Consumption Pattern of Prebiotics and Plant extracts among Young Adults and Implementation of Digital Health Intervention for Promoting Healthy Gut Microbiome

SRINITHYA.G
(20PFN023)

A THESIS SUBMITTED TO

AVINASHILINGAM INSTITUTE FOR HOME SCIENCE AND
HIGHER EDUCATION FOR WOMEN
COIMBATORE-6410 043

IN PARTIAL FULFILLMENT OF THE REQUIREMENTS
FOR DEGREE OF
MASTER OF SCIENCE IN FOOD SCIENCE AND NUTRITION

MAY 2022

CERTIFICATE

Consumption Pattern of Prebiotics and Plant extracts among Young Adults and Implementation of Digital Health Intervention for Promoting Healthy Gut Microbiome

SRINITHYA.G

(20PFN023)

A THESIS SUBMITTED TO
AVINASHILINGAM INSTITUTE FOR HOME SCIENCE AND
HIGHER EDUCATION FOR WOMEN
COIMBATORE-6410 043

IN PARTIAL FULFILLMENT OF THE REQUIREMENTS
OF THE DEGREE OF
MASTER OF SCIENCE IN FOOD SCIENCE AND NUTRITION

MAY 2022

20/5/22
Signature of the Supervisor

M. Sylvia
20/5/22
Signature of the Head of the Department

DECLARATION

DECLARATION

I hereby declare that the dissertation entitled **"Consumption Pattern of Prebiotics and Plant extracts among Young Adults and Implementation of Digital Health Intervention for Promoting Healthy Gut Microbiome"**, submitted to the Avinashilingam Institute for Home Science and Higher Education for Women, Coimbatore, in partial fulfilment of the requirement forthe award of the **Degree of Master of Science in Food Science and Nutrition** is a record of originalresearch work done by me under the supervision and guidance of **Prof. (Mrs.). C.A. Kalpana,** Department of Food Science and Nutrition, Avinashilingam Institute for Home Scienceand Higher Education for Women, Coimbatore and that it has not formed the basis for the award of any Degree/ Diploma/ Associateship/ Fellowship or similar title to any candidate of any otherUniversity and it represents entirely an independent work on the part of the candidate.

20/5/22

Signature of the Supervisor

Srinithya G.

Signature of the Candidate

ACKNOWLEDGEMENT

ACKNOWLEDGEMENT

First and foremost, the investigator places her humble salutations at the feet of**God Almighty** who has given sound wisdom, knowledge, strength and opportunity to do the investigation effectively.

The investigator owes her respectful gratitude to **Late Prof. (Thiru) T.S. Avinashilingam**, Founder and First Chancellor of Avinashilingam Institute for Home Science and Higher Education for Women Coimbatore, for providing this temple of learning to do this research.

The investigator records her reverential gratitude to **Late Hon. Colonel Prof. (Tmt.) Rajammal P. Devadas, M.A., M.Sc., Ph.D (Ohio State), Hon. D.Sc.(Madras, Hon D.H.L.(Oregon State), Hon. D.H.L.(Ohio State), D.S.C.(Kanpur), Hon.D.Sc. (Northern Ireland),** Former Chancellor, Avinashilingam Institute for Home Science and Higher Education for Women, Coimbatore, for being a perennial source of inspiration for conducting the study.

The investigator expresses her heartfelt thanks and deep sense of gratitude to**Prof. S. P. Thyagarajan, Ph.D., M. D, D. Sc, FAMS, FNASc, FIMSA, FABMS, FFTM (Glasgow, UK), Chancellor**, Avinashilingam Institute for Home Science and Higher Education for Women, Coimbatore for providing the infrastructural facilities for the smooth conduct of the study.

The investigator offers her deepest gratitude to **Prof. T.S.K. Meenakshisundaram, M.A., M.Phil., Ph.D., Managing Trustee**, Sri Avinashilingam Education Trust Institutions, Coimbatore, for providing the opportunity to conduct the study.

The investigator owes her special thanks to **Prof. (Mrs.). Bharathi Harishankar,** Vice Chancellor, Avinashilingam Institute for Home Science andHigher Education for Women, Coimbatore for the amenities provided for the successful completion of the study.

The investigator records her sincere gratitude to **Prof. (Mrs.). S. Kowsalya, M.Sc., M.Phil., Ph. D.,** Registrar, Avinashilingam Institute for Home Science and Higher Education for Women, Coimbatore for providing all help in the smooth conduct of the study.

The investigator owes her heartfelt thanks to **Prof. (Mrs.) N. Vasugi, M.sc., M.B.A., M.Phil., Ph.D.,** Dean, Faculty of Home Science, Avinashilingam Institute for Home Science and Higher Education for Women, Coimbatore, for her kind support and encouragement for the conduct of the study.

It gives the investigator an immense pleasure and proudness to offer profound gratitude to **Prof. (Mrs.) M. Sylvia Subapriya, M.Sc., M.Phil., B.Ed., Ph.D.**, Professor and Head, Departmentof Food Science and Nutrition, Avinashilingam Institute for Home Science and higher Education for Women, Coimbatore, for the keen interest, valuable help, concern and encouragement which were helped in the successful completion of the study.

The investigator expresses her deep sense of gratitude to **Prof. C.A. Kalpana, M.Sc., B.Ed., M.Phil., Ph.D., SLET., NET.,** Professor, Department of Food Science and Nutrition, Avinashilingam Institute for Home Science and Higher Education forWomen, Coimbatore, for her meticulous guidance, deep concern, constructive suggestions and sincere help from the initial to the final level of the study.

Out of deep sense of indebtedness, the investigator expresses her sincere thanks to all the **Staff Members** of the **Department of Food Science and Nutrition**, Avinashilingam Institute for Home Science and Higher Education for Women, Coimbatore who helped her with their constructive suggestions at all times.

The investigator also wishes to express her deep indebtedness and gratefulness to her **Parents, Sisters, Friends and All Well Wishers** for their patience, motivation and constant support throughout the course of the study.

CONTENTS

CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF PLATES

LIST OF APPENDICES

Introduction

I. INTRODUCTION

A microbial community, known as the microbiome, resides in the mammalian gut. Bacteria, archaea, viruses, and eukaryotic microorganisms inhabit interactive interfaces that are exposed to or connected to the external environment in the human body. The human microbiota is a collection of microorganisms that comprises around 100 trillion microbial cells, and the genes encoded by these microbes collectively create the human microbiome. The human gut microbiota consists of trillions of microbes that form a complex ecosystem. Although some researchers have suggested that the number of microbes in the human gut is tenfold the total number of human somatic cells, a recent estimate has calculated that the numbers are of the same order, with the total number of bacteria in the human body being around 3.8×10^{13}.

Microbiota and host have a mutually beneficial symbiotic relationship. The gut microbiota supports the development of the metabolic system and the maturation of the intestinal immune system by providing beneficial nutrients, such as the synthesis of vitamins and short-chain fatty acids, and the host provides crucial habitat and nutrients for the microbiome. Therefore, the interaction between the microbiome and intestinal immune system is critical to maintaining mucosal homeostasis (Shi *et al.,* 2017).

Microbial colonization of the human gut begins at birth. The infant's intestines are believed to be sterile or contain a very low level of microbes at birth, but the GIT is quickly colonized during and after delivery. As a neonate passes through the birth canal, he or she is exposed to the microbial population of the mother's vagina. This process influences the development of an infant's intestinal microbiota, which shows similarities to the vaginal microbiota of his or her mother. Infants who were delivered through cesarean section showed reduced microbial numbers in the gut at 1 month when compared with those who were delivered vaginally, although these differences do not remain detectable at 6 months of age (Sharma *et al.,* 2019).

Infants delivered vaginally harbor microbial communities, dominated by Lactobacillus spp. and Bifidobacterium spp., which are similar to their mother's vaginal canal. Conversely, infants delivered by cesarean section are colonized by microbial communities composed of common skin microbes with Staphylococcus as the predominant genus. These studies suggest that neonatal acquisition of the intestinal microbiome is dependent on the organisms encountered in the first hours and days of life from the mother and environment. These early colonizers are enriched for genes governing the metabolism of sugars found in milk as well as those involved in the de novo synthesis of folate, representing critical metabolic functions in the developing host gut (Barko *et al.,* 2018).

The gut microbiome provides a broad range of functions. Most importantly, it collects indigestible particles from food into faecal waste and assimilates nutritional particles, such as vitamins and minerals. It acts with the liver to detoxify and excrete xenobiotics; ubiquitous harmful foreign chemicals present in the environment. An individual's systemic and intestinal immune systems depend greatly on the gut microbiome's function of epithelial cell renewal and management of intestinal integrity. Without a healthy intestinal wall, bacteria migrate across the gut into the general circulation increasing systemic inflammation. This migration occurs through a mechanism of intestinal permeability sometimes referred to as "leaky gut". With a leaky gut, junctions, composed of various proteins that link adjacent intestinal epithelial cells, are weak and fail to act as an integral barrier to migrating pathogens (Edwards *et al.,* 2017)

Most of the contributions made by the gut microbiota to the physiology of the human superorganism are related to microbial metabolism. The colon is the major site of this fermentation, as its relatively high transit time and pH coupled with low cell turnover and redox potential present more favourable conditions for the proliferation of bacteria. The three macronutrients consumed in the human diet, carbohydrates, proteins, and fat, can reach the colon upon either escaping primary digestion, Several factors can influence digestive efficiency, which in turn modulates the substrates available to the gut microbiota for consumption, including the form and size of the food particles (affected by cooking and processing), the composition of the meal (affected by the relative ratios of macronutrients and presence of anti-nutrients such as α-amylase inhibitors), and transit time (Oliphant *et al.,* 2019).

Fruits, vegetables, and cereals are major components other human diet providing essential carbohydrates and dietary fibres, (Mills *et al*., 2019) identified only 17 enzymes within the human genome to break down carbohydrate nutrients which included starch, lactose, and sucrose. Thus, plant cell wall polysaccharides and resistant starch, which constitute most dietary fibres and cannot be digested or absorbed in the small intestine, enter the large intestine and undergo microbial breakdown and subsequent fermentation.

Collectively, the carbohydrates consumed by the microbiota have been termed "microbiota accessible carbohydrates" (MACs). Carbohydrate active enzymes (CAZymes) break down MACs into fermentable monosaccharides. For example, the gut bacterium Bacteroides thetaiotaomicron was recently shown to metabolize the most structurally complex plant polysaccharide known, rhamnogalacturonan-II, using a highly specific enzyme system. Bifidobacterium longum strains derived from the infant's gut were shown to be capable of metabolizing human milk oligosaccharides (Ndeh *et al.,* 2017, Arboleya *et al.,* 2018).

The systemic effect of microbiota is mediated by microbial metabolites such as short-chain fatty acids (SCFAs), and the gases hydrogen sulfide, ammonia, hydrogen, methane, carbon monoxide, and carbon dioxide. SCFAs, which comprise mainly acetate, propionate, and butyrate, are produced under anaerobic conditions in the large intestine by fermentation of dietary fibres. Consequently, SCFAs have multiple effects on the host, including acting as an energy source, promoting glucose and energy homeostasis, regulating immune responses and inflammation, regulating anorectic hormones which have a role in appetite control, tumor suppression (especially butyrate), and regulating central and peripheral nervous systems (Mohajeri *et al.,* 2018).

The intestinal mucosal immune system constitutes the largest immune component in vertebrates, functioning closely with the intestinal microbiome. The balance of the intestinal mucosa immune system plays a key role in host homeostasis and defense. Epithelial cells are the second physical barrier of the intestinal mucosal immune system, and they directly participate in the immune surveillance of the gut. The microbiome produces metabolites, such as butyrate and tryptophan decomposition metabolites that can enhance gut integrity and stimulate innate lymphoid cells group 3 (ILC3) to produce Inter Leukin-22 (Shi *et al.,* 2017).

An impaired interaction between intestinal microbiota and the mucosal immune system is associated with the pathogenesis of inflammatory diseases, such as Inflammatory bowel disease (IBD), Rheumatoid arthritis (RA), Systemic lupus erythematosus (SLE), Ankylosing spondylitis (AS), etc., and it highlights the importance of exploring the function of microbiota in such diseases (Shi *et al.,* 2017).

In the past 10 years, considerable information has been accumulated on the action of microbiome on the central nervous system (CNS) and "brain-gut-microbiota axis" conception was proposed. The CNS regulates the permeability, secretion, motility, and immunity of the digestive tract by exerting its effect on the enteric nervous system, muscle tissue and the mucous layer of the intestine through the efferent autonomic nervous pathways. In turn, the intestinal microbiome is able to influence brain functions through afferent signaling pathways and through the secretion of biologically active substances (Askarova *et al.,* 2020).

Studies carried out on laboratory animals are confirmed by clinical data obtained in the study of the intestinal microbiome of the elderly. The association of brain amyloidosis with pro-inflammatory intestinal bacterial taxa and peripheral markers of inflammation in people of old age suffering from cognitive disorders was shown (Cattaneo et al., 2016). The results of this study demonstrated that, in dementia patients with amyloidosis, an increased level of pro-inflammatory cytokines in the blood (IL-6, CXCL2, NLRP3, and IL-1β) was accompanied by a reduced content of E. rectale and an increased content of Escherichia/Shigella in stool samples (Askarova *et al.,* 2020).

In recent years, there has been a growing appreciation for the ability of the gut microbiota to produce neurochemicals that can influence the peripheral enteric and central nervous systems. For example, gamma-aminobutyric acid (GABA) is a major inhibitory neurotransmitter in the brain and neuropsychiatric disorders, including anxiety and depression, have been linked to GABA system dysfunction. Strains of culturable lactobacilli and Bifidobacteria from the human intestine were shown to produce GABA, namely Lactobacillus Brevis, Bifidobacterium dentium, adolescentis, and infantis. Furthermore, GABA was found to serve as a growth factor for a previously uncultured gut bacterium, Flavonifractor sp. which was shown to ferment GABA (Mills *et al.,* 2019).

Clostridium difficile is a spore-forming, Gram-positive anaerobe, producing toxins A and B; the latter is responsible for colonic inflammation and the development of pseudomembranous colitis. The traditional treatment for CDI has been with metronidazole or vancomycin, and removal of the offending trigger antibiotic; however, this is proving increasingly ineffective with recurrence rates up to 50% and increasing incidence of fulminant disease. correcting underlying dysbiosis through fecal microbiota transplant (FMT) is more effective and durable than antibiotic therapy for recurrent CDI (Sidhu *et al.,* 2017).

The use of antibiotics limits not only the activity of pathogenic bacteria but also the commensal microbial population living in the gut. Several reports suggest that a shift in the gut microbial population due to antibiotic usage may be associated with the progression of DM.

Antibiotic treatment could modulate fat mass and SCFA levels. Infants with the onset of diabetes are characterized by less diversity of gut microbiome due to over-usage of antibiotics. This transformation has been considered a prediabetic microbial signature (Sharma *et al.,* 2019).

Therapeutic manipulation of the intestinal microbiome is generally achieved through modification of the diet, administration of prebiotics, probiotics, antibiotics, more recently, fecal microbiome transplantation (FMT). These therapies are meant to shift microbial community states associated with dysbiosis to those associated with health (Barko *et al.,* 2018).

Fermentation of dietary prebiotics in the gut involves metabolic cross-feeding where the products of fermentation by one or more bacterial species provide the substrate(s) for other bacterial species. This complex cooperative activity of the gut microbiota is essential for good health (Nahoum *et al.,* 2016).

In a three-group randomized intervention study, infants fed prebiotic GOS+inulin supplemented milk had comparable numbers of fecal *Bifidobacteria* and *lactobacilli* to infants who were breast fed, whereas infants fed standard formula milk had significantly lower numbers of both bacterial genera. Incidence of gastrointestinal and upper respiratory tract infections was significantly lower in breast fed infants or the ones fed prebiotic supplemented milk compared to standard formula milk. Similarly, allergic reactions to food and milk were significantly higher in the standard formula milk group (Mohajeri *et al.,* 2018).

