who indicated participation in college-level nutrition and/or genetics course and those who did not. There was a significant effect for students who indicated participation in a college-level genetics course, ($p = 0.04$).

Mean nutrigenomic perception scores according to departmental level (100level, 200level, 300level, 400level, 500level student) are highlighted in Table 8. One way ANOVA revealed a significant difference in the perception scores between the five-level ranking groups ($p = 0.001$) and the Tukey test was used to detect where significant differences were found. Juniors ($p = 0.038$) and seniors ($p = 0.005$) scored significantly higher than freshman, indicating more positive perceptions. Seniors also scored significantly higher than graduate students ($p = 0.014$), indicating more positive perceptions.

A one-way ANOVA was conducted comparing perceptions of genetic testing for personalized nutrition among majors and results are reported in Table 9. Majors were categorized into four groups including; 1) Health and Medicine, 2) Social Sciences 3) Business, Math, Science & Technology, and 4) Arts, Humanities, & Others. A statistically significant difference was found among majors, $F(3, 2895)=8.17$, $p \leq 0.001$ and Tukey post-hoc test was used to see where significant differences were found. While there was no significant difference in perception among 'Health and Medicine' majors and 'Business, Math, Science, and Technology' majors ($p \geq 0.05$), 'Health and Medicine' majors had a significantly more positive perception than 'Social Science' ($p = .002$) and 'Arts and Other' ($p = .003$) majors. Overall 'Health and Medicine' majors (n=705) had the most positive perception toward nutrigenomics, while 'Art and Other'.

Table 6: Awareness and Perception of Respondent toward Nutrigenomics

| **Perception** | **Mean ± SD[a]** | **A/SA (n)** | **NEU % (n)** | **D/SD % (n)** |
|---|---|---|---|---|
| Screening for known genes is the way forward for medicine and nutrition. | 3.83 ± 1.06 | 77.5 (303) | 12.5 (49) | 10 (39) |
| Gene testing for personalized nutrition will lead to the prevention of some diseases. | 4.94 ± 0.98 | 84.4 (330) | 7.4 (29) | 8.2 (32) |
| In my lifetime, I expect to see significant medical improvements due to the use of genetics in nutrition. | 4.30 ± 2.17 | 86.6 (338) | 9.5 (37) | 3.8 (15) |
| I am concerned that my genetic information will be made available for research purposes. | 3.59 ± 1.04 | 63.3 (242) | 18.8 (72) | 17.8 (68) |
| My genes have influenced my health. | 3.88 ± 1.12 | 72.3 (281) | 15.2 (59) | 12.6 (49) |
| Nutrigenomics knowledge for personalized nutrition is too hard to understand. | 2.92 ± 1.12 | 31.4 (120) | 29.6 (113) | 39 (149) |
| I would like to know about future diseases through the knowledge of nutrigenomics. | 3.97 ± 0.92 | 80.4 (314) | 12 (47) | 7.7 (30) |
| I think there is too much focus on genetics when money could be spent on the world's starving population. | 2.84 ± 1.24 | 30 (117) | 26.9 (105) | 43.1 (168) |
| Genetic testing for personalized nutrition should be available to everyone. | 4.11 ± 0.89 | 72.5 (282) | 15.2 (59) | 12.4 (50) |
| I am concerned that not enough will be done to protect | 3.24 ± 1.16 | 45.5 (176) | 26.9 (104) | 27.6 (107) |

| | | | | |
|---|---|---|---|---|
| the confidentiality and privacy of my genetic information. | | | | |
| Having Knowledge about nutrigenomics allows individuals to control their lifestyle more easily. | 4.01 ± 0.96 | 84.4 (330) | 7.4 (29) | 8.2 (32) |
| Genetic knowledge for personalized nutrition will result in discrimination. | 2.76 ± 1.95 | 23.9 (93) | 26.1 (101) | 50 (194) |
| Nutri-genetic for personalized nutrition will help people to live longer. | 3.92 ± 0.96 | 79.1 (312) | 11.2 (44) | 9.7 (38) |
| All individuals should be made aware of nutrigenomics for personalized nutrition. | 4.21 ± 2.26 | 84.9 (332) | 9.5 (37) | 5.7 (22) |

Table 6 Continued

| **Perception** | **Mean ± SD[a]** | **A/SA % (n)** | **NEU % (n)** | **D/SD % (n)** |
|---|---|---|---|---|
| I am concerned that not enough will be done to protect the confidentiality and privacy of my genetic information. | 3.24 ± 1.16 | 45.5 (176) | 26.9 (104) | 27.6 (107) |
| Having Knowledge about nutrigenomics allows individuals to control their lifestyle more easily. | 4.01 ± 0.96 | 84.4 (330) | 7.4 (29) | 8.2 (32) |
| Genetic knowledge for personalized nutrition will result in discrimination. | 2.76 ± 1.95 | 23.9 (93) | 26.1 (101) | 50 (194) |
| Nutrigenetics for personalized nutrition will help people to live longer. | 3.92 ± 0.96 | 79.1 (312) | 11.2 (44) | 9.7 (38) |
| All individuals should be made aware of nutrigenomics for personalized nutrition. | 4.21 ± 2.26 | 84.9 (332) | 9.5 (37) | 5.7 (22) |
| Nutrigenomics knowledge would cost too much and would only be available to the educated. | 3.28 ± 1.21 | 48.7 (191) | 22.2 (87) | 29.1 (114) |
| I am worried that nutrigenetics testing may lead to eugenics (the science of improving the human population by controlling breeding to increase desirable characteristics). | 3.31 ± 1.15 | 49.9 (194) | 26.5 (103) | 23.6 (92) |
| Nutrigenomics knowledge for personalized nutrition will make medical cures for diseases more possible. | 4.16 ± 2.26 | 317 (81.3) | 48 (12.3) | 24 (6.2) |
| Nutrigenomics knowledge for personalized nutrition should be promoted extensively. | 4.14 ± 0.94 | 83.8 (326) | 11.2 (43) | 4.9 (19) |
| I do not believe that nutrigenomics for personalized nutrition is backed by sound science. | 2.61 ± 1.09 | 20.2 (77) | 31.8 (121) | 48.1 (183) |
| Genetic testing for personalized nutrition goes against my religious beliefs. | 2.02 ± 1.14 | 51 (13.3) | 10.4 (40) | 76.2 (292) |
| I believe it is essential to assign more money to nutrigenomic developments. | 3.97 ± 0.93 | 299 (76.9) | 58 (14.9) | 32 (8.2) |

a = calculated from a 5-point Likert style scale where (1) equals ***strongly disagree*** and (5) equals ***strongly agree***. Abbreviations*:* **A/SA**, agree/strongly agree; **NEU**, neutral; **D/SD**, disagree/strongly disagree; SD, standard deviation; (n), number of members in sample.

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| Item | Mean ± SD | (n)% | p-Value |
|---|---|---|---|
| **Gender** | | | |
| Male | 3.45 ± 0.55 | 151 | 0.337 |
| Female | 3.40 ± 0.48 | 243 | |
| **Have you heard or read about these genetics fields?** | | | |
| Yes | 3.43 ± 0.51 | 243 | 0.611 |
| No | 3.39 ± 0.50 | 139 | |
| **Nutrition course participation** | | | |
| Yes | 3.43 ± 0.48 | 197 | 0.510 |
| No | 3.39 ± 0.52 | 184 | |
| **Genetic course participation** | | | |
| Yes | 3.41 ± 0.53 | 272 | 0.046 |
| No | 3.45 ± 0.40 | 112 | |

Table 7: Differences in Perceptions Gender, Genetics/Nutrition course participation, and familiarity to Nutrigenomics fields

Note. Mean scores were calculated from a 5-point Likert style scale where (1) equals strongly disagree and (5) equals strongly agree.
*Show t-test statistical significance, where statistical significance was set at $p \leq 0.05$.
Abbreviations: **SD**, standard deviation; **n**, number of members in the sample.

| Test Variable | Group Variable | p-Value | Test Variable (Mean ± SD) |
|---|---|---|---|
| 100L | 200L | .990 | |
| | 300L | 1.000 | 3.46 ± 0.44 |
| | 400L | .999 | |
| | 500L | 1.000 | |
| 200L | 100L | .990 | |
| | 300L | .947 | 3.35 ± 0.49 |
| | 400L | 1.000 | |
| | 500L | .985 | |
| 300L | 100L | 1.000 | |
| | 200L | .947 | 3.46 ± 0.52 |
| | 400L | .991 | |
| | 500L | 1.000 | |
| 400L | 100L | .999 | |
| | 200L | 1.000 | 3.36 ± 0.58 |
| | 300L | .991 | |
| | 500L | .999 | |
| 500L | 100L | 1.000 | |
| | 200L | .985 | 3.45 ± 0.51 |
| | 300L | 1.000 | |
| | 400L | .999 | |

Table 8: Differences in Perceptions of Nutrigenomic among class level

*. The mean difference is significant at the ≤ 0.05 level.