Two recent studies showed that the detrimental effects of high fat diets on penetrability of the mucus layer and metabolic functions could be prevented through dietary administration of inulin (Zou *et al.,* 2018). Overall, these findings, together with the role of butyrate in preventing oxygen induced gut microbiota dysbiosis, provide a strong rational to enrich dietary fibre consumption to maintain intact mucosal barrier function in the gut (Ray, 2018).

Probiotics are formulations of live organisms that confer beneficial effects on the recipient when delivered in adequate amounts. Proposed mechanisms through which probiotics improve host health include reducing intestinal permeability by upregulation of tight junction proteins, increasing mucin secretion by goblet cells, increasing the secretion of defensins which prevent pathogen colonization, production of SCFAs, stimulation of IgA secretion, decreasing luminal pH, and enhancing and directing immune cells to promote tolerance to commensals while maintaining protection against pathogens (Grzeskowiak *et al.,* 2015).

The most commonly used probiotic organisms include Lactobacillus and Bifidobacterium. Additional bacteria used include Bacillus and Streptococcus as well as the yeast, Saccharomyces boulardii. It is essential to remember that probiotic organisms are often strain-specific. To remain viable, probiotics must survive the acidic environment of the stomach and bile acid to colonize the intestines. However, probiotics appear to confer benefits without changing the microbiome permanently and transient colonization is still associated with beneficial effects in the host (Barko, *et al.,* 2018).

Fecal microbiome transplantation entails the transfer of feces from a healthy donor into the intestinal tract of a diseased recipient. The first modern record of FMT, for the treatment of humans with pseudomembranous colitis, was reported in 1958, and all 4 patients that were treated survived. The route of delivery varies between studies and includes oral capsules, nasogastric, nasoduodenal, and colonoscopic administration, and via enema (Choi *et al.,* 2016).

The first condition where the FDA has granted investigational new drug status for FMT in the United States was Clostridium difficile infection. Patients with recurrent C. difficile (RCDI) have decreased proportions of fecal Bacteroidetes and Firmicutes, and an ~90% cure rate is expected after FMT. In patients with RCDI after FMT, the recipient's fecal microbiome mirrors that of the donor, up to 24 weeks after FMT (McMichael *et al.,* 2018).

An online survey is a structured questionnaire so that the targeted audience can easily complete it over the internet generally by filling out a form. An online survey is one of the most famous data-collection sources, here a set of questions is sent out to a target sample and the study participants can complete the questions over the world wide web. The subjects receive survey forms through various mediums such as social media, email, the website, etc.

Unlike a traditional survey, an online survey offers a way to collect information from a huge audience for very little cost. The most crucial element is that the survey form should be as concise as possible; otherwise, study participants may become agitated and abandon the concept of completing the forms. The reason for conducting an online survey is first, survey forms can be sent them out from the researcher's desktops or laptops. Secondly, the study participants can have the option to respond to the surveys whenever the time is better for them. The advantages of conducting an online survey include serving as a faster medium to reach the target audience, Real-time analysis (software is available for analyzing the collected data), cost-efficient (much cheaper than other survey methods), an online survey can be answered with a click and saves the researcher’s time.

With this in view, the present study was undertaken with the following objectives.
To-

- Assess the knowledge of young adults on Gut microbiome.
- Study the consumption pattern of Prebiotics and Plant among young adults.
- Develop and implement digital health intervention for promoting healthy Gut microbiome.
- Evaluate the impact of Digital health intervention.

Review of Literature

II. REVIEW OF LITERATURE

The review of literature pertaining to this study entitled "Consumption pattern of Prebiotics and Plant extracts among young adults and Implementation of Digital Health Intervention for Promoting Healthy Gut Microbiome" is discussed under the following headings:

A. Gut microbiome- An Insight
B. Plant food components and health
C. Prebiotics and Gut microbiome
D. Dietary fibre and gut microbiota composition
E. Digital health intervention for promoting gut health.

A. GUT MICROBIOME- AN INSIGHT

The life forms on this earth can be clustered into three broad domains: namely Archaea, Bacteria, and Eukaryota. All life has evolved from a simple unicellular common ancestor over billion years of evolution giving rise to the complexity of cells within an organism. The human is a superorganism that functions in harmony with trillions of symbiotic bacteria and eukaryotic cells. The host and its symbionts together are called a "holobiont," and their collective genome is known as a "hologenome". Variation in the hologenome either by changes in the host genome or the microbiome may occur with reasonable fidelity maintaining the plasticity of the holobiont (Adak *et al.,* 2019).

The gut microenvironment mainly favours the growth of bacteria from seven predominant divisions (Firmicutes, Bacteroidetes, Actinobacteria, Fusobacteria, Proteobacteria, Verrucomicrobia and Cyanobacteria) (Backhed *et al.,* 2015).

Among these seven divisions, the Bacteroidetes and Firmicutes constitute more than 90% of the total population. Most of the species under the phylum Bacteroidetes belong to the genera of *Bacteroides* and *Prevotella*. Bacterial species under the phylum Firmicutes such as *Clostridium* clusters IV and XIVa which include the genera *Clostridium*, *Eubacterium* and *Ruminococcus* are predominant in gut. *Methanobrevibacter smithii* a hydrogen-consuming methanogen and halophilic *Haloferax alexandrinus* and *Haloferax massiliensis spp*. nov. from Archaea had been reported from human gut (Lagier *et al.,* 2016).

In the LI, the number of anaerobes outnumbers the aerobes by a factor of 100–1000. The bacterial density reaches to 10^{12} CFU/ml and is mainly dominated by Firmicutes and Bacteroidetes. In the lumen of LI, bacterial genera such as *Bacteroides*, *Bifidobacterium*, *Streptococcus*, *Enterobacteriaceae*, *Enterococcus*, *Clostridium*, *Lactobacillus,* and

Ruminococcus are predominant, whereas *Clostridium*, *Lactobacillus*, *Enterococcus,* and *Akkermansia* are associated with the mucosa. In addition, a few pathogens including *Campylobacter jejuni*, *Salmonella enterica*, *Vibrio cholera*, *E Coli,* and *Bacteroides fragilis* may present in the LI with lower abundance (0.1%) (Adak, *et al.,* 2019).

Gut microbiota performs its function on four different landscapes in the human body: metabolic, protective, structural, and neurological. The carbohydrates that escape from the digestion and absorption in SI are utilized by a number of microbes present in LI. The saccharolytic activities of the microbes present in LI ferment the undigested carbohydrates resulting in SCFAs production, viz. acetate, propionate and butyrate. SCFAs are either transported or diffused into host cells and sensed by binding with G protein-coupled receptors such as GPR41, GPR43 and GPR109A on epithelial and immune cells (Rooks *et al.,* 2016).

Butyrate is essential for epithelial cells to consume large amounts of oxygen through β oxidation, generating a state of hypoxia that maintains oxygen balance in the gut, preventing gut microbiota dysbiosis (Byndloss *et al.,* 2017). Propionate is transferred to the liver, where it regulates gluconeogenesis and satiety signaling through interaction with the gut fatty acid receptors. Acetate—the most abundant SCFA and an essential metabolite for the growth of other bacteria—reaches the peripheral tissues where it is used in cholesterol metabolism and lipogenesis, and may play a role in central appetite regulation (Morrison *et al.,* 2016).

Randomized controlled trials have shown that higher production of SCFAs correlates with lower diet-induced obesity and with reduced insulin resistance. Butyrate and propionate, but not acetate, seem to control gut hormones and reduce appetite and food intake in mice. Gut microbial enzymes contribute to bile acid metabolism, generating unconjugated and secondary bile acids that act as signaling molecules and metabolic regulators to influence important host pathways (Long *et al.,* 2017).

Normal gut microbiota is our first internal line of defense against pathogens and toxins, protecting the body against disease in tandem with the host immune system. One of the key functions of a healthy microbiome is to prevent the colonization of pathogens through a barrier effect. This occurs through the production of antimicrobial compounds such as bacteriocin and the outcompeting of pathogens for nutrients and attachment sites through sheer force of numbers.

Gut bacteria are also integral to the development of the mucosal innate immune system through direct interactions with intestinal epithelial cells. Early exposure to a variety of bacteria provides a kind of training for the immune system such that normal protective responses occur to commensals and appropriate inflammatory responses occur with exposure to pathogens.

Conversely, reduced microbial diversity and exposure early in life can lead to an immune system that over-reacts to antigens, predisposing to autoimmune and allergic diseases (Khodor, *et al.,* 2017).

Activities of gut microbiota can control the ENS as well as CNS via (1) production, expression and turnover of neurotransmitters and neurotrophic factors, (2) maintaining the intestinal barrier and tight junction integrity, (3) modulating the enteric sensory afferents, (4) production of bacterial metabolites and (5) mucosal immune regulation. The ENS can sense more than 30 neurotransmitters most of which are found in the CNS, such as acetylcholine, dopamine and serotonin. More than 90% of serotonin and 50% of dopamine originate in the gut which are mainly produced by the gut microbiota. These two neurotransmitters play an important role in transmission of "fight to fight" message to the brain in controlling of mood, happiness and pleasure of an individual (Sarkar *et al.,* 2016).

The concept of probiotics, presently defined as "live microorganisms which, when administered in adequate amounts confer health benefit to the host". Over 60% of the human population suffers from lactose intolerance due to lower level and activity of lactase enzyme. The lactose intolerance depends on several factors, such as age, race and integrity of the SI membrane and transit time. The probiotics can produce lactase which promote the digestion of unabsorbed lactose and prevent acid and gas formation (Oak *et al.,* 2018).

A randomized double-blind placebo-controlled study of a formulation of probiotics with fermented milk containing (*S. salivarius subsp. thermophilus, E. faecium, L. rhamnosus GG, L. acidophilus, L. plantarum, L. paracasei, L. delbrueckii subsp. Bulgaricus, B. breve and B. animalis subsp. lactis*) and fructooligosaccharides (FOS) was found to be effective in management of constipation associated with Parkinson's disease (Barichella *et al.,* 2016).
Another formulation of probiotics in which consumption of milk (200 ml/day) containing *L. acidophilus, L. casei, B. bifidum and L. fermentum* (2 × 109 CFU/g for each) for 12 weeks was shown to improve cognitive function in elderly Alzheimer's patients without effecting the biomarkers of oxidative stress and inflammation, fasting plasma glucose and lipid profiles (Akbari *et al.,* 2016).

Gibson and Roberfroid (1995) defined prebiotics as a class of compounds that stimulate the growth and/or activity of a limited number of beneficial bacteria (Lactobacilli and/or Bifdobacteria) in the colon to improve host health. However, this definition has now been broadened and included carbohydrate and non-carbohydrate substances that confer microbiota-mediated health benefits (Gibson *et al.,* 2017).

In the GI tract, prebiotics can resist gastric acidity and can reach in LI where their selective utilization by microbiota produces SCFAs. Prebiotics such as FOS and GOS including the patented GOS produced by Bimuno (B-GOS) modulate neural growth factors such as brain-derived neurotrophic factor, neurotransmitters and synaptic proteins including synaptophysin and NMDA receptor subunits (Williams *et al.,* 2016).

Faecal microbiota transplantation (FMT) refers to a “stool transplant” into the GI tract from a healthy individual to a patient for the treatment of specific diseases. In United States, the FDA has considered human faeces as an experimental drug since 2013. Now, FMT has been used experimentally to treat GI diseases including colitis, constipation, IBD, and chronic fatigue syndrome, Parkinson’s disease, multiple sclerosis (Rossen *et al.,* 2015).

In recent techniques of FMT, enemas, nasogastric intubation, enteric intubation, colonoscopes and gastroscopes are used for faecal transplantation. The treatment of CDI with antibiotics including metronidazole, vancomycin, or fidaxomicin may cause recurrent infection, antibiotics resistance and dysbiosis of normal gut microbiota (Bagdasarian *et al.,* 2015).

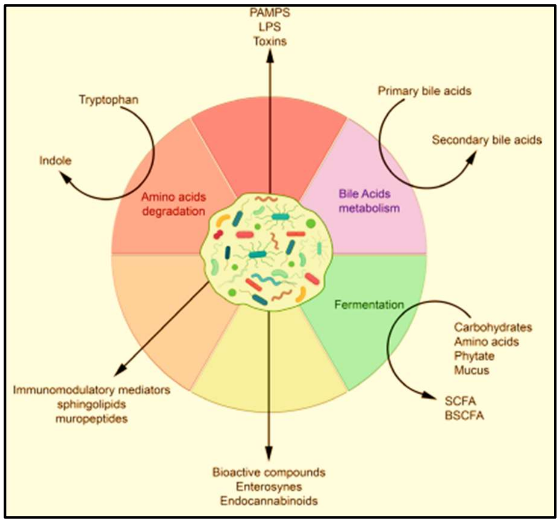


Figure 1: Molecules and metabolites produced by the gut microbiota according to the nutrients or metabolic source and their derived compounds. BSCFA, branched SCFA; LPS, lipopolysaccharides; pathogen-associated molecular patterns; SCFA, short chain fatty acids (de vos *et al.,* 2022).

B. PLANT FOOD COMPONENTS AND HEALTH

Plant-based foods are generally classified into fruits, vegetables, legumes, grains, nuts, and seeds; their derived processed counterparts such as breads, pasta, breakfast cereals, cooked and fermented vegetables and legumes, and fruit purées, juices, and jams; and their derived ingredients such as oleaginous seed–derived oils, sugars, and some herbs and spices. What differentiates them from animal-based foods is that their fibre fraction is made of indigestible compounds, mainly cellulose, hemicellulose, pectins, and/or resistant starch. Among grain products, legumes, cereals/pseudo cereals, and nuts/seeds are characterized by their high carbohydrate, protein, and lipid contents, respectively. In addition to fibre, plant-based foods all possess macro- (proteins, lipids, and carbohydrates), micro- (minerals, trace elements, and vitamins), and phytonutrients (e.g., polyphenols and carotenoids). Each of them helps the plant to survive within its environment and reproduce itself (Fardet *et al.,* 2017).

By definition, a bioactive compound has a biological effect on a human organism, tissues, or cells, being likely to have preventive effects on pathophysiological processes. In plant-based foods, all compounds or nutrients are therefore potentially bioactive within human organisms, but their protective effect will depend on several factors such as the health status or physiological state, the degree of food processing, and the presence of other compounds within the food matrix, and the quantity consumed. Even antinutritional factors, such as phytates, may have potential protective effects, emphasizing the dual nature of plant bioactive compounds (Fardet *et al.,* 2017).

Polyphenols are natural antioxidants that are chiefly derived from medicinal plants and food, for instance, vegetables, fruits, cereals, medicinal herbs, beverages, spices, and mushrooms. Phenolic acids, flavonoids, and anthocyanins, amongst others, are classes of polyphenols. Natural antioxidants, especially carotenoids and polyphenols, have been reported to possess several biological attributes, such as anti-cancerous, anti-aging, and anti-inflammatory properties (Xu *et al.,* 2017).

The consumption of vegetables and fruits is recommended as they are a rich source of natural antioxidants, for example, vitamin E (tocopherols) and vitamin C (ascorbic acid). Antioxidants have several health-promoting attributes including the regulation of immune functioning, reducing DNA damage, and ameliorating lipid peroxidation. Vitamin C exists as ascorbic acid and dehydroascorbic acid, with the former being the predominant form in plants (Kim *et al.,* 2016).

Phenolic components are known to be primary antioxidative or free radical inhibitory agents because of their capability to donate hydrogen atoms or electrons (Singh *et al.,* 2016). Antioxidative components derived from fruits and vegetables can decrease heart disorders, arthritis, neurodegenerative diseases, cancer, arteriosclerosis, and regulate brain dysfunction (Singh *et al.,* 2015). Several bioactive peptides isolated from rice, barley, oats, wheat, and cereals have been revealed to present antihypertensive activity (Majid *et al.,* 2020).