Note. Statistical significance was set at p. 0.05. Mean scores were calculated from a 5-point Likert style scale where (1) equals strongly disagree and (5) equals strongly agree. Abbreviations: **SD**, standard deviation; **n**, number of members in the sample.

| Test Variable | Group Variable | p-Value | Test Variable (Mean ± SD) |
|---|---|---|---|
| **COLANIM** | COLPLANT | 0.361 | |
| | COLFHEC | 0.791 | 3.65 ± 0.44 |
| | COLBIOS | 0.362 | |
| **COLPLANT** | COLANIM | 0.361 | |
| | COLFHEC | 0.847 | 3.54 ± 0.60 |
| | COLBIOS | 0.999 | |
| **COLFHEC** | COLANIM | 0.791 | |
| | COLPLANT | 0.847 | 3.59 ± 0.44 |
| | COLBIOS | 0.818 | |
| **COLBIOS** | COLANIM | 0.362 | |
| | COLPLANT | 0.999 | 3.53 ± 0.42 |
| | COLFHEC | 0.818 | |

Table 9: Differences in Perceptions of Nutrigenomic among class level

*. The mean difference is significant at the ≤ 0.05 level.
Note. Statistical significance was set at p ≤ 0.05. Mean scores were calculated from a 5-point Likert style scale where (1) equals strongly disagree and (5) equals strongly agree. Abbreviations: **SD**, standard deviation; **n**, number of members in the sample.

d) Factors influencing the awareness about Nutrigenomics for personalized nutrition

This section of the survey addressed common factors affecting participation in genetic testing for personalized nutrition. Results from this assessment are displayed in Table 10. On a modified 5-point Likert style scale, ranging from (1) 'not at all likely' to (5) ' completely likely, with (3) indicating 'moderately likely,' participants were most likely to be encouraged to know about nutrigenomics because of family history of a particular disease. The most common reason they would not participate, as indicated by survey responses, was a lack of money to pay for testing or possible treatments. Participants scored lowest against participation on factors regarding beliefs, privacy concerns, or think it's useless.

Independent sample t-tests were conducted (Table 10) comparing the likelihood of factors to influence participation in nutrigenomic testing between males and females. There was no significant difference between genders on all factors (p. 0.05), except I believe there is no expert to handle this field both in the health and education sector (p = 0.007). Overall, female respondents indicated that they were significantly more encouraged to participate than male respondents. Among free answer responses, many students indicated that they might not interested in knowing about nutrigenomic due to limited understanding, interest, and evidence of accurate results. Other common barriers included worry about inappropriate use of genetic information, especially by insurance companies. Common reasons for wanting to undergo a nutrigenomic test were improved health, fitness, and quality of life.

| Factors | Gender | Mean ± SD | (n) | p-Value |
|---|---|---|---|---|
| Dogmatic belief towards traditional Medicine | Male | 2.58 ± 1.29 | 149 | 0.106 |
| | Female | 2.37 ± 1.18 | 233 | |
| I believe is still a hypothesis | Male | 2.74 ± 1.12 | 149 | 0.741 |
| | Female | 2.70 ± 1.14 | 239 | |
| Availability of more detailed Information | Male | 3.62 ± 1.11 | 146 | 0.476 |
| | Female | 3.40 ± 1.12 | 230 | |

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| | | | | |
|---|---|---|---|---|
| I believe there are no expectations to handle this field both in health and education sector | Male<br>Female | 2.66 ± 1.14<br>2.84 ± 1.34 | 147<br>238 | 0.007 |
| Family or friend's advice* | Male<br>Female | 3.05 ± 1.25<br>3.04 ± 1.36 | 150<br>235 | 0.332 |
| Family history of particular disease* | Male<br>Female | 2.45 ± 1.33<br>2.57 ± 1.40 | 150<br>240 | 0.195 |
| Lack of money to pay for testing treatments or possible | Male<br>Female | 3.22 ± 1.30<br>3.13 ± 1.35 | 147<br>238 | 0.468 |
| Lack of time | Male<br>Female | 2.99 ± 1.60<br>2.96 ± 1.37 | 146<br>233 | 0.507 |
| Fear to discover some fact about my genetic makeup and what type of food to Eat | Male<br>Female | 2.67 ± 1.32<br>3.05 ± 1.51 | 144<br>236 | 0.713 |
| I think it's useless | Male<br>Female | 1.88 ± 1.27<br>1.86 ± 1.16 | 145<br>239 | 0.600 |
| It is not within my course specification | Male<br>Female | 2.24 ± 1.36<br>2.20 ± 1.33 | 140<br>229 | 0.718 |
| It is an invasion of privacy | Male<br>Female | 2.05 ± 1.20<br>2.07 ± 1.23 | 148<br>235 | 0.597 |

Table 10: Factors influencing the awareness about Nutrigenomics for personal nutrition among respondent

Table 10 Continued

| **Item** | **Gender** | **Mean ± SD** | **(n)** | **p-Value** |
|---|---|---|---|---|
| Nutrigenomics use many difficult fields to access and search for understanding | Male<br>Female | 3.12 ± 1.28<br>3.17 ± 1.23 | 150<br>234 | 0.767 |
| I don't have a lecturer that has a major Degree in the field unlike every other first. | Male<br>Female | 2.32 ± 1.30<br>2.37 ± 1.24 | 150<br>232 | 0.713 |
| It is just a recent advance in the field of nutrition and health though have gained large the ground in the developed Country | Male<br>Female | 2.96 ± 1.33<br>3.12 ± 1.26 | 150<br>234 | 0.876 |
| It requires sophisticated equipment to carry out genetic testing | Male<br>Female | 3.60 ± 1.23<br>3.08 ± 1.26 | 151<br>237 | 0.473 |
| Little or no Hospital facilities have the capability in term of trained staff to carryout genetic test for Personalized | Male<br>Female | 3.35 ± 1.21<br>3.08 ± 1.30 | 150<br>230 | 0.506 |

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| | | | | |
|---|---|---|---|---|
| Nutrition | | | | |
| I dislike anything that has to deal with Gene | Male<br>Female | 1.85 ± 1.16<br>1.86 ± 1.15 | 149<br>237 | 0.958 |
| Nutrigenomics as a course is very difficult to Understand | Male<br>Female | 2.32 ± 1.44<br>2.37 ± 1.34 | 147<br>237 | 0.129 |
| The tools of study used to understand nutrigenomics (e.gepigenomics, proteomics, metabolomics, etc.) are difficult to understand. | Male<br>Female | 2.66 ± 1.20<br>2.68 ± 1.19 | 150<br>237 | 0.703 |

Note. The mean was calculated from data from a 5-point Likert style scale where one equals 'Not at all likely' and five equals 'completely likely'. *Show statistical significance, where statistical significance was set at $p \leq 0.05$.
Abbreviations: **SD**, standard deviation; **n**, number of members in the sample.

*B. Discussion*

The main essence of this study was to examine college students' knowledge and perceptions of nutrigenomics for personalized nutrition. The study results showed that among college students, there was approximately 57% (n=229) genetic knowledge, college students perceive nutrigenomics for personalized nutrition as benefits that outweigh the risks, and there was no significant difference between males and females in the perception of nutrigenomics for personalized nutrition.

a) Characteristics of the Study Population

The study was conducted at the Federal Agricultural University in Abeokuta, Ogun State, and involved 400 students, 38.7% of whom were men and 61.3% were women. This shows a mirror result with respondents from Julianne G. Wilkins (2017), where the majority of respondents were female (73%). Respondents used in the study ranged in age from 17 to 35 years, in contrast to the study by Julianne G. Wilkins (2017), which ranged in age from 18 to 60 years. Respondents were selected using a multi-stage sample, in which four colleges were selected using simple random sampling techniques. From the randomly selected colleges, two departments were also randomly selected using simple random sampling techniques, and from each department respondents were selected on the basis of male to female ratio, in contrast to Julianne G. Wilkins (2017) where respondents were selected using targeted selection.

This study revealed that 50.8% of respondents were reported to have taking a college-level nutrition course, and 69.9% were reported to have taking a college-level genetics course. This result contrasts with the results of the Human Genome Education Model Project, where 80% of 3,600 health professionals reported that they had received no formal training in genetics in either their graduate or undergraduate programs (Lapham et al., 2000; Wilkins, 2017). These results are indicative of an improvement in the curriculum of higher institutions for college-level genetic education. These results also imply that if this group of graduate students work as healthcare professionals, knowledge may be abundant due to the improvement and availability of college genetics courses.

b) Awareness and Knowledge of Nutrigenomics

Majority of the students (60%) reported to have heard or read about nutrigenomics. The data from the present study isin contrasts with previous similar research among Canadian consumers, healthcare professionals and the public servant, which also revealed limited awareness and limited general knowledge about the omics science under study (i.e. Nutrigenomics)(Morin, 2009; Wilkins, 2017). Compared to a national survey conducted in the United States, where only 14% of respondents said they were aware of nutrigenomic tests, this study indicates greater awareness among students. In the same national survey, education and age under 55 were significant independent predictors of familiarity with nutrigenomics (Goddard et al., 2009; Wilkins, 2017). As university students tend to be younger and of higher academic

status than most Nigerians, this may explain university students' increased awareness of nutrigenomic testing and also suggest that they are a well-fitting population of potential consumers and/or advocates.

In the present study, university students correctly answered an average of 57% of the genetic knowledge questions. This finding reveal a mirror result with that of Julianne G. Wilkins (2017), where college students correctly answered an average of 55% of the genetic knowledge questions, indicating a general lack of genetic knowledge in this population. Other surveys conducted in the Netherlands found that around half to three quarters of chronic disease patients reported having little or no knowledge of genetics, with older respondents reporting significantly less than younger respondents (Wilkins, 2017). In another survey of 600 dietitians in the UK who also assessed genetic knowledge, the results were generally poor, averaging 41% correct on a validated multiple choice test (Whelan et al., 2008). Similarly, in a study by the Academy of Nutrition and Dietetics, only about half of the dietitians surveyed (n=913) said the definition of nutrigenomics was clear (Wilkins, 2017). The same patterns are seen among general practitioners, gynecologists, and paediatricians, where the results were on average 40%, 52%, and 62% correct, respectively (Wilkins, 2017). These findings support previous findings about significant gaps in genetic knowledge among health professionals (Rolfes SR, 2006) and imply that college programs may be an appropriate target to fill these gaps and provide a foundation of genetic background knowledge.