Phenolics are a group of compounds with ≥1 aromatic rings possessing ≥1 hydroxyl groups. Phenolics are the products of secondary metabolism in plants; play vital roles in the reproduction, growth, and metabolism of the plants; act as defense mechanisms against pathological virus and fungus infections, parasites, and predators; and contribute to the color of plants. In addition to their functions in plants, phenolic compounds in our diet may reduce the risk of chronic diseases such as cancer, heart disease, and diabetes. Fruits and vegetables are good sources of dietary phenolics (Martínez *et al.,* 2020).

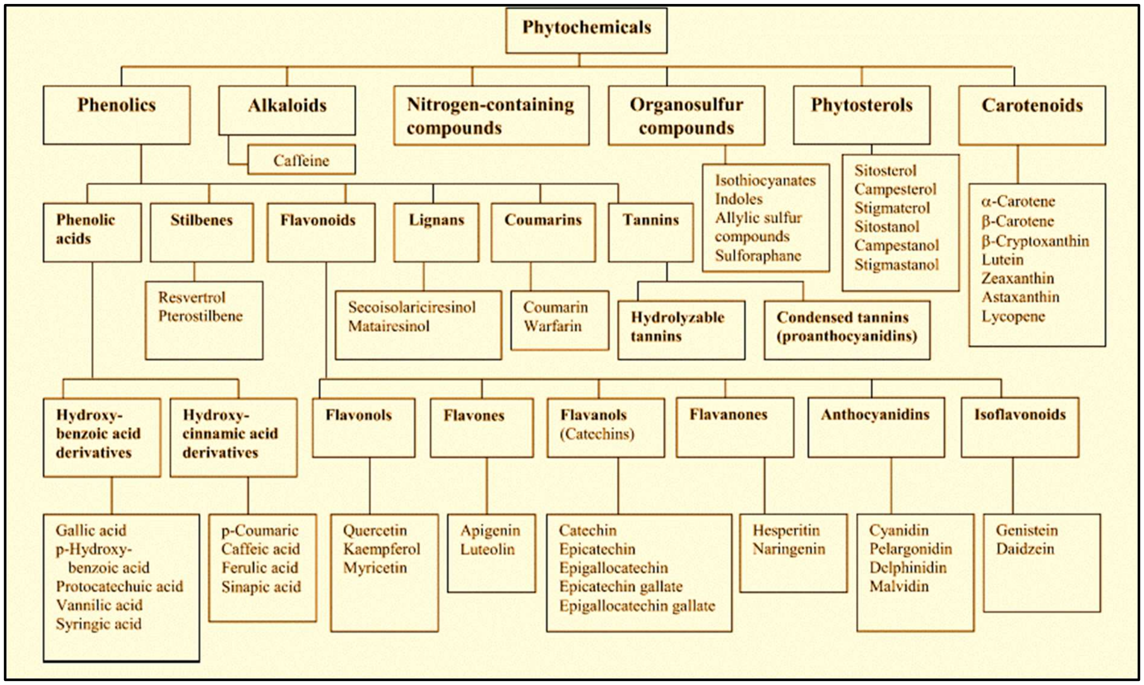


Figure 2: Classification of dietary phytochemicals (Liu, 2004)

Among 27 common vegetables consumed in the United States, spinach had the highest phenolic content, followed by red pepper, beets, broccoli, Brussels sprouts, eggplant, asparagus, and green pepper, in order of phenolic content. The rest of the vegetables in order of phenolic content were yellow onion, cauliflower, cabbage, radish, chili pepper, mushroom, sweet potato, carrot, sweet corn, potato, squash, white onion, green pea, tomato, green bean, celery, lettuce, romaine lettuce, and cucumber.

Flavonoids are a major group of phenolic compounds that commonly have a generic structure consisting of 2 aromatic rings (A and B rings) connected by 3 carbons that are usually in an oxygenated heterocycle ring, or C ring. Fruits, vegetables, and other plant foods are rich sources of flavonoids, which have been linked to reducing the risk of major chronic diseases, such as heart disease, cancer, stroke, diabetes, Alzheimer's disease, cataracts, and age-related functional decline.

Carotenoids are classified into hydrocarbons (carotenes) and their oxygenated derivatives (xanthophylls), with a 40- carbon skeleton of isoprene units. b-Carotene, a-carotene, and b-cryptoxanthin have pro-vitamin A activity and can be converted to retinol (vitamin A) after being metabolized in humans. Zeaxanthin and lutein are the essential carotenoids in the macular region (yellow spot) of the retina of the eyes in humans. A diet rich in zeaxanthin and lutein has been associated with a reduced risk of the development of cataracts and macular degeneration. range and yellow vegetables and fruits, including carrots, spinach, pumpkins, papayas, sweet potatoes, winter squash, mangoes, cantaloupes, and red peppers, are rich sources of b-carotene. Dark green leafy vegetables, including spinach, kale, turnip greens, broccoli, Brussels sprouts, and collards, are rich sources of lutein and zeaxanthin. Tomatoes, watermelons, pink grapefruits, apricots, and pink guavas are the most common sources of lycopene (Samtiya *et al.,* 2021).

One of the main results of the DASH study is that fruit and vegetable consumption was associated with a significant decrease in blood pressure, in which the effect was more pronounced in hypertensive patients than in normotensive participants. This might be attributed to an increase in the intake of potassium, magnesium, or some other component in fruits and vegetables, or alternatively a reduced intake of sodium.

Several components of fruit and vegetables have cholesterol-lowering properties, particularly dietary fibe. Similarly, ingestion of large quantities of phytosterols (>2 g per day) lowers plasma LDL-cholesterol levels. Since the available evidence demonstrates that viscous fibres, plant sterols, vegetable proteins, and nuts can each independently lower serum cholesterol by 5–10%. The large randomized controlled trial, which demonstrated a positive effect of increased fruits and vegetable intake on blood pressure, showed no effect on blood levels of total cholesterol.

A link has been proposed between increased consumption of green leafy vegetables and reduced incidence of diabetes, albeit is based on a limited number of studies with other classes of fruits and vegetables, such as root vegetables, also potentially playing a role

Accumulating evidence indicates that the combination of increased fruit and vegetable intake, together with other dietary recommendations, might promote satiety and weight loss in overweight individuals. Although the effect of fruit and vegetable consumption on weight control has been scarcely investigated in clinical settings, it has been found that decreased fat intake combined with increased fruit and vegetable intake results in greater weight loss when compared with low-fat diets alone (Alissa *et al*., 2017).

Table 1. Promising health benefits of plant originated bioactive compounds.

Plant Food	**Bioactive Components**	**Health Benefits**
Eggplant	Glycoalkaloids Anthocyanins	Anti-cancer activity Reduction of cholesterol levels
Soy	Isoflavone genistein Isoflavonoids aglycones	Anti-cancer activity Improved insulinotropic activity
Moringa Oleifera	Isothyocynate	Improved oxidative stress and brain health cholesterol-lowering effects
Blueberries	Pterostilbene, Anthocyanins	Anti-cancer activity
Quinoa	Bioactive peptides	Anti-cancer activity Anti-diabetic effects
Grape	Proanthocyanidins Polyphenols	Gut health Reduction of cardiovascular disease
Cranberry	Polyphenols	Gut health
Black currants	Anthocyanins	Anti-diabetic activity (type-2 diabetes)
Lettuce	Polyphenols	Anti-diabetic effects
Sorghum	Phenolics	Anti-cancer activity
Tea	Gallocatechin gallate	Reduction of cholesterol
Lemon seeds	Flavonoids	Improvement in oxidative damage

(Samtiya *et al.*, 2021).

C. Prebiotics and Gut microbiome

Prebiotics are a subgroup of dietary fibres with resistance to gastric acidity and the digestive enzymes of mammals, which confer a variety of health benefits. Gibson in 2004 states that main characteristic of prebiotics is their selective stimulation of the growth and/or activity of intestinal bacteria associated with health and well-being (Pluta *et al.,* 2020).

Resistant starch fulfils the definition of a prebiotic. It provides prebiotic-type fermentation in the colon and confers many metabolic benefits, such as increasing bile salt turnover and laxation, reducing the risk of gastrointestinal tract cancers, and lowering the postprandial glucose response and blood lipid levels (Bindels *et al.,* 2015). Moreover, it contributes to epithelial cell growth and proliferation by increasing the butyrate concentration via its fermentation by the gut microbiota (Ozgun *et al.,* 2017).

Except that the differences in the genetic level of intestinal bacteria lead to different utilization of prebiotics, prebiotics can selectively stimulate intestinal bacteria by cross-feeding, a process through which the growth of intestinal bacteria is indirectly stimulated via the utilization of metabolites produced by other community members (Holscher, 2017). For example, Bifidobacterium and Lactobacillus spp. ferment fructans to produce lactate and acetate, which are used as energy sources by many other bacterial species, including Eubacterium, Roseburia, and Faecalibacterium (Schwiertz, 2016). Recently, the cross-feeding strategies toward utilization of fucose by other bifidobacterial strains like *B. bifidum, B. kashiwahonense, B. breve*, and *B. longum subsp. infantis* has been demonstrated in the formation of 1,2-propandiol (Bunesova, Lacroix, & Schwab, 2016, 2018; Schwab *et al.,* 2017).

Substrate cross-feeding has also been reported in other species, such as *Bacteroides, Faecalibacterium, Roseburia, Ruminococcus,* and *Eubacterium*. The co-culture of *B. uniformis* and *E. coli* promoted their utilization of agaro-oligosaccharides more than the monoculture of these strains. *F. prausnitzii* has been reported to use the acetate produced by *B. thetaiotaomicron* in vivo (Wang *et al*., 2020).

These complex carbohydrates, which include resistant starch and plant cell-wall polysaccharides, constitute an important portion of the human diet, with a daily amount of 20–60 g reaching the colon, and act as fermentation substrates for the gut microbiota. As a result of fermentation, SCFAs, mainly butyrate, acetate, and propionate, are produced in the gut. They confer a number of health benefits on the host, such as acting as an energy source for colorectal tissues, stimulating cellular mechanisms that retain tissue integrity, contributing to the immune system, and possibly having anti-inflammatory effects (Markowiak *et al.,* 2017).

Human breast milk is rich in biologically active compounds that exhibit antimicrobial and immunomodulatory activities, in addition to lipids and sugars such as lactose that directly provide nutrition to infants. It also contains human milk oligosaccharides (HMOs), carbohydrates that are not digestible by the infant but instead influence the gut microbiome (Andreas *et al.,* 2015).

B. longum subsp. infantis, *B. longum subsp. longum, B. breve, and B. pseudocatenulatum*, internalize HMOs via ATP-binding cassette (ABC) transporters and hydrolyze these oligosaccharides using intracellular glycosyl hydrolases. This strategy protects the infant by giving an ecological advantage to these Bifidobacteria, preventing potential pathogens from colonizing the gut (Charbonneau *et al.,* 2016).

Recently, due to the progress in the research of indigenous microorganisms and the expansion of the concept of prebiotics, a broader range of intestinal bacteria, such as Bacteroides, Faecalibacterium, Roseburia, Ruminococcus, Eubacterium, and Akkermansia, has been expected to be good targets to prebiotics (Takumi, Yoshihiro, Toshio, & Yasuhiro, 2018). A human trial indicated that the supplementation of FOS induced higher levels of butyrate-producing microbes like Faecalibacterium, Ruminococcus, and Oscillospira in the feces (Tandon *et al*., 2019).

An in vivo trial showed a 10-fold increase in the number of F. prausnitzii in the adults' feces after an intake of 1-kestose at 5 g/day for 8 weeks (Takumi *et al*., 2018). Lemon peel waste oligosaccharides could increase the level of F. prausnitzii and Roseburia intestinalis as well as E. rectale via in vitro fermentability assessment using fecal inocula (Gómez, Gullón, Yáñez, Schols, & Alonso, 2016).

However, 5-carbon oligosaccharides connected by βbonds (e.g., XOS and arabinoxylan-oligosaccharides) are more narrowly utilized in the digestive tract than 6-carbon sugars connected by α bonds (e.g., FOS, inulin and resistant starch) (Saville & Saville, 2018). It has been reported that HMOs Lacto-fucopentaose I could be selectively utilized by B. longum subsp. infantis, but not B. animalis subsp. lactis (Zhao *et al*., 2016).

The relative abundance of A. muciniphila in the fecal samples of mice increased more than 100-fold after the ingestion of FOS under a high-fat diet. Similarly, the administration of fruits rich in polyphenols such as Concord grape and California table grape could also increase the abundance of *A. muciniphila* in the feces of mice (Baldwin *et al*., 2016). Moreover, Martinez et al. revealed that the administration of resistant starch type 2 (RS2) could significantly raise the proportions of R. bromii and E. rectale in the feces of humans.

Some biomedical reports and clinical trials indicated that some specific strains of beneficial bacteria can be enriched via prebiotic treatment. An in vitro fecal fermentation assay showed that the supplementation of XOS successfully enriched *B. longum subsp. longum* CR15

(Kok *et al.,* 2019). Subsequent genome assembly and annotation indicated that proteins (glycosyl hydrolases GH43 and GH120 and carbohydrate-binding molecules CBM6 and CBM22) and genes encoding d-xylulose 5-phosphate, xylose isomerase, and xylulokinase are associated with the XOS transport or utilization of this strain.

The structures and chain lengths of prebiotics (including candidate prebiotics) are critical determinants of fermentability. In addition, the glycosidic linkage type and monomer composition could affect the resistance of prebiotics to hydrolysis in the small intestine, further causing a difference in selective fermentation by microbiota in the large intestine (Ferreira-Lazarte *et al.,* 2019). For instance, β1-4-linked oligosaccharides are especially effective for the selective stimulation of Bifidobacterium spp. and can also be fermented by some strains of Lactobacilli and Bacteroides.

TABLE 2: Prebiotics and their beneficial outcomes

Prebiotic oligosaccharides	**Proposed responsible microorganism**
Human milk oligosaccharides (HMOs)	*Bifidobacterium longum subsp. infantis, Bacteroides*
Fructooligosaccharides (FOS)	Bifidobacteria, *Faecalibacterium prausnitzii*, Bacteroidetes
Inulin	Bifidobacteria, Bacteroidetes
Galactooligosaccharides (GOS)	Bifidobacteria, lactobacilli
Mannan-oligosaccharides (MOS)	Lactobacilli
Xylooligosaccharides (XOS)	Bifdobacteria, lactobacilli

(Enam *et al.,* 2019)

D. Dietary fibre and gut microbiota composition

Most countries adopted the definition of the Codex Alimentarius commission from 2009, which defines the dietary fibre as edible carbohydrate polymers with three or more monomeric units that are resistant to the endogenous digestive enzymes and thus neither hydrolyzed nor absorbed in the small intestine, and that belong to the following categories: (1) edible carbohydrate polymers naturally occurring in foods such as fruits, vegetables, legumes, and cereals; (2) edible carbohydrate polymers obtained from food raw materials by physical, enzymatic, and chemical means that have a proven physiological benefit; and (3) synthetic carbohydrate polymers with a proven physiological benefit.

Although most national authorities adhere to this definition, some differences are found between dietary fibre definitions, and they mainly concern (1) considering some non-carbohydrates such as lignin and other substances present in cell walls linked to polysaccharides as dietary fibres (Stephen *et al*., 2017) and (2) the minimum number of carbohydrate monomers to be included.

Dietary fibres are subdivided either into polysaccharides (nonstarch polysaccharides [NSPs], resistant starch [RS], and resistant oligosaccharides [ROs]) or insoluble and soluble forms (Deehan *et al*., 2017). Most insoluble forms such as cellulose and hemicellulose have a fecal bulking effect, as they reach the colon and are not, or only slowly, digested by the gut bacteria. Most soluble fibres do not contribute to fecal bulking, but are fermented by the gut bacteria and thus give rise to metabolites such as short-chain fatty acids (SCFAs). In contrast to ROs, most soluble NSPs, especially polymers with high molecular weight such as guar gum, certain pectins, b-glucans, and psyllium, are viscous, meaning that they are able to form a gel structure in the intestinal tract that can delay the absorption of glucose and lipids influencing post-prandial metabolism (Deehan *et al*., 2017).