The present study also showed that those students in the College of Biological Science, which can be considered a major, who reported having taken a college-level genetics course demonstrated a higher understanding of basic genetics concepts in knowledge assessment. These results are consistent with a survey of gynecologists in the United States, where physicians with formal training in genetics perform significantly better than physicians without training on a range of questions related to genetic knowledge (Wilkins, 2017). This discovery is important because other surveys of healthcare professionals indicate a lack of confidence in the provision of genetic services among those without genetic education, and therefore confirm the value of providing genetic education beginning at the college level (Lapham et al., 2000; Wilkins, 2017).

Overall, the results of the current study indicate high participation in genetic education at the college level, along with an overall low level of genetic knowledge among college students. This could help explain the lack of genetics and nutrigenomics knowledge among trusted healthcare providers, an issue corroborated by several other studies. The relationship between genetic education and genetic knowledge among college students found in the present study, combined with previous reports of low confidence among physicians without genetic education, confirms the value of genetic education in college programs and beyond, especially for those who wish to apply nutrigenomics directly in the clinical setting.

In the present study, participants in the higher grades (400s and 500s) performed worse on the genetic knowledge assessment than those in the lower grades (100s, 200s, and 300s). Although this result was somewhat unexpected, it can be explained by the broad nature of the lower grade program, which typically includes courses from a variety of subjects, potentially giving lower grade students a more up-to-date exposure to concepts of genetics. Alternatively, lower scores at higher grade levels could be explained by their narrower focus of study and limited current exposure as they pursue more specialized degrees. Another possible explanation for the differences in genetic knowledge between grade levels could be related to the proportion of participants in the higher grades (400 and 500 levels) and lower grades (100, 200 and 300 levels) with science and health backgrounds. For example, the mean knowledge score for higher grade students (400s and 500s) might have been influenced by a lower proportion of participants with no health or medical educational background.

Furthermore, it is worthy of note in this study to refer to the outstanding and outwitting performance of students majoring in biological science areas as compare to those students majoring in agricultural sciences and physical science majors. These results make sense given that life sciences-related studies are more likely to include genetic disciplines than those focused on other areas. In particular, at the Federal Agricultural

University, Abeokuta, many biology, chemistry, biochemistry, and other programs require courses in genetics, while many other programs lack genetic prerequisites.

c) Perceptions of Nutrigenomic Testing

Overall, participants agreed more strongly with positive statements about nutrigenomic tests, while agreeing less with negative statements. Some previous studies have suggested support for genetic testing (Wilkins, 2017), but many of these are not specific to the use of nutrigenomics in nutritional care. So, this study was designed to assess the knowledge and perception of students toward the use, acceptance, social implication and perceive benefits of nutrigenomic knowledge. In this study, college students were most in agreement with the statement, "Nutrigenomics for personalized nutrition will lead to the prevention of some diseases" and were most concerned that nutrigenomics for personalized nutrition would cost too much and only be available to the wealthy. Overall, participants were most likely to agree with statements about the possibility of nutrigenomics to support disease prediction and prevention and were less likely to agree with statements about promoting and providing more money for nutrigenomic developments. This result mirrors the results of other survey research studies in which both patients and physicians reported that genetic testing would have a significant impact on the motivation to make healthier behavior changes (Grimaldi et al., 2017; Wilkins, 2017), and in which the costs greatest obstacle to nutrigenomic knowledge. Thispresent study agreed to the assertion made by Keith (2013), in his research and other similar previous researches that asserted that college students, along with other consumers, are concerned that genomic testing may be too expensive and excessive cost may be a critical factor influencing the decision to adopt nutrigenomic technology as a diet care tool use.

Privacy issues, religious beliefs, and fear of discovering disease susceptibility were all concerns cited as barriers to nutrigenomics in previous research studies (Fallaize et al., 2013; Grimaldi et al., 2017; Wilkins, 2017). The present study shows that these are not major concerns for college students. College students disagreed most strongly with the statement "Nutrigenomics for personalized nutrition contradicts my religious beliefs" and also showed limited agreement with the statement "I am concerned that not enough is being done to protect the confidentiality and privacy of my genetic information." This Findings may indicate an open-minded mindset with a greater focus on potential benefits that nutrigenomic testing could offer for nutritional care, which in turn makes university students a potential group of supporters and consumers.