Soluble and insoluble fibres are found in different food sources such as legumes, vegetables, nuts, seeds, fruits, and cereals in different proportions. However, not all types of fibres are present in the same food categories. RS can only be found in starchy foods such as cereals, legumes, tubers, and non-mature fruits like green bananas, while pectins are more enriched in fruits and some vegetables, whereas b-glucans and arabinoxylans are present in cereals (Lovegrove *et al.,* 2017).

Dietary Fibre Regulates the Composition of the Gut Microbiota Dietary fibre can have a major impact on the composition, diversity, and richness of the microbiome, providing a plethora of substrates for fermentation reactions carried out by specific species of microbe that possess the necessary enzymatic machinery to degrade these complex carbohydrates. There are numerous microbiota species defined as fibre fermenters in the large intestine, while there are different types of dietary fibre, all of which are broken down. Increasing dietary fibre consumption alters the nutritional niches in the intestine allowing these bacteria to expand their population. Individuals consuming diets low in fibre tend to have reduced microbial diversity (Makki *et al.,* 2018).

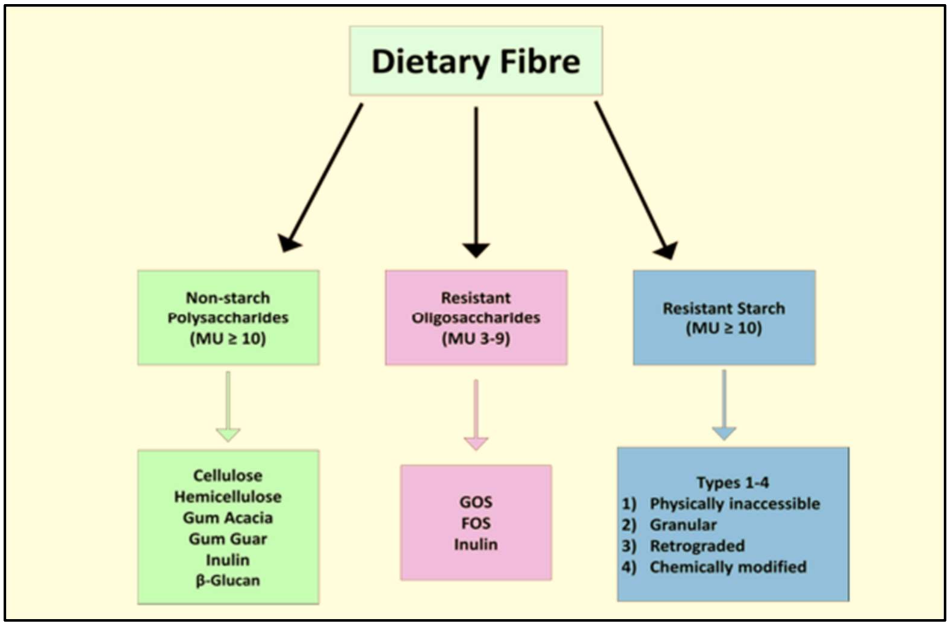


Figure 3: Schematic highlighting the different types of fibre divided by a number of monomeric units. Abbreviations: monomeric units (MU), galactooligosaccharides (GOS), and fructo-oligosaccharide (Cronin *et al.,* 2021).

Some of these compounds are considered ‘‘prebiotics’’ on the premise that they exert health benefits by selectively inducing beneficial bacterial populations in the gut. However, the assignment of only certain fibres as prebiotics based on these criteria is somehow arbitrary.

Dietary administration of fibre alters the niche environment in the gut by providing substrates for microbial growth, allowing microbial species that are able to utilize these substrates to expand their populations. Together, the gut microbiome harbors 130 glycoside hydrolase, 22 polysaccharide lyase, and 16 carbohydrate esterase families, which provide the microbiome flexibility to switch between different energy sources of fibres depending on availability. Species belonging to Firmicutes and Actinobacteria are the main responders to dietary fibre, although they contain relatively few fibre-metabolizing enzymes per organism. However, they generally have more specialized roles such as the initiation of complex substrate degradation (Deehan *et al*., 2017).

It is not only the enzymatic capacity (as a primary fibre degrader) that determines the ability of a microbe to benefit from dietary fibre, but also its ability to ‘‘adhere’’ to a substrate, tolerate the environmental conditions changed through the fibre (e.g., increased acidity through fermentation), and benefit from carbohydrate breakdown products (secondary fibre degraders) and metabolites (through cross-feeding) (Deehan *et al*., 2017).

Primary fibre degraders can hereby function as ‘‘keystone’’ species that initiate the utilization of a complex fibre through what can be considered a ‘‘guild’’ of species (Zhao *et al*., 2018). For example, *R. bromii* is considered a keystone species for the degradation of RS and contributes significantly to butyrate production in the colon, although the species itself does not produce butyrate. Similar keystone species are likely to exist for other dietary fibre types but have not yet been identified.

The impact of dietary fibre on microbiota composition displays several consistent characteristics. First, the observed shifts induced by non-digestible carbohydrates in humans, regardless if they are accepted prebiotics or not, are restricted to a limited number of taxa. Second, the magnitude of the induced changes can be substantial, with specific species constituting more than 30% of the total sequences obtained by amplicon sequencing of the fecal microbiota. However, these changes are only maintained so long as the substrate is consumed (Makki *et al.,* 2018). Third, the microbial response to dietary fibre is highly individualized. The reason for this individuality is not yet understood. Individuals may lack keystone species or lack strains that possess the enzymatic capacity to utilize a specific substrate (Zhao *et al*., 2018).

Dietary fibres are important energy sources for cecum and colon-residing microbiota. Anaerobic bacteria under specific intestinal conditions activate their machinery, constituted of key enzymes and metabolic pathways, which can metabolize complex carbohydrates, thus leading to the production of metabolites such as SCFAs. SCFAs are organic products mainly composed of acetate, propionate, and butyrate. SCFAs possess key roles in regulating host metabolism, immune system, and cell proliferation (Koh *et al*., 2016).

SCFAs are found at high concentrations in the cecum and proximal colon, where they are used as energy sources in colonocytes (especially butyrate), but can also be transported to the peripheral circulation via the portal vein to act on the liver and peripheral tissues. Although the levels of SCFAs are low in the peripheral circulation, it is now well accepted that they act as signaling molecules and regulate different biological processes in the host (Koh *et al*., 2016).

Compositional differences between various types of resistant starch have been found to have differential effects on the host microbiota. In vivo studies have found that RS4 consumption in humans increased the abundance of the phyla Actinobacteria and Bacteroidetes, while Firmicutes were decreased. Furthermore, RS4 was shown to increase the abundance of Parabacteroides distasonis and Bifidobacterium adolescentis. In the same study, the dietary supplementation of RS2 had no effect on phylum, while at the species level population increases of Ruminococcus bromii and Eubacterium rectale were detected. In vitro experimentation found that Ruminococcus bromii is a keystone species required for the fermentation of RS2 and RS3 (Cronin *et al.,* 2021).

A prolonged lack of dietary fibres damages the mucus barrier and is associated with an increased abundance of mucin-degrading bacteria such as Akkermansia muciniphila (Desai *et al*., 2016). Furthermore, when the diet is devoid of dietary fibres some gut bacteria switch their metabolism to use mucin glycans by inducing gene expression of mucin-degrading enzymes. Consistent with this, Western-diet feeding (very low fibre content) of mice increases the penetrability of the inner mucus layer and lowers growth rate, rendering the mucus penetrable, and may thus increase the susceptibility to infections (Makki *et al*., 2018).

D. Digital health intervention for promoting gut health

“The term ‘digital health’ refers to a wide range of technologies directed at delivering healthcare, providing information to lay people and helping them share their experiences of health and illness, training and educating healthcare professionals, helping people with chronic illnesses to engage in self-care and encouraging others to engage in activities to promote their health and wellbeing and avoid illness” (Lupton *et al.,* 2018).

New technologies generate streams of digital data about human bodies. Online searching for health and medical information on the Internet is probably the simplest and most popular digital practice, gaining popularity in spite of the doubts about the accuracy of information. Telemedicine as a remote healthcare consultation is emerging as a time-, energy-, and cost-saving alternative to the classic doctor-patient setting. Digitized patient self-care and self-monitoring in chronic diseases, sensors, robotic care providers, and medical apps support patients in their daily self-care. Persuasive computing and gamification as ways of addiction prevention or motivators for lifestyle change also contribute to patient empowerment. This kind of empowerment and cost efficiency are seen as positive outcomes of digital health technologies (Lupton *et al.,* 2018).

Regarding hardware, internet access, mobile phone, and smartphone penetration have been increasing. Medical technologies such as artificial narrow intelligence, robotics, genomics, telemedicine, and virtual and augmented reality are becoming disruptive. Regarding the software/information component, an enormous amount of medical information, peer support, and open access to clinical studies and guidelines are becoming widely available. It does not only lead to potentially better quality and a larger quantity of information being obtained in healthcare but also to the opportunity for self-care (Mesko *et al.,* 2017).

According to the US Food and Drugs Administration (FDA), “the broad scope of digital health includes categories such as mobile health (mHealth), health information technology (IT), wearable devices, telehealth and telemedicine, and personalized medicine”. These categories rely heavily on human health data. Conventionally, the collection of health data is mediated by officially licensed medical devices, such as diagnostic instruments or genome sequencers, operated by health professionals in clinical environments and under strict regulatory conditions. Digital health, in turn, entails connecting health-related data, including data generated by patients themselves, and harnessing the medical potential of technological tools of common usage, such as smartphones, wellness bands, apps, social media, and sensing devices disseminated in our dwelling environment. Most of these tools are not initially conceived for medical use and are not marketed as medical devices. Notably, however, some prominent digital health technologies already cut across the rigid distinction between licensed and ordinary gadgets, and the latter have also started to receive official designation as medical devices (Vayena *et al.,* 2018).

Similarly, a study was carried out to access the smartphone app (MyHealthyGut), to promote effective self-management of celiac disease and improve gut health. Preliminary findings of successful evidence-based mHealth interventions come from the field of weight loss and management of type 1 diabetes. For example, Burke and colleagues report the findings of using personal digital assistants (PDA) compared to paper diaries to assist in a weight loss intervention for obese adults. Participants who lost the most weight were those who used the PDA and received individualized feedback. In addition, compared to participants who used paper diaries, participants who used PDAs had better adherence to self-monitoring records (Dowd *et al.,* 2018).

In a study, the digital therapeutics care provided to subjects, informed by genetic and baseline gut microbiome and their interaction with participant’s lifestyle, seemed to effectively reduce symptom severity of FGIDs, including IBS, diarrhea, and constipation. Our earlier study supported the use of this care as a therapy for insulin resistance, empowering subjects to manage their inflammation by awareness of the impact of processed foods and foods to which they are sensitive as per their genomic SNPs and microbiome results. Dietary fibre coaching also results in increased vegetable diversity and quantity. Whereas further research is required to better understand the effect of different components of the care (e.g., fibre types) on modulating the microbial taxa and genomic SNPs identified in the models and their corresponding effect on reduction of FGIDs symptom severity, this preliminary retrospective study generates testable hypotheses for associations of a number of biomarkers in the prognosis of FGIDs symptomatology (Kumbhare, *et al.,* 2021).

The app myIBDcoach utilizes interactive eLearning (electronic learning) modules about medications, adherence, smoking cessation, nutrition, symptom management, fatigue, work productivity, anxiety, and depression. In addition to eLearning modules, Constant Care gives a disease-specific lecture during the onboarding process and provides access to an eHealth nurse and educational video clips. Constant Care researchers report that this has been valuable in empowering IBD patients to perform individualized, self-administered therapy. At the end of 12 months, a study of 333 participants showed significant improvement in general knowledge about IBD ($P<.001$) and medications ($P=.001$) in the Danish cohort of the study compared to controls, as measured by the Crohn's and Colitis Knowledge Score (Yin *et al.,* 2019).

Methodology

III. METHODOLOGY

The methodology followed in the present study entitled "Consumption Pattern of Prebiotics and Plant extracts among young adults and Implementation of Digital Health intervention for promoting healthy Gut Microbiome" comprises the following phases:

PHASE I
- Selection of area and study participants (Selected district- Coimabtore, Dharmapuri, Erode, Krishnagiri, Namakkal, Salem, Tiruppur), N=384

PHASE II
- Selection of tool
- Conduct of survey

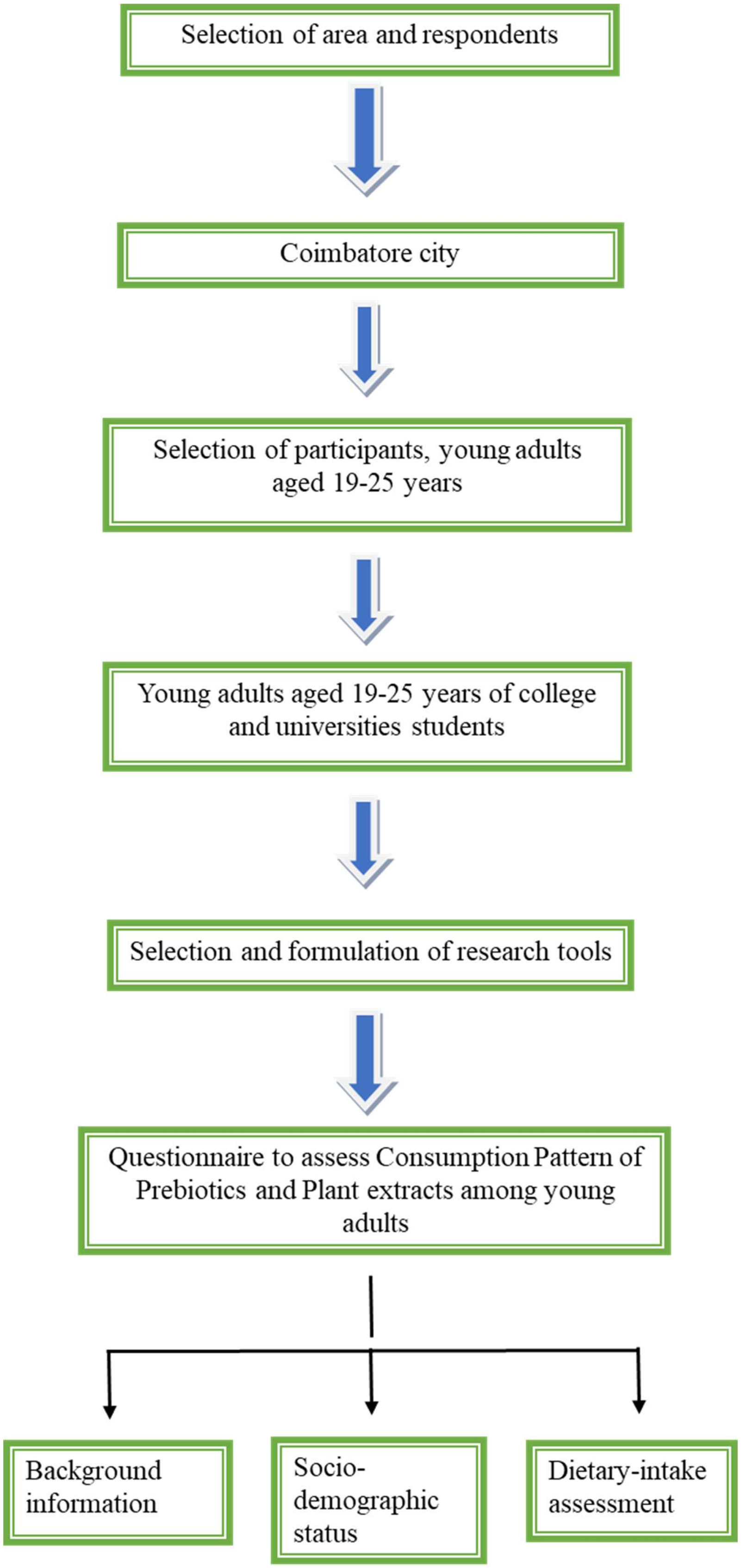
PHASE III
- Development and implementation of digital health intervention on Gut Microbiome

PHASE IV
- Impact evaluation on Knowledge, Attitude and Practice.

PHASE 1: Identification of area and subjects for the study

A. Selection of Study Area and subject

Selected districts from Tamilnadu a state in India includes district-Coimbatore, Dharmapuri, Erode, Krishnagiri, Namakkal, Salem, Tirupur was selected as the area of study of the Consumption Pattern of Prebiotics and Plant extracts among young adults about gut health. The investigator surveys a familiar area, to assess the consumption pattern of prebiotics and plant extracts among young adults. A total of 384 samples were selected from selected districts of Tamilnadu. The sample size is calculated using a sample size table. The selected population size is 2,50,000 at a 5 percent level of confidence the sample size calculated is N=384. The sample is selected from the sampling frame, which consists of a list of all members of the population of interest. Necessary permission and consent letters were obtained for selecting adults to participate in the study.


Selection of area and respondents
Coimbatore city
Selection of participants, young adults aged 19-25 years
Young adults aged 19-25 years of college and universities students
Selection and formulation of research tools
Questionnaire to assess Consumption Pattern of Prebiotics and Plant extracts among young adults
Background information
Socio-demographic status
Dietary-intake assessment

Contd…

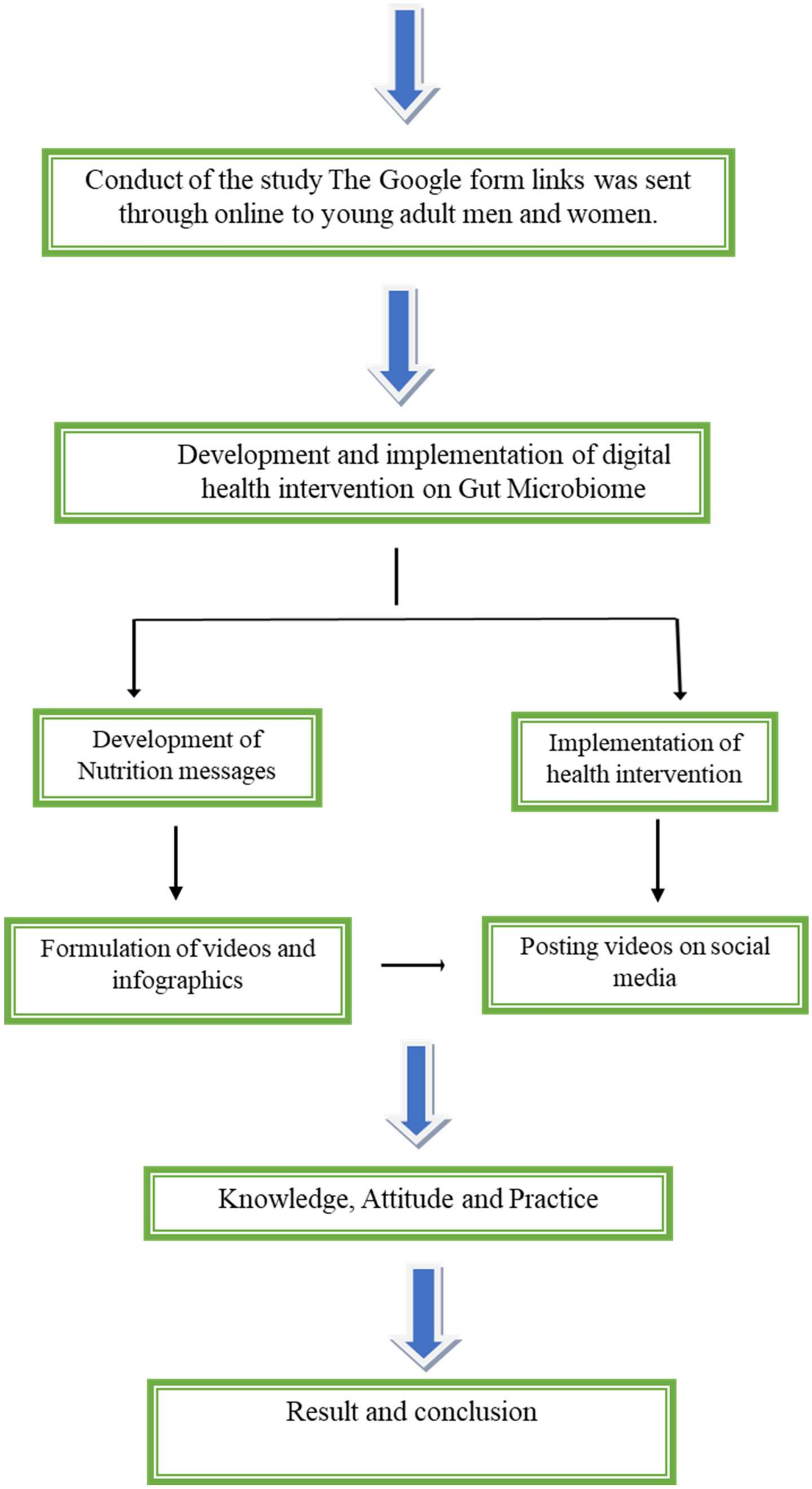


Figure:4

RESEARCH DESIGN

The target population of the study was young adults between the age group of 18-25 years college-going students were selected. The survey aims to assess prebiotic consumption and plant extracts among young adults. Acute dietary changes among young adults impact the microbial communities within the gut. The diet rich in plant-based foods provide varied types of dietary fibres thereby supporting a more diverse microbiota composition. Consumption of prebiotics is a dietary strategy through which the gastrointestinal microbiota can be modified. Most people lack awareness of the gut microbiome and its potential health benefits to the host. Diet serves as an important factor in nourishing the Gut Microbiome and its impact on human health. Thus, this survey aims to create awareness in the community to increase the consumption of a plant-based diet for the betterment of Gut health.

The investigator selected random sampling techniques to select for the study with the following inclusion and exclusion criteria.

Inclusion criteria:

- Young adults aged 18-25 years.
- Vegetarians and Non-vegetarians.
- Men and women.
- Who agreed to take part in this study.

Exclusion criteria:

- Individuals who are less than 18 and more than 25 years of age.
- Individuals with any infectious and other degenerative diseases such as diabetes/ cardiovascular disease/ cancer.
- Pregnant women and lactating mothers.
- Women on hormone replacement therapy
- Individuals on a specific diet (such as for a religious purpose or weight loss)
- Individuals on medication (such as for weight loss)

The survey was conducted based on the inclusion and exclusion criteria to avoid ambiguity in the final results and findings. The questionnaire form was only circulated to the study participants who are eligible and limited to them. The exclusion criteria are specifically framed to not survey the study participants who are not eligible for this survey. So that accurate results can be obtained. Based on the above-listed criteria the study participants were selected for the survey and clearly explained the title of this survey named "Dietary consumption pattern of prebiotics and plant extracts among young adults". Before the survey, the study participants were informed of the benefits and the goal of the survey.

PHASE II:

A. FORMULATION OF TOOLS:

A set of questionnaires was prepared to elicit information on the designed questionnaire to assess the socio-economic dietary pattern of selected study participants (young adults). Questionnaires are the most commonly used tool in the survey. Subjects were informed about the benefits of participating in this study. A close-ended questionnaire was formulated to assess the consumption pattern of prebiotics. Information on various socio-economic and demographic parameters was collected from the subjects. The socio-demographic profile consisted of details like the Name of the participant, Age of the participant, gender, designation of the student, location of the participants, and area. The questionnaire contains five questions on socio-demographic profile and fifteen questions on dietary intake. The questionnaire is given in Appendix (I).

B. CONDUCT OF ONLINE SURVEY

The investigator formulated a questionnaire to elicit information on designed dietary and food consumption patterns, fibre food consumption, prebiotic-rich foods consumption, and herbal extracts.

The google form was circulated to all university and college-going students, both men and women via social media. The study participants were instructed to fill the questions in the form. The guidelines and instructions were provided along with a link to a Google Form to help students comprehend the survey and fill out the form to collect the study group's background information. The form was circulated to many students to obtain the targeted response. The study participants were already informed about the benefits of participating in this study. At present most people do not consume a wide variety of plant-based foods, the questionnaire alone raised awareness among the participants. They follow the monotony for their convenience, but they are deficient in important nutrients that are necessary for proper body functioning. This survey form contains a wide variety of questions including cereals, pulses, green leafy vegetables, other vegetables, roots and tubers, fruits, and probiotic food consumption, all these questions make participants be aware that there is a wide variety of plant-based foods that need to be consumed for better health and it has to be continually followed on an everyday diet.

The primary data was collected from the respondents on socio-demographic status, dietary and food consumption patterns, before imparting knowledge on the Gut microbiome. Finally, all the responses to the survey are retrieved from the google form. The consumption pattern of young adults can be deduced from the responses. The responses are also stored in a Google spreadsheet, making it simple to conduct further statistical analysis. The spreadsheet view of the collected data may also be accessed.

The consent letter was received from the study participants. It was clearly stated to them that the information gathered from the study participants will be kept confidential and will not be disclosed under any circumstances.

PHASE III:

DEVELOPMENT AND IMPLEMENTATION OF A DIGITAL HEALTH INTERVENTION ON THE GUT MICROBIOME

Digital health intervention was given to the study participants on the Gut Microbiome via WhatsApp, YouTube, and Infographics after the survey.

The selected tools for digital health intervention include Videos, and Infographics consisting of information and facts about the gut microbiome and its potential health benefits to host. Educational videos are a powerful tool for connecting the study participants. Videos enable them to develop a better understanding and create awareness.

A total of 5 videos were generated, to increase awareness. Articles from PubMed, Google Scholar, and other sources were used to create the videos. The materials were completely read, and the video addressed all of the essential topics.

Infographics, according to this adage, a picture is worth a thousand words, therefore infographics were made to help the community comprehend the gut microbiota. Gut health, microorganisms in the gut, gut microbial composition, and other topics are covered in detail in infographics. Articles, videos, and research papers were used to compile the material. The list of topics is selected for videos to make understand the gut microbiome from birth, development of microbiota, to its role and functions to host, how diet positively manipulates the gut microbiota composition. All these topics were explained through videos and infographics to create awareness for the community.

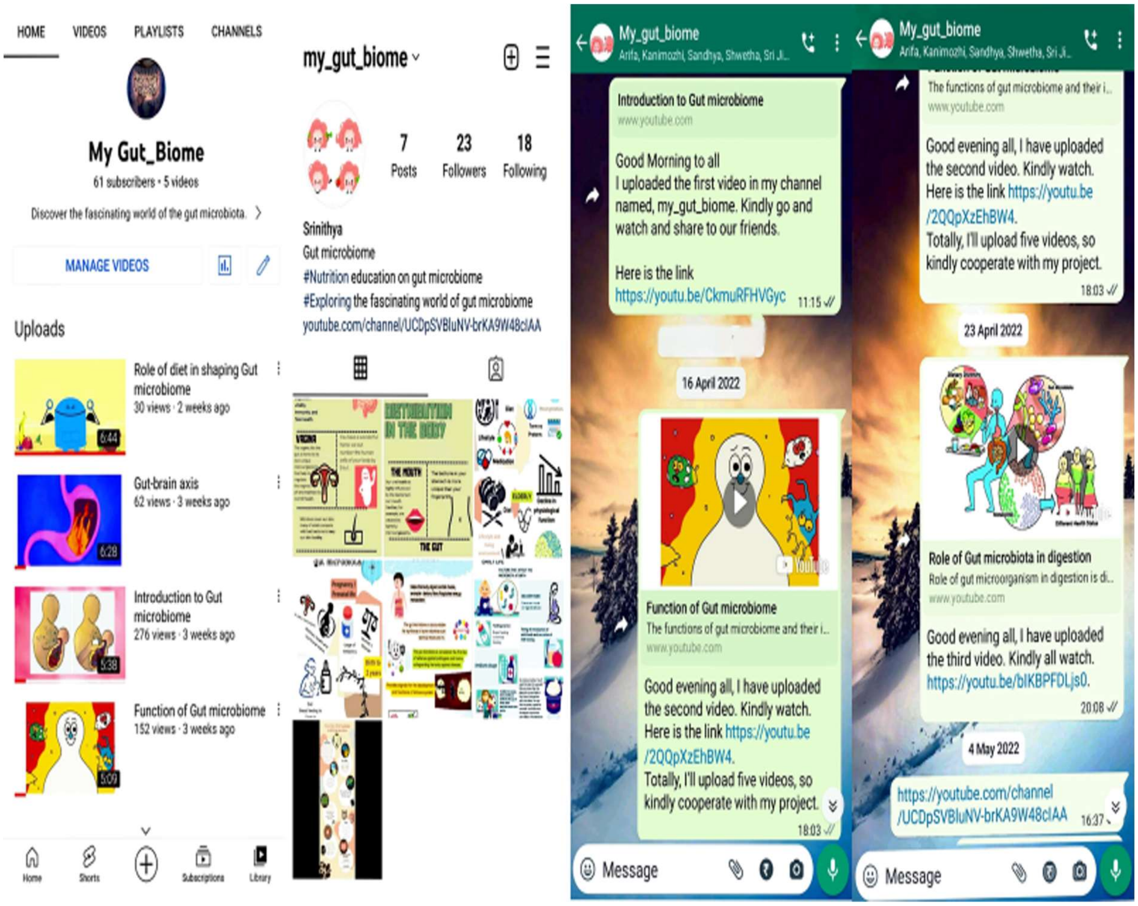
According to the Oxford, infographics (or information graphics) is “a visual representation of information or data”. Infographics are considered valuable tools for visual communication.

Infographics are being employed as a digital health intervention tool for the "Gut Microbiome" (gut microbiota for health by European Society of Neurogastroenterology & motility). For a better knowledge of the gut microbiome, infographics were made containing a lot of information and photographs about the gut microbiome and microorganisms present in the gut. To raise awareness, a total of five infographics were prepared. Infographics will be shared on social media platforms such as WhatsApp and Instagram.

The WhatsApp group was created by adding all the participants. The videos and infographics were sent out every week for a total of five weeks. Every week, the group received two videos and one infographic. This was continued for all five weeks. Short video clips were sent to the WhatsApp group.

A channel was created on YouTube dedicated to disseminating information about the gut microbiome. Every week, the channel featured new videos. The YouTube video URLs were shared on social media to reach a broader audience. YouTube is a popular digital medium for reaching out to new audiences and spreading awareness.

This raises awareness of the Gut Microbiome and its importance in improving one's health. Digital health intervention is a valuable tool for sharing knowledge and awareness about the gut microbiome. Because most people are ignorant of the gut microbiome. Even the majority of individuals are oblivious that bacteria exist in their large intestines. This bacteria is extremely beneficial to one's health. As a result, increasing awareness of the gut microbiome can help people better understand the role of bacteria in the host, encouraging them to eat a wider variety of plant-based diets. As a result, the gut microbiome consortium can be improved.



My Gut_Biome

61 subscribers • 5 videos

Discover the fascinating world of the gut microbiota.

Role of diet in shaping Gut microbiome
30 views · 2 weeks ago

Gut-brain axis
62 views · 3 weeks ago

Introduction to Gut microbiome
276 views · 3 weeks ago

Function of Gut microbiome
152 views · 3 weeks ago

7 Posts 23 Followers 18 Following

Srinithya
Gut microbiome
#Nutrition education on gut microbiome
#Exploring the fascinating world of gut microbiome
youtube.com/channel/UCDpSVBluNV-brKA9W48cIAA

My_gut_biome
Arifa, Kanimozhi, Sandhya, Shwetha, Sri Ji...

Introduction to Gut microbiome
www.youtube.com

Good Morning to all
I uploaded the first video in my channel named, my_gut_biome. Kindly go and watch and share to our friends.