d) Factors Influencing Decision to Participate in Nutrigenomic Testing

Previous research has shown that many factors influence individuals and populations when they decide to engage in the use of new technologies, and that they are more likely to engage in related behavior when the potential benefits outweigh the potential risks. Because nutrigenomics research is limited, the present study is the second to examine what factors might influence college students' decisions to take nutrigenomics tests. The results of the present study are based on findings from previous research, which highlighted a number of factors that could either encourage or discourage participation (Wilkins, 2017). However, in the present study, college students reported that they were more encouraged to use nutrigenomics than discouraged from using it. In addition, this research found that students were most encouraged by "family history of a particular illness" and most discouraged by "lack of funds for testing or possible treatment." This finding is consistent with another study in which the percentage of participants who said they would be willing to take a genetic test dropped from 48% to 5% after being told it would cost £250 (Keith, 2013). , and acknowledging the value of advances in nutrigenomics, cost is a major concern for these and other populations. Collectively, these findings underscore the need to develop more affordable means of discovering genetic susceptibility to disease so that nutritional genomics can be used to prevent chronic Illnesses can be used in all socioeconomic groups.

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# CHAPTER FIVE

# CONCLUSION AND RECOMMENDATION

## *A. Conclusions*

Experts believe nutrigenomics has great potential to lead to evidence-based nutritional intervention strategies that restore health and fitness and reduce the incidence and impact of complex diseases, which currently account for nearly two-thirds of deaths worldwide (Bauer et al., 2011; Wilkins, 2017). However, public support for the "omics" technology is unclear due to several obstacles and in particular excessive costs for consumers. With millennial university students representing the largest generation in Nigeria's history, the knowledge and perceptions of this populace can be critical in driving advances in this developing field. This study and previous studies aimed to explore and communicate the current perceptions of an influential generation about nutrigenomics. Examining these discoveries could help researchers and healthcare providers strategize, identify future opportunities, and address potential challenges, allowing nutrigenomic technology to thrive in the years to come.

To successfully use genetic blueprints for dietary disease prevention, researchers and scientists must uncover the mechanisms that drive the link between diet and the external expression of our genes (Afman& Müller, 2006; Wilkins, 2017) and then determine how these dietary interventions lead to improved health outcomes. As these goals are met and nutrigenomic knowledge and testing becomes more available, scientific initiatives and legislation must be developed to address ethical concerns and protect the public interest. Additional research is needed to better understand how nutrigenomic knowledge for personalized nutrition is perceived by university students and other populations. In addition, researchers need to more accurately interpret the interaction between genes and diet and establish evidence-based practices for the use of nutrigenomics technology so that healthcare professionals and consumers can find confidence in this scientific field.

## *B. Recommendations*

Based on the results of this study and the results derived from it, I will hereby recommend the following in order to promote the improvement of subsequent results in relation to this field of study:

- Awareness raising about nutrigenomics for personalized nutrition should be done through mass media to educate the public about this field as the majority of Nigerians are not aware that this field even exists.
- This study, if repeated, could be improved by examining the family histories of participants with chronic illnesses and their impact on knowledge and perceptions of nutrigenomics.
- The readability of some survey questions should also be addressed to improve clarity. In addition, validity and reliability studies on all questions would improve the credibility of subsequent research.
- Public awareness should be created and this should start with social mobilization and advocacy to increase engagement of key stakeholders who can positively influence and improve this area novel science.
- More research is needed to validate previous researches and dispel the major doubts that may exist among the Nigerian population.
- In-service trainings for healthcare professionals are required to understand the complexity of this area.
- Technology for a proper understanding of this field should be made available at the relevant institutes (both private and public) that are a concern in order to promote efficiency and raise the level of students and professionals studying this field and related ones study courses.

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## APPENDIX

## FEDERAL UNIVERSITY OF AGRICULTURE ABEOKUTA
## COLLEGE OF FOOD SCIENCE AND HUMAN ECOLOGY
## DEPARTMENT OF NUTRITION AND DIETETICS

Dear Respondent,

The researcher is a final year student of the Federal University of Agriculture, Abeokuta, carrying out a study on knowledge and perception of undergraduate students towards nutrigenomics for personalized nutrition therapy in the Federal University of Agriculture, Abeokuta**.** This study involves a Paper survey questionnaire designed to understand how college students perceive the use of Nutrigenomics to develop personalized nutrition regimens. The questionnaire is only meant for research purpose, your honest information will help in meeting the objectives of this research work, your response will only be used for survey purposes and will be kept confidential. Thank you very much for your time.

Respondent's consent: I---------- (Respondent Signature) hereby confirm that I have willingly agreed to participate, as a respondent in the above-named survey. I understand that any information I provide will be confidential, I do not have to go ahead if I do not wish to, and that there will be no harm or benefit to me from participating.

**Note**: If you are 18 years of age or older, understand the statements above, and freely consent to participate in the study, TICK the "I Agree" column to begin the survey.