Here is the link
https://youtu.be/CkmuRFHVGyc 11:15

16 April 2022

Function of Gut microbiome
The functions of gut microbiome and their i...
www.youtube.com

Good evening all, I have uploaded the second video. Kindly watch.
Here is the link https://youtu.be/2QQpXzEhBW4.
Totally, I'll upload five videos, so kindly cooperate with my project. 18:03

My_gut_biome
Arifa, Kanimozhi, Sandhya, Shwetha, Sri Ji...

The functions of gut microbiome and their i...
www.youtube.com

Good evening all, I have uploaded the second video. Kindly watch.
Here is the link https://youtu.be/2QQpXzEhBW4.
Totally, I'll upload five videos, so kindly cooperate with my project. 18:03

23 April 2022

Role of Gut microbiota in digestion
Role of gut microorganism in digestion is di...
www.youtube.com

Good evening all, I have uploaded the third video. Kindly all watch.
https://youtu.be/bIKBPFDLjs0. 20:08

4 May 2022

https://youtube.com/channel/UCDpSVBluNV-brKA9W48cIAA 16:37

PLATE 1

Snapshots of Digital Health Intervention

PHASE IV:

IMPACT EVALUATION ON KNOWLEDGE, ATTITUDE, AND PRACTICE:

Knowledge, Attitude, and Practice were assessed before and after the digital intervention as part of the digital intervention's pre- and post-assessment. The Knowledge, Attitudes, and Practices (KAP) survey is designed to gather information on knowledge (Gut Microbiome), attitudes (food myths and taboos), and practices (following a plant-based diet, consuming fibre-rich foods). The KAP Survey is necessary for assessing the health intervention program. For each knowledge, attitude, and practice, questions will be framed. The KAP survey questionnaire was created to gather data on common habits and beliefs. Interviewers gather data using a standardized, standard questionnaire that may include both quantitative and qualitative information. KAP is used to determine how often people consume a plant-based diet in their regular diet and whether they consume fibre-rich diets.

KAP Survey:

KAP survey was conducted before and after digital intervention. The digital health intervention was planned for 5 weeks. The KAP survey consist of three sections of a questionnaire for Knowledge, Attitude, and Practice as a pre- and post-assessment of digital health intervention. In section one, a knowledge-based question was about the gut microbiota. The second section addressed dietary attitudes and beliefs as well as any changes in consumption patterns as a result of a health intervention. Finally, questions about the frequent consumption of dietary fibre, Prebiotics, Plant-based diets, and other foods are included in section three. KAP is used to assess study participants' attitudes toward food intake, knowledge of the gut microbiome, and how often they consume Plant-based foods and dietary fibre as part of their usual diet. For the KAP survey, a series of yes/no type questions were framed and distributed to all study participants. To elicit the most responses, the questions were constructed as briefly as possible.

Specific objectives of the KAP survey may include the following:

- To assess the knowledge, attitudes, and practices regarding consumption of Plant-based diets, fibre-rich foods, Prebiotics consumption, Plant extracts and their role in health and knowledge on plant components and their benefits to health among young adults.
- To evaluate the impact of the Gut Microbiome interventions on Knowledge, Attitude, and practices regarding consumption of plant-based diets, fibre-rich foods, probiotics consumption, Plant extracts, and their role in health and knowledge on plant components and their benefits to health among young adults, following the digital health intervention.

A sample of KAP survey questionnaire form was given in the Appendix (I).

Statistical analysis and interpretation of data:

The data collected were checked for the completeness and consistency. Then it was edited,organized, coded and entered to Microsoft Excel 2016. Statistical Package for Social

Science (SPSS) version 26.0 was used to analyze the data and assess the effectiveness of digital health intervention and impact of the education given on Gut microbiome among the respondents.

Pearson’s chi square as used to analyze whether there is any association between demographic profile and fibre rich food consumption among young adults.

Student’s t-distribution was used to analyze whether there is any significant difference between the mean scores obtained before and after imparting the education through digital health intervention.

Pearson correlation test was used to analyze whether there is any significant difference between the mean score obtained on food consumption pattern before and after imparting education through digital health intervention.

Results and Discussion

IV. RESULTS AND DISCUSSION

The results and discussion of the study entitled. "**Consumption Pattern of Prebiotics and Plant extracts among Young Adults and Implementation of Digital Health Intervention for Promoting Healthy Gut Microbiome"** is presented under the following headings:

1. Demographic profile of young adults
    - 1.1 Age of young adults
    - 1.2 Gender
    - 1.3 Educational qualification
    - 1.4 Place of residence
    - 1.5 Area of residence
2. Diet survey
    - 2.1 Frequency of food consumption among young adults
    - 2.2 Association of consumption pattern of fibre rich foods and plant extracts, age and location
    - 2.3 Association of consumption pattern of fibre rich foods and plant extracts with age factor
    - 2.4 Association of consumption pattern of fibre rich foods and plant extracts with gender factor
    - 2.5 Association of consumption pattern of fibre rich foods and plant extracts and place of residence
3. Impact Evaluation
    - 3.1 Impact of digital health intervention on Knowledge attitude and practice of gut microbiome
    - 3.2 Impact of digital health intervention on knowledge about gut microbiome
    - 3.3 Impact of digital health intervention on attitude towards gut microbiome
    - 3.4 Impact of digital health intervention on practices facilitating gut microbiome.
    - 3.5 Impact of digital health intervention and dietary modification on food intake of young adults.

1. DEMOGRAPHIC PROFILE OF YOUNG ADULTS

The socio-economic and demographic profile is biologically and socially acquired and controlled in a hierarchical and systematic order of certain interrelated elements, including age, education, and gender (Abdullahi, 2019). A total of three hundred eighty-four young adults have participated in the survey. Table No. 1 shows the background information of the study participants taken for investigation.

Table No. III

Background information of the study participants

Parameters	**Criteria**	**Respondents (N=384)**	
		No. of Response	**Percentage (%)**
Age (in years)	18-20	230	59.9
	21-25	154	40.1
Gender	Male	135	35.2
	Female	249	64.8
Education	Undergraduate	292	76.0
	Postgraduation	72	18.8
	PhD	20	5.2
Place of residence	Coimbatore	102	26.6
	Dharmapuri	51	13.3
	Erode	64	16.7
	Krishnagiri	39	10.2
	Namakkal	28	7.3
	Salem	34	8.9
	Tirupur	66	17.2
Area of residence	Rural	178	46.3
	Urban	206	53.7

1.1. Age of respondents

The distribution of age of the respondents is given in Figure 3.

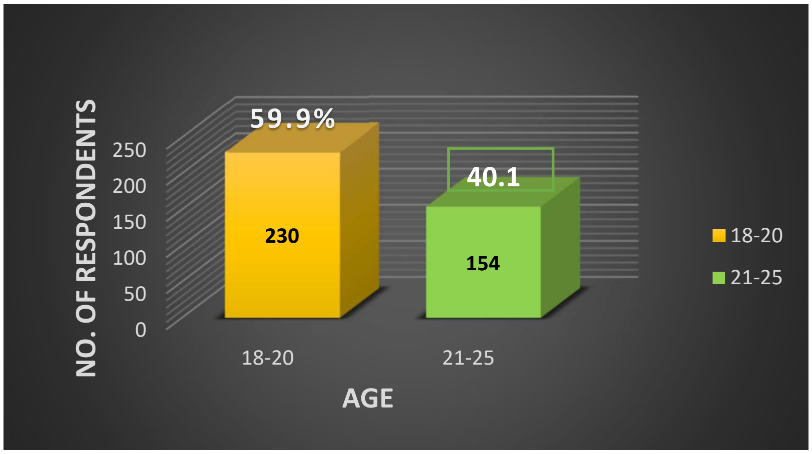


Figure 5: Age of Respondents

Figure 5 shows that 59.9% percent of the respondents were in the age group of 18-20 years. 40.1 percent were in the age group of 21-25 years. These observations are supported by census data from 2011, which show that 8.6% of Tamilnadu's population is between the age group of 15-19, and 8.89 percent is between the age group of 20-25. (Census 2011).

1.2. Gender of respondents

The distribution of gender of the respondents is given in Figure 2.

(N=384)

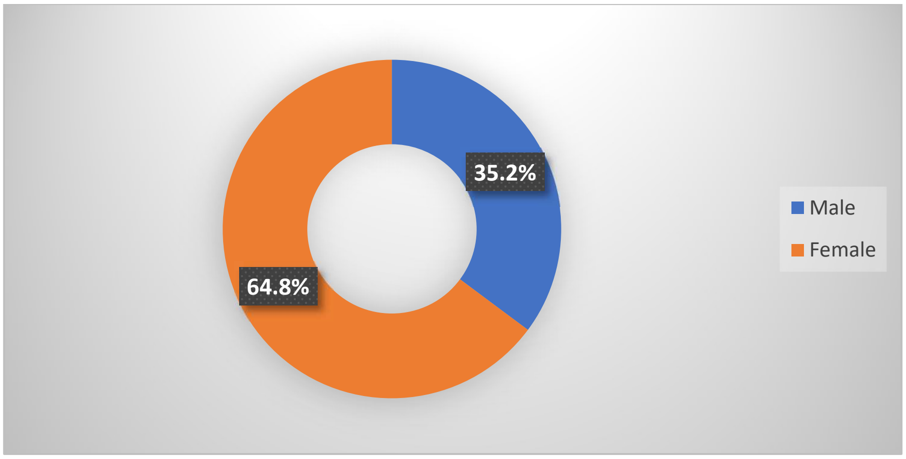


Figure 6: Gender of Respondents

As evident from Figure 6, 64.8 percent of the respondents were female and 35.2 percent of the respondents were male.

According to Census 2011 data, Tamilnadu’s population of 7.21 crores of people, of which 36,137,975 are male and 36,009,055 are female (Census, 2011).

1.3.Educational Qualifications of young adults

The distribution of educational qualifications of the respondents is given in Figure 4.

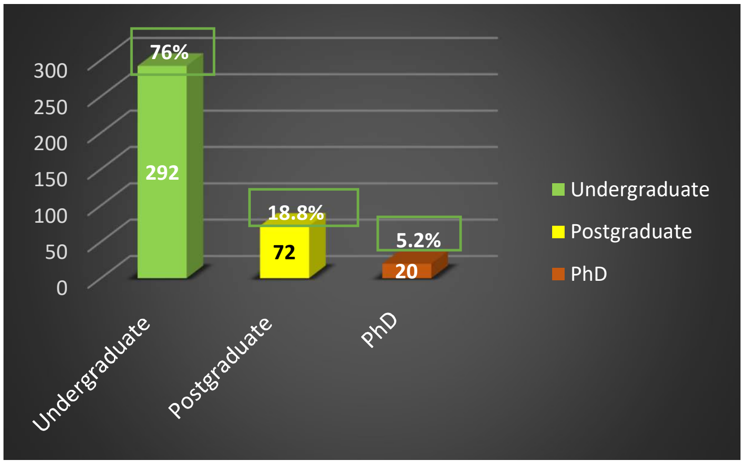


Figure 7: Educational Qualification of young adults

The survey revealed that 76.0 percent of the respondents were found to be pursuing undergraduate followed by 18.8 percent postgraduate and 5.2% Ph.D. in different disciplines.

Tamilnadu's literacy rate has risen to 80.09 percent according to the 2011 population census. Male literacy rates are 86.77 percent, while female literacy rates are 73.44 percent. Tamilnadu had a literacy rate of 73.45 percent in 2001, with male and female literacy rates of 82.42 percent and 64.43 percent, respectively (Census, 2011).

The total number of literates in Tamilnadu is 51,837,507, with 28,040,491 males accounting for 54.09 percent of the total literates and 23,797,016 females, accounting for 45.9 percent of the total literates in the state (wb.gov.in).

1.4.Place of residence

The distribution of the place of residence of the respondents is given in Figure 8.

As evident from Figure 5, majority of the respondents i.e., 26.6 percent belonged to Coimbatore, followed by 17.2 percent Tirupur, 16.7 percent Erode, 13.3 percent Dharmapuri, 10.2 percent Krishnagiri, 8.9 percent Salem, and 7.3% Namakkal.

According to the Census data of 2011, which revealed that, out of the total population of Tamilnadu, 18.56 percent lived in Coimbatore, 29.11 percent in Tirupur, 11.66 percent in Erode, 16.34 percent in Dharmapuri, 15.44 percent in Salem, 20.41 percent in Krishnagiri, and 15.61 percent in Namakkal (Census, 2011).

(N=384)

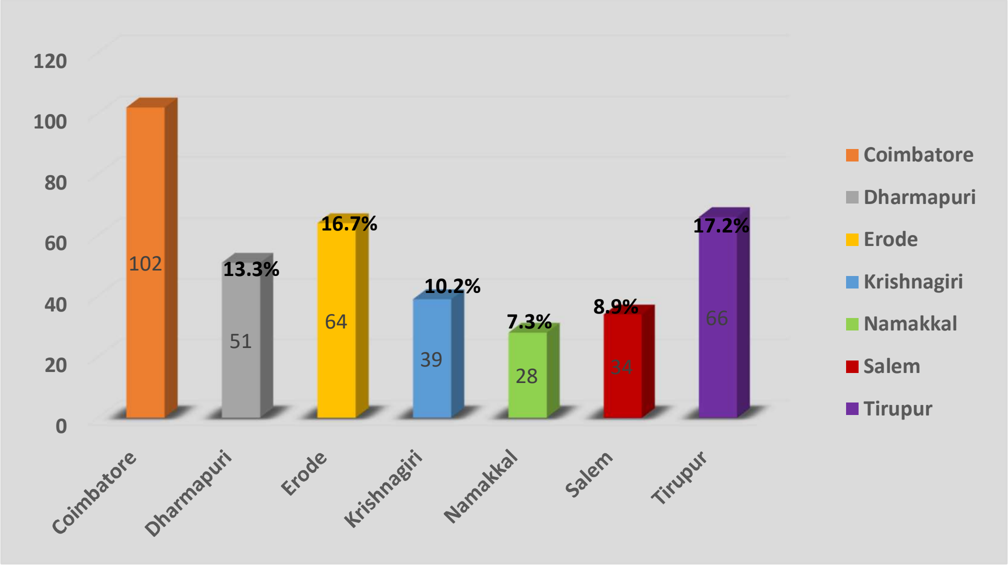


Figure 8: Place of residence

1.5.Area of Residence of Respondents

The distribution of the area of residence of the respondents is given in Figure 9.

(N=384)

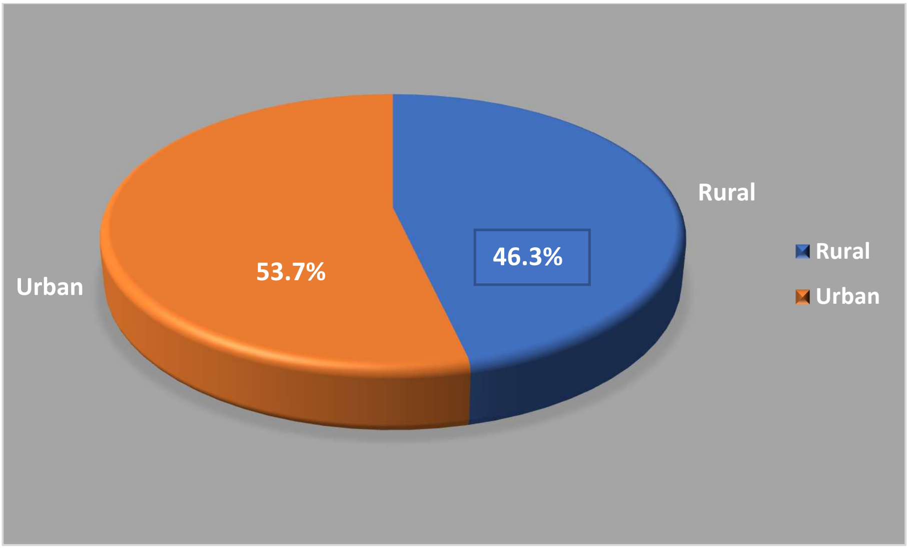
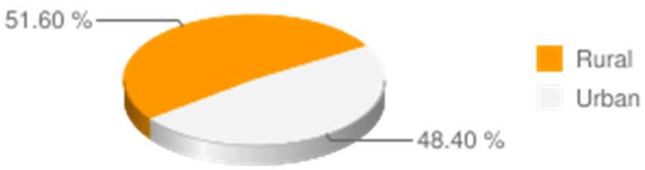


Figure 9: Area of residence

As evident from Figure 9, the majority of the respondents i.e., 53.7 percent belonged to urban areas, while the remaining 46.3 percent of the respondents belonged to rural areas.

According to the Census data of 2011, which revealed that, out of total population of Tamilnadu, 48.4 percent of people lived in urban regions. The total figure for the population living in urban areas was 34,917,440 of which 17,458,910 are males and while remaining 17,458,530 are females. The same data revealed that 48.40 percent of the population lived in rural areas (Census, 2011).



(Census, 2011)

Figure 10: Distribution of area of residence

2. DIET SURVEY

A diet survey aids in visualizing an individual's or a population's food intake. The current study employed data from the frequency of food consumption as indicators of young adults' food intake.

2.1 Frequency of food consumption among the Young adults

Table IV presents the frequency of food consumption among young adults

The frequency of consumption of foods from different food groups varied between food among the young adults. The consumption of cereals and millets revealed that rice is the staple food was consumed daily by 89 per cent, while wheat was mostly (80-83%) consumed weekly among young adults irrespective of age. Ragi is a prebiotic, rich source of dietary fibre. Among young adults' millets like ragi, Thinai, Varagu, Samai, Kutharaivali and Cholam were consumed weekly or occasionally.

The consumption pattern of pulses was not on daily basis among young adults weekly three-to-four-time pattern was observed. The pulses such as Channa dal, green gram dal, Soyabean, Horse gram, Rajmah, Red gram dal, Black gram dal and bengal gram dal were consumed weekly. Fifty to fifty-three per cent of the young adults in all the age groups consumed black gram dhal daily as part of the idly or dosa batter.

Table IV

Frequency of food consumption among young adults

Food groups	18-20 years (N=230)										21-25 years (N= 154)									
	Daily		**Weekly**		**Monthly**		**Occasionally**		**Never**		**Daily**		**Weekly**		**Monthly**		**Occasionally**		**Never**	
	No.	**%**	**No.**	**%**	**N0.**	**%**	**No.**	**%**	**No.**	**%**	**No.**	**%**	**No.**	**%**	**No.**	**%**	**No.**	**%**	**No.**	**%**
Cereals and millets																				
Rice	119	88.1	15	11.1	1	0.7	-		-		223	89.5	23	9.2	3	1.2	-	-	-	-
Wheat	16	11.8	110	81.4	7	5.1	2	1.4	-	-	29	11.6	203	81.5	13	5.2	4	1.6	-	-
Ragi	7	5.1	62	45.9	38	28.1	20	14.8	8	0.7	15	6.02	107	42.9	77	30.9	33	12	17	6.8
Kambu	4	2.9	41	30.3	39	28.8	33	24.4	17	12	7	2.8	72	28.9	88	35.5	46	18.1	37	14
Thinai	1	0.7	34	25.1	37	27.4	29	21.4	33	24.4	5	2.0	59	23.6	71	28.5	67	26.9	48	19.2
Varagu	3	2.2	29	21.4	37	27.4	28	20.7	37	27.4	9	3.61	48	19.2	72	28.9	65	26.1	56	22.4
Samai	2	1.4	29	21.4	41	30.3	62	45.9	54	40	12	4.8	55	22.0	67	26.9	29	11.6	33	13.2
Kutharaivali	1	0.7	32	23.7	41	30.3	28	20.7	32	23.7	7	2.8	50	20	68	27.3	60	24	65	26.1
Cholam	2	1.4	43	31.8	48	35.5	27	20	14	10.3	11	4.41	69	27	87	34.9	50	20.09	33	13.2
Pulses																				
Black gram dal	50	37.0	71	52.5	9	6.6	2	1.4	1	0.7	90	36.1	131	52	20	8.03	5	2.0	5	2.0
Channa dal	12	0.7	90	66.6	27	20	-	-	3	2.2	24	9.6	182	53	34	13.6	7	2.8	5	2.0
Bengal gram dal	32	3.7	79	58.5	19	14.0	2	1.4	-	-	66	26.5	149	60	24	9.6	8	3.2	5	2.4
Green gram dal	13	9.6	93	0.7	21	15.5	2	1.4	3	2.2	17	6.8	194	77	29	11.6	6	2.4	6	2.4
Soyabean	4	0.7	64	47.7	48	35.5	11	8.1	5	3.7	13	5.2	138	55	76	31.7	16	6.4	9	3.6
Horse gram	2	1.4	67	49.6	35	0.7	15	11.1	13	5.2	138	55	76	31.7	16	6.4	9	3.6	17	14.2
Rajmah	1	0.7	44	32.5	47	34.8	14	10.3	26	19.2	9	3.6	83	34	92	36.9	31	12.4	37	14.8

Red gram dal	24	0.7	65	16.9	27	7.03	8	2.08	8	2.08	57	22.8	125	50	43	17.2	17	6.8	10	4.01
Moong dal	10	7.4	85	62.9	25	18.5	10	7.4	2	1.4	39	15.6	150	60	42	16.8	14	0.4	7	2.8
Roots and tubers																				
Potato	17	12.5	104	77.0	10	7.4	1	0.7	-	-	41	16.4	191	77	17	6.8	1	0.4	2	0.8
Sweet potato	4	2.9	52	38.5	44	32.5	26	19.2	6	4.4	11	4.4	99	40	86	34.5	46	18	10	4.0
Carrot	16	11.8	103	76.2	10	7.4	3	2.2	-	-	43	17.2	186	74	18	7.2	4	1.6	1	0.4
Radish	6	4.4	90	60.6	24	17.7	7	5.1	5	3.7	15	6.02	181	82	34	13.6	15	6.2	7	2.8
Tapioca	8	5.9	45	33.3	44	32.5	27	20	8	5.9	16	8.4	88	35	82	32.9	54	21	12	4.8
Greenleafy vegetables																				
Agathi	30	22.2	41	30.3	33	0.74	28	20.7	-	-	45	18.0	105	42	43	17.2	59	23	-	-
Amaranthus	24	17.7	31	22.9	34	25.1	43	31.8	-	-	37	14.8	95	38	43	17.2	77	31	-	-
Drumstick leaves	25	18.5	73	54.0	19	14.0	15	11.1	-	-	44	17.6	147	59	32	12.8	29	11	-	-
Fenugreek leaves	19	14.0	38	28.1	30	22.2	45	33.3	-	-	38	15.2	93	37	48	19.2	73	29	-	-
Ponangani Keerai	17	12.5	38	28.1	38	28.1	39	28.8	-	-	35	14.0	97	38	55	22.0	65	26	-	-
Parupu Keerai	15	11.1	57	42.2	30	22.2	20	22.2	-	-	39	15.6	112	44	54	21.6	47	18	-	-
Manathakkali Keerai	21	15.5	50	37.0	34	25.1	27	20	-	-	32	12.8	108	43	55	22.0	57	22	-	-
Other vegetables																				
Tomato	108	80	18	13.3	4	2.9	1	0.7	1	0.7	202	81.1	44	17	3	1.2	-	-	3	1.2
Beans	21	15.5	12	8.8	8	5.9	1	0.7	-	-	32	12.8	203	81	13	5.2	1	0.4	3	0.7
Drumstick	14	10.3	103	76.2	8	5.9	6	4.4	1	0.7	27	10.8	191	76	24	9.6	6	2.4	4	1.6
Cauliflower	11	8.1	86	63.7	24	17.7	9	6.6	2	1.4	20	8	176	70	41	16	10	4.0	5	2.0

Ladies finger	8	5.9	102	75.5	14	10.3	7	5.1	1	0.7	25	10	196	78	23	9.2	5	2.0	3	1.2
Gourd vegetables	10	7.4	86	63.7	20	14.8	10	7.4	6	4.4	15	6.02	182	73	36	14.4	11	4.4	8	3.2
Plantain flower	7	5.1	83	61.4	21	15.5	6	4.4	2	1.4	28	11.2	176	70	28	11.2	6	2.4	14	5.6
Brinjal	20	14.8	83	61.4	21	15.5	6	4.4	2	1.4	28	11.2	176	70	28	11.2	6	2.4	14	5.6
Knol-khol	4	2.9	48	35.5	25	18.5	24	17.7	31	5.2	13	5.2	114	17.6	24	9.6	57	23	17	4.4
Fruits																				
Apple	27	20	44	32.5	33	24.6	28	20.7	-	-	59	23.6	98	39	56	22.4	39	14	-	-
Guava	33	24.4	52	38.5	31	22	16	11.8	-	-	65	26.1	113	45	51	20.4	23	9.2	-	-
Papaya	14	10.3	59	43.7	35	25	24	17.7	-	-	47	18.8	108	43	54	21.6	43	17	-	-
Pomegranate	32	23.7	56	41.1	34	25	10	7.4	-	-	65	16.1	123	49	53	21.2	11	4.4	-	-
Sapota	21	15.5	41	30.3	37	27	33	24.4	-	-	40	16	93	37	69	27.7	50	20	-	-
Seethaphal	16	11.8	32	23.7	42	31	42	31.1	-	-	39	15.6	75	30	72	28.9	66	26	-	-
Banana	51	37.7	22	16.2	40	29	19	14.0	-	-	89	35.6	68	27	61	24.4	34	13.6	-	-
Grapes	23	17	55	40.7	38	28	16	11.8	-	-	52	20.8	113	45	65	26.1	22	8.8	-	-
Fleshy foods																				
Meat	7	5.1	68	50.3	30	22.4	8	5.9	19	14.6	15	6.02	119	47	57	22.8	17	6.8	44	17
Chicken	4	2.9	83	61.4	28	20	4	2.9	13	9.6	11	4.4	156	62	50	20.0	12	4.8	23	9.2
Egg	23	17.0	87	64.4	12	8.8	3	2.2	7	5.1	50	20.0	158	63	27	10.8	2	0.8	15	6.0
Organ meat	3	2.2	29	21	28	20.7	16	11.8	56	41.3	8	3.2	56	22	55	22.0	29	11	104	41
Beverages																				
Milk	88	65.1	15	11	3	2.2	8	5.9	18	13.2	170	68.2	34	13.2	6	2.4	17	6.8	25	10
Tea	74	54.8	17	12.5	2	1.4	13	9.6	26	19.2	145	58.2	39	15	4	1.6	19	7.6	45	18.2
Coffee	62	45.9	20	14	8	5.9	10	7.4	32	23.4	119	47.7	55	22.1	13	5.2	24	9.6	41	16.4

Among the roots and tubers potato, carrot, and radish were consumed once or twice a week followed by an occasional consumption pattern among the adults disregarding the age. The green leafy vegetables such as Agathi, drumstick leaves, Parupu Keerai and Manathakkali Keerai were consumed once a week and sometimes occasionally. Ponangani, fenugreek leaves, and Amaranthus were not preferred by 28 to 34 percent of the adults.

Other vegetables such as brinjal, beans, drumstick, and ladies' finger were consumed once or twice a week by above 70 per cent of young adults in all age groups. In nearly, 80 per cent of the adults, the consumption of tomatoes was daily.

But among the young adults only 68 to 70 per cent of them consumed cruciferous vegetables weekly. Plantain flower, and Knol-khol were consumed once in a week by 42.9 per cent and 35.5 per cent respectively. Among the fruits, banana consumption a daily (35-35%) consumption was observed. Other fruits such as apple, pomegranate, guava, papaya, sapota, and Seethaphal were consumed once or twice a week 36.9 per cent, 46.6 per cent, 42.9 per cent, 42.9 per cent, 43.4 per cent, 34.8 per cent, and 27.8 per cent respectively.

Consumption of flesh foods like chicken, mutton, and fish was weekly twice or thrice in most young adults irrespective of their age. Weekly consumption of egg was observed in 63 to 64 per cent of young adults in all age groups. 41 per cent of did not consume organ meat and 21 percent consumed organ meat weekly.

Among the young adults, 65.1 per cent, and 68.2 per cent in the age group of 18-20 years, and 21-25 years, consumed milk. In 18-20 years, and 21-15 years, most of the milk was consumed as tea or coffee. Thirty four per cent of the young adults consumed panner and cheese by weekly.

2.2 Association of consumption pattern of fibre rich foods, age, gender and location

Dietary fibre delays the intestinal transit of the food consumed. Dietary fibre is important for proper bowel function, to reduce chronic constipation, diverticular disease, haemorrhoids coronary heart diseases, diabetes and obesity. They also reduce plasma cholesterol. The protective role of dietary fibre against colon cancer has long been recognised (NIN, 2011).

Not all fibres can be classified as prebiotics; however, most prebiotics can be classified as dietary fibres. Consumption of prebiotics is a dietary strategy by which the gastrointestinal microbiota can be modified for health benefit (Holscher, 2017). Prebiotics were originally defined in 1995 by Gibson and Roberfroid as "a non-digestible food ingredient that beneficially affects the host by selectively stimulating the growth and/or activity of one or a limited number of bacteria in the colon, and thus improves host health.

Without good food composition data, nutrition research cannot establish or explain the interrelationship between diet and its influence on health. The latest new 'Indian Food Composition Tables, 2017' provides values with widest possible coverage of nutrient and bioactive components of key foods representing all major food groups. High fibre foods and their amount per 100 grams from selected food groups are given in the Table V.

TABLE V

LIST OF HIGH FIBRE FOODS FROM FOOD GROUPS

Food groups	**Dietary fibre (g)**	**Food groups**	**Dietary fibre (g)**
Cereals and millets		**Pulses**	
Wheat	11.23	Soybean	21.55
Bajra	11.49	Rajmah	17.74
Jowar	10.22	Black gram dal	11.93
Ragi	11.18	Bengal gram dal	15.15
Green leafy vegetables		**Roots and tubers**	
Agathi	8.60	Tapioca	4.61
Drumstick	8.21	Carrot	4.18
Ponangani	6.74	Sweet potato	2.65
Fenugreek	4.90	Radish	3.99
Other vegetables		**Fruits**	
Beans	8.63	Sapota	9.60
Drumstick	6.83	Guava	8.59
Plantain flower	4.08	Gooseberry	7.75
Ladies finger	5.25	Custard apple	5.10

(Approximately per 100g)

2.3 Association of consumption pattern of fibre rich foods and age

The information pertaining to the frequency of consumption pattern of fibre rich foods in association with age factor is given as follows:

TABLE VI

Frequency of consumption of fibre rich foods in association with age

Food groups	**18-20 years (N=230)**					**21-25 years (N=154)**					**Association with age**		
	D	**W**	**M**	**O**	**N**	**D**	**W**	**M**	**O**	**N**	**X^2**	**df**	**p-value**
Cereals and millets													
Bajra	8	64	79	46	33	4	47	48	34	21	3.5	7	0.834^{NS}
Wheat	28	183	14	4	1	18	127	25	2	0	2.6	7	0.913^{NS}
Ragi	14	100	65	35	16	8	68	49	20	9	10.9	7	0.143^{NS}
Jowar	9	60	78	49	32	3	50	57	30	14	7.5	7	0.375^{NS}
Pulses													
Soybean	12	126	71	13	8	5	76	53	14	6	6.06	7	0.532^{NS}
Rajmah	9	75	84	28	34	1	52	55	17	29	6.66	7	0.464^{NS}
Black gram dal	64	133	21	8	4	34	95	22	2	1	6.67	7	0.464^{NS}
Bengal gram dal	85	120	16	5	4	55	82	13	2	2	2.95	7	0.889^{NS}
Green leafy vegetables													
Agathi	39	97	40	54	-	36	49	36	33	-	7.95	6	0.241^{NS}
Drumstick	40	133	30	26	-	28	87	21	18	-	1.62	6	0.951^{NS}
Ponangani	31	90	49	60	-	21	45	44	44	-	14.6	6	0.024^{*}
Fenugreek	34	84	45	67	-	23	47	33	51	-	6.33	6	0.387^{NS}
Roots and tubers													
Tapioca	13	76	78	51	12	11	57	48	30	8	3.92	6	0.687^{NS}
Carrot	39	169	17	4	1	20	120	11	3	0	2.59	6	0.858^{NS}
Sweet potato	9	87	82	44	8	6	67	48	28	8	3.01	6	0.807^{NS}
Radish	15	165	30	13	7	6	106	28	9	5	4.58	6	0.597^{NS}
Other vegetables													
Beans	31	183	12	1	3	22	122	9	1	0	3.24	6	0.777^{NS}
Drumstick	24	176	20	6	4	17	118	12	6	1	2.57	6	0.860^{NS}
Plantain flower	13	114	56	24	23	8	70	41	22	13	3.06	6	0.801^{NS}
Ladies finger	23	178	21	5	3	10	120	16	7	1	3.98	6	0.679^{NS}

Fruits													
Sapota	33	85	63	49	-	26	49	43	34	-	6.29	7	0.509^{NS}
Guava	56	104	47	22	-	41	61	35	17	-	3.76	7	0.806^{NS}
Gooseberry	48	91	52	38	-	37	51	37	29	-	4.47	7	0.723^{NS}
Custard apple	33	67	66	64	-	22	40	48	44	-	3.88	7	0.793^{NS}
Plant extracts													
Tulsi	25	58	39	41	60	15	39	24	24	52	3.467	7	0.839^{NS}
Hibiscus tea	12	34	29	41	115	3	26	18	23	84	6.096	7	0.529^{NS}
Karupurvalli tea	11	33	23	40	123	6	28	14	23	82	3.813	7	0.801^{NS}
Sangu poo tea	11	28	15	33	12	6	23	11	19	93	3.013	7	0.884^{NS}

NS- Not significant. Df- degree of freedom *- Significant

Table No. VI shows a significant ($P > 0.05$) no association between age factor and frequency of high fibre food consumption of the respondents. The values are not significant.