**Questionnaire No ……**

### SECTION A
### Socio-demographic characteristics

**Instruction:** Write and tick the appropriate option that best communicates your response to the question below.

Q1. Age at last birthday?.....…….
Q2. Gender? (a) Male (b) Female
Q3. What is your Department? _____
Q4. What level are you in? (a) 100L (a) 200L (c) 300L (c) 400L (d) 500L

### SECTION B
### General Question
**Instruction:** Tick the appropriate option that best communicate your response for the question below.

Q5. Have you ever taken a departmental level course on Animal/Human nutrition? (a) Yes (b) No
Q6. Have you ever taken a departmental level genetics course? (a) Yes (b) No If yes,
Q7. Nutrigenomics is the study of the interaction between nutrition and genes. Some courses deal with genetics that enhances the understanding of nutrigenomics for personalized nutrition therapy. (Example includes Single Nucleotide Polymorphism, Nucleic acid, Metabolomics, Epigenomics, Interleukin Genetics, etc.) Have you heard or read about these genetics fields? (a) Yes (b) No
Q8. Personalized nutrition means giving of nutrition therapy to individuals base on personal needs or individual requirements. Nutrition therapy in the past has been based on generalized dietary management, but nutrigenomics thought about the effect of a nutrient on gene expression. Do you think this field of study can improve the management and prevention of disease conditions? (a) Yes (b) No

### SECTION B
### Knowledge and Perception of university students toward Nutrigenomics for Personalized Nutrition

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Q9. The following statements are about the knowledge of nutrigenomics for personalized nutrition. To what extent do you agree or disagree with each statement? Tick as appropriate the correct option that best communicates your response.

| **Questions** | Strongly disagree (1) | Disagree (2) | Neither agree nor disagree (3) | Agree (4) | Strongly agree (5) |
|---|---|---|---|---|---|
| Screening for known genes is the way forward for medicine and nutrition. (Q9_1) | | | | | |
| Gene testing for personalized nutrition will lead to the prevention of some diseases. (Q9_2) | | | | | |
| In my lifetime, I expect to see significant medical improvements due to the use of genetics in nutrition. (Q9_3) | | | | | |
| I am concerned that my genetic information will be made available for research purposes. (Q9_4) | | | | | |
| My genes have influenced my health. (Q9_5) | | | | | |
| Nutrigenomics knowledge for personalized nutrition is too hard to understand. (Q9_6) | | | | | |
| I would like to know about future diseases through the knowledge of nutrigenomics. (Q9_7) | | | | | |
| I think there is too much focus on genetics when money could be spent on the world's starving population. (Q9_8) | | | | | |
| Genetic testing for personalized nutrition should be available to everyone. (Q9_9) | | | | | |
| I am concerned that not enough work will be done to protect the confidentiality and privacy of my genetic information. (Q9_10) | | | | | |

Q9 **Continued**. The following statements are about the perception of nutrigenomics for personalized nutrition. To what extent do you agree or disagree with each statement? Tick as appropriate the correct option that best communicates your response.

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| **Questions** | Strongly disagree (1) | Disagree (2) | Neither agree nor disagree (3) | Agree (4) | Strongly agree (5) |
|---|---|---|---|---|---|
| Having Knowledge about nutrigenomics allows individuals to control their lifestyle more easily. (Q9_11) | | | | | |
| Genetic knowledge for personalized nutrition will result in discrimination. (Q9_12) | | | | | |
| Nutri-genetic for personalized nutrition will help people to live longer. (Q9_13) | | | | | |
| All individuals should be made aware of nutrigenomics for personalized nutrition. (Q9_14) | | | | | |
| Nutrigenomics knowledge would cost too much and would only be available to the educated. (Q9_15) | | | | | |
| I am worried that nutrigenetic testing may lead to eugenics (the science of improving the human population by controlling breeding to increase desirable characteristics). (Q9_16) | | | | | |
| Nutrigenomics knowledge for personalized nutrition will make medical cures for diseases more possible. (Q9_17) | | | | | |
| Nutrigenomics knowledge for personalized nutrition should be promoted extensively. (Q9_18) | | | | | |
| I do not believe that nutrigenomics for personalized nutrition is backed by sound science. (Q9_19) | | | | | |
| Genetic testing for personalized nutrition goes against my religious beliefs. (Q9_20) | | | | | |
| I believe it is essential to assign more money to nutrigenomic developments. (Q9-21) | | | | | |

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**SECTION C**

**Factors influencing the awareness towards the knowledge of Nutrigenomics**,
Q10. To what extent do the following reasons allow you to OR disallow you from the knowledge of nutrigenomic for personalized nutrition? Tick as appropriate the correct option that best communicates your response.

| **Questions** | Not at all likely (1) | Slightly likely (2) | Moderately likely (3) | Very likely (4) | Completely likely (5) |
|---|---|---|---|---|---|
| Dogmatic belief towards traditional medicine (Q10_1) | | | | | |
| I believe is still a hypothesis (Q10_2) | | | | | |
| Availability of more detailed information (Q10_3) | | | | | |
| I believe there is no expert to handle this field both in health and education sector (Q10_4) | | | | | |
| Family or friend's advice (Q10_5) | | | | | |
| Family history of a particular disease (Q10_6) | | | | | |
| Lack of money to pay for testing or possible treatments (Q10_7) | | | | | |
| Lack of time (Q10_8) | | | | | |
| Fear to discover some fact about my genetic makeup and what type of food to eat (Q10_9) | | | | | |
| I fear that some of my favorite food might be incompatible with my genetic makeup. | | | | | |
| I think it's useless (Q10_10) | | | | | |
| It is not within my course specification (Q10_11) | | | | | |
| It is an invasion of privacy (Q10_12) | | | | | |
| The tools of study used to understand nutrigenomics (e.gepigenomics, proteomics, metabolomics, etc.) are difficult to understand(Q10_13) | | | | | |
| Nutrigenomics use many difficult fields to access and search for understanding such as biochemistry, physiology, Genetics, Epidemiology, Molecular Biology, etc.(Q10_14) | | | | | |
| I don't have a lecturer that has a major degree in the field unlike every other first. (Q10_15) | | | | | |

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| | | | | | |
|---|---|---|---|---|---|
| It is just a recent advance in the field of nutrition and health though it has gained large ground in the developed country. (Q10_16) | | | | | |
| It requires sophisticated equipment to carry out genetic testing. (Q10_17) | | | | | |
| Little or no Hospital facilities have the capability in term of trained staff to carry out a genetic test for Personalized Nutrition(Q10_18) | | | | | |
| I dislike anything that has to deal with a gene. (Q10_19) | | | | | |
| Nutrigenomics as a course is very difficult to understand. (Q10_20) | | | | | |

**SECTION D**

**Knowledge of genetics among undergraduate towards an understanding of nutrigenomics**

The following questions are designed to assess your knowledge of genetics. Please read each question carefully. If you do not understand or don't feel comfortable answering a question, please choose "Don't know." Please do not guess if you do not know the answer. Instead, choose "Don't know." Tick as appropriate the correct option that best communicates your response.

Q10. A gene is a portion of DNA, which codes for protein, which leads to a trait.
(a) True ( ) (b) False ( ) (c) Don't know ( )

Q11. Males inherit two X-chromosomes at birth, one from their mother and one from their father. (a) True ( ) (b) False ( ) (c) Don't know ( )

Q12. The human genome project has estimated that humans have between 20,000 and 25,000 genes. (a) True ( ) (b) False ( ) (c) Don't know ( )

Q13. Genes contain chromosomes.
(a) True ( ) (b) False ( ) (c) Don't know ( )

Q14. A genotype is the genetic make-up of an organism.
(a) True ( ) (b) False ( ) (c) Don't know ( )

Q15. In humans, each cell normally contains 23 pairs of chromosomes, for a total of 46. (a) True ( ) (b) False ( ) (c) Don't know ( )

Q16. A phenotype is a physical expression of alleles (brown eyes or blue eyes).
(a) True ( ) (b) False ( ) (c) Don't know ( )

Q17. A mutation occurs when the structure of a gene changes.
(a) True ( ) (b) False ( ) (c) Don't know ( )

Q18. Mutations always lead to negative health outcomes.
(a) True ( ) (b) False ( ) (c) Don't know ( )

Q19. An allele is the different forms of a gene, represented by letters.
(a) True ( ) (b) False ( ) (c) Don't know ( )

Q20. A dominant trait is the trait which is hidden in F1 generation.
(a) True ( ) (b) False ( ) (c) Don't know ( )

Q21. Epigenetics is the study of changes in an organism's gene expression without a change in the genetic code. (a) True ( ) (b) False ( ) (c) Don't know ( )

Q22. DNA repair is a collection of processes where a cell identifies and repairs DNA molecules that encode its genome. (a) True ( ) (b) False ( ) (c) Don't know ( )

Q23. A point mutation is a type of mutation that causes a single nucleotide base substitution, insertion, or deletion. (a) True ( ) (b) False ( ) (c) Don't know ( )

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Q24. An example of a genotype that is heterozygous is AA.
(a) True ( ) (b) False ( ) (c) Don't know ( )

Q25. An example of a genotype that is homozygous is cc.
(a) True ( ) (b) False ( ) (c) Don't know ( )

Q26. Mutations can create variations in protein "switches" that control protein function. (a) True ( ) (b) False ( ) (c) Don't know ( )

Q27. Mutations cannot be reversed through DNA repair.
(a) True ( ) (b) False ( ) (c) Don't know ( )

Q28. A recessive trait can be carried in a person's genes without appearing in their phenotype. (a) True ( ) (b) False ( ) (c) Don't know ( )

Q29. RNA contains the genetic information which is encoded in gene preserve for generation to come.(a) True ( ) (b) False ( ) (c) Don't know ( )