Since the staple food of the Indian population was the cereal-based proportion of cereal consumption pattern of young adults was 99.9% among both men and women. The consumption of cereals was included in the daily meal with the majority preferring rice and wheat. Rice is a staple diet of Tamilnadu, unsurprisingly it is consumed daily by all the study participants. Millets are a type of coarse grain that is high in protein, fibre, vitamins, and minerals. The practice of including millets in one's everyday diet is not new. Millets were a key staple meal in central and southern India, as well as hilly areas. Millet's consumption seemed to be less in the study group. It is clear from the above table that soluble fibre and micronutrients rich cereals and millets (Thinai, ragi, Samai, bajra, Varagu, Kutharaivali) are not frequently consumed by the study group. Similar, dietary diversity of cereal consumption was observed in Bhavani and Prabhavathy Devi (2019) in India.

2.4 Association of consumption pattern of fibre rich foods and gender

The information pertaining to the frequency of consumption pattern of fibre rich foods in association with gender factor is given as follows:

TABLE VII

Frequency of consumption of fibre rich foods and plant extract in association with gender

Food groups	Male (N=230)					Female (N=154)					Association with gender		
	D	**W**	**M**	**O**	**N**	**D**	**W**	**M**	**O**	**N**	**X^2**	**df**	**p-value**
Cereals and millets													
Bajra	4	41	39	33	17	7	72	88	46	37	18.25	7	0.011^{NS}
Wheat	16	110	7	2	-	29	203	13	4	-	2.45	7	0.931^{NS}
Ragi	7	62	38	20	8	15	107	77	33	17	2.10	7	0.954^{NS}
Jowar	2	43	48	27	14	11	113	127	79	54	4.77	7	0.688^{NS}
Pulses													
Soybean	4	64	48	11	5	13	138	76	16	9	6.49	7	0.483^{NS}
Rajmah	1	44	47	14	26	9	83	92	31	37	5.56	7	0.592^{NS}
Black gram dal	50	71	9	2	1	90	131	20	5	5	3.26	7	0.859^{NS}
Bengal gram dal	32	79	19	2	0	66	149	24	8	5	6.15	7	0.522^{NS}
Green leafy vegetables													
Agathi	30	41	33	28	-	45	105	43	59	-	7.40	6	0.285^{NS}
Drumstick	25	73	19	15	-	44	147	32	29	-	1.53	6	0.957^{NS}
Ponangani	17	38	38	39	-	35	97	55	65	-	12.1	6	0.058^{NS}
Fenugreek	19	38	30	45	-	38	93	48	73	-	7.27	6	0.296^{NS}
Roots and tubers													
Tapioca	8	45	44	27	8	16	88	82	54	12	2.39	6	0.880^{NS}
Carrot	16	103	10	3	-	43	186	18	4	1	2.84	6	0.828^{NS}
Sweet potato	4	52	44	26	6	11	99	86	46	10	0.93	6	0.988^{NS}
Radish	6	90	24	7	5	15	181	34	15	7	4.04	6	0.671^{NS}
Other vegetables													
Beans	21	12	8	1	-	32	203	13	1	3	3.97	6	0.680^{NS}

Drumstick	14	103	8	6	1	27	191	24	6	4	3.94	6	0.684^{NS}
Plantain flower	7	58	35	21	11	14	126	62	25	25	5.27	6	0.509^{NS}
Ladies finger	8	102	14	7	1	25	196	23	5	3	5.64	6	0.464^{NS}
Fruits													
Sapota	21	41	37	33	-	40	93	69	50	-	6.03	7	0.536^{NS}
Guava	33	52	31	16	-	65	113	51	23	-	5.61	7	0.586^{NS}
Gooseberry	27	44	33	28	-	59	98	56	39	-	4.56	7	0.713^{NS}
Custard apple	16	32	42	42	-	39	68	61	72	-	6.38	7	0.496^{NS}
Plant extracts													
Tulsi	24	69	44	44	70	15	28	19	21	49	6.075	7	0.531^{NS}
Hibiscus tea	12	41	33	45	122	3	19	14	19	77	4.792	7	0.685^{NS}
Karpuravalli tea	13	41	26	44	128	4	20	11	19	78	3.767	7	0.806^{NS}
Sangu poo tea	11	35	18	37	151	6	16	10	15	85	1.818	7	0.969^{NS}

NS- Not significant. df- degree of freedom

D-Daily **W**- Weekly **M-** Monthly **O**-Occasionally **N**-Never

Table No. VII shows a significant (P >0.05) no association between gender factor and frequency of high fibre food consumption of the respondents. The values are not significant.

This finding can be supported by another study done to investigate- How does food consumption pattern vary between Indian adult men and women. The study found that there is a strong and significant pro-rich inequality in diet diversity among adults in India. (Dhillon *et al.,* 2020).

Another study done by (Arganini *et al.,* 2012) found that attitude reflected by dietary profiles in terms food intake pattern, showed consistent trends according to gender. Women show a tendency to perform healthier food choices and are much more concerned about the importance of food choice and eating behaviour to stay in a good physical shape than men.

2.5 Association of consumption pattern of fibre rich foods and location

The information pertaining to the frequency of consumption pattern of fibre rich foods in association with gender factor is given as follows:

Frequency of consumption of fibre rich foods in association with place of residence of respondents

TABLE VIII

CEREALS AND MILLETS

Criteria	**Parameters**	**Wheat**					**Bajra**					**Jowar**					**Ragi**				
		D	**W**	**M**	**O**	**N**	**D**	**W**	**M**	**O**	**N**	**D**	**W**	**M**	**O**	**N**	**D**	**W**	**M**	**O**	**N**
Place of residence	Coimbatore	18	75	5	2	0	2	31	33	25	9	5	27	38	24	7	9	43	27	18	3
	Dharmapuri	3	45	2	1	0	1	18	17	7	8	0	20	13	11	7	0	27	14	8	2
	Erode	7	53	2	1	0	1	19	18	13	13	1	19	18	14	12	1	29	18	7	9
	Krishnagiri	2	33	3	1	0	0	13	16	7	3	2	11	15	6	5	0	19	12	6	2
	Namakkal	4	20	4	0	0	1	6	9	6	6	3	6	11	4	4	0	8	11	6	3
	Salem	3	25	4	1	0	3	6	12	7	4	1	9	13	9	2	2	13	14	5	0
	Tirupur	9	58	1	0	0	4	16	22	15	11	3	18	27	11	9	10	29	18	5	6
Association with place of residence	X^2	37.36					30.36					42.19					59.75				
	Df	42					42					42					42				
	p-value	0.674^{NS}					0.909^{NS}					0.463^{NS}					0.037^{NS}				

NS- Not Significant df- degree of freedom

D- Daily **W**- Weekly **M**- Monthly **O**- Occasionally **N**- Never

Table No. VIII shows a significant ($P > 0.05$) no association between place of residence and frequency of high fibre food consumption of the respondents among cereal food group. The values are not significant.

TABLE IX
PULSES

Criteria	Parameters	Soybean					Rajmah					Black gram dal					Bengal gram dal				
		D	**W**	**M**	**O**	**N**	**D**		**M**	**O**	**N**	**D**	**W**	**M**	**O**	**N**	**D**	**W**	**M**	**O**	**N**
Place of residence	Coimbatore	4	47	39	5	5	3	32	34	17	14	39	52	7	1	7	25	60	13	1	1
	Dharmapuri	1	29	16	4	1	0	26	18	1	6	22	23	3	2	1	13	29	5	4	0
	Erode	4	31	20	4	5	2	19	22	5	16	25	33	3	0	3	15	42	4	0	3
	Krishnagiri	0	19	17	3	0	1	11	17	5	5	10	23	4	2	0	12	23	4	0	0
	Namakkal	1	20	4	2	1	0	11	10	3	4	9	16	2	1	0	8	18	1	1	0
	Salem	4	18	8	3	1	0	10	15	5	4	12	15	5	1	1	7	17	8	1	1
	Tirupur	3	38	20	6	1	4	18	23	9	14	23	40	5	0	0	18	39	8	3	0
Association with place of residence	X^2	37.13					41.24					35.8					39.05				
	Df	42					42					42					42				
	p-value	0.684^{NS}					0.504^{NS}					0.736^{NS}					0.601^{NS}				

NS- Not Significant df- degree of freedom

D- Daily **W**- Weekly **M**- Monthly **O**- Occasionally **N**- Never

Table No. IX shows a significant ($P > 0.05$) no association between place of residence and frequency of high fibre food consumption of the respondents among Pulses food group. The values are not significant.

TABLE X

GREEN LEAFY VEGETABLES

Criteria	Parameters	Agathi					Drumstick					Ponangani					Fenugreek				
		D	**W**	**M**	**O**	**N**	**D**	**W**	**M**	**O**	**N**	**D**	**W**	**M**	**O**	**N**	**D**	**W**	**M**	**O**	**N**
Place of residence	Coimbatore	18	33	26	23	-	14	55	15	16	-	9	30	31	30	-	12	33	21	34	-
	Dharmapuri	12	17	13	9	-	14	26	8	3	-	10	15	15	11	-	9	16	11	15	-
	Erode	15	19	9	21	-	14	36	5	9	-	10	26	9	19	-	11	20	12	21	-
	Krishnagiri	8	19	8	4	-	6	28	3	2	-	2	19	8	10	-	4	12	14	9	-
	Namakkal	6	11	5	6	-	8	16	2	2	-	6	11	4	7	-	7	12	3	6	-
	Salem	4	18	6	6	-	1	22	8	3	-	3	14	9	8	-	4	14	8	8	-
	Tirupur	12	29	9	18	-	12	37	10	9	-	12	20	17	19	-	10	24	9	25	-
Association with place of residence	X^2	32.93					48.52					30.34					31.84				
	Df	36					36					36					36				
	p-value	0.612^{NS}					0.079^{NS}					0.734^{NS}					0.667^{NS}				

NS- Not Significant df- degree of freedom

D- Daily **W**- Weekly **M**- Monthly **O**- Occasionally **N**- Never

Table No. X shows a significant ($P > 0.05$) no association between place of residence and frequency of high fibre food consumption of the respondents among Green leafy vegetables. The values are not significant.

TABLE XI

ROOTS AND TUBERS

Criteria	Parameters	Tapioca					Carrot					Sweet potato					Radish				
		D	**W**	**M**	**O**	**N**	**D**	**W**	**M**	**O**	**N**	**D**	**W**	**M**	**O**	**N**	**D**	**W**	**M**	**O**	**N**
Place of residence	Coimbatore	6	33	34	23	4	15	72	11	2	0	6	35	35	23	1	9	64	21	4	2
	Dharmapuri	6	15	16	13	1	7	41	3	0	0	1	20	19	9	2	3	36	5	5	2
	Erode	2	22	20	14	6	11	45	4	3	1	2	21	24	11	6	2	47	10	10	2
	Krishnagiri	2	11	13	9	4	5	32	2	0	0	0	17	17	4	1	0	27	6	6	1
	Namakkal	1	11	12	3	1	7	19	1	1	0	2	16	4	5	1	2	22	2	2	0
	Salem	3	14	11	6	1	3	27	3	1	0	1	12	11	9	1	0	28	5	5	0
	Tirupur	4	28	20	13	3	11	53	4	0	0	3	30	20	11	4	5	47	9	9	5
Association with place of residence	X^2	29.14					31.47					30.6					32.2				
	Df	36					36					36					36				
	p-value	0.784^{NS}					0.684^{NS}					0.722^{NS}					0.647^{NS}				

NS- Not Significant df- degree of freedom

D- Daily **W**- Weekly **M**- Monthly **O**- Occasionally **N**- Never

Table No. XI shows a significant ($P > 0.05$) no association between place of residence and frequency of high fibre food consumption of the respondents among Roots and tubers. The values are not significant.

TABLE XII

OTHER VEGETABLES

Criteria	Parameters	Beans					Drumstick					Plantain flower					Ladies finger				
		D	**W**	**M**	**O**	**N**	**D**	**W**	**M**	**O**	**N**	**D**	**W**	**M**	**O**	**N**	**D**	**W**	**M**	**O**	**N**
Place of residence	Coimbatore	15	76	9	0	0	13	69	14	2	2	6	44	27	15	8	8	78	9	4	1
	Dharmapuri	7	42	2	0	0	4	41	4	1	1	2	28	10	7	4	4	36	9	2	0
	Erode	10	50	1	1	2	9	48	2	4	0	7	27	14	9	7	7	50	4	1	2
	Krishnagiri	4	31	2	1	1	4	30	3	2	0	0	21	11	3	4	2	33	2	2	0
	Namakkal	4	24	0	0	0	3	23	1	1	0	2	17	3	3	3	2	26	0	0	0
	Salem	1	29	4	0	0	1	30	2	1	0	1	18	10	4	1	3	25	4	2	0
	Tirupur	12	53	3	0	0	7	53	6	1	1	3	29	22	5	9	7	50	9	1	1
Association with place of residence	X^2	38.07					28.76					33.52					27.6				
	Df	36					36					36					36				
	p-value	0.375^{NS}					0.798^{NS}					0.587^{NS}					0.840^{NS}				

NS- Not Significant df- degree of freedom

D- Daily **W**- Weekly **M**- Monthly **O**- Occasionally **N**- Never

Table No. XII shows a significant (P >0.05) no association between place of residence and frequency of high fibre food consumption of the respondents among Other vegetables. The values are not significant.

TABLE XIII

FRUITS

Criteria	Parameters	Sapota					Guava					Gooseberry					Custard apple				
		D	**W**	**M**	**O**	**N**	**D**	**W**	**M**	**O**	**N**	**D**	**W**	**M**	**O**	**N**	**D**	**W**	**M**	**O**	**N**
Place of residence	Coimbatore	14	36	31	18	-	26	43	22	8	-	21	41	21	16	10	15	26	31	27	-
	Dharmapuri	7	18	11	15	-	13	26	6	6	-	10	16	15	11	6	8	16	10	17	-
	Erode	9	22	20	13	-	18	27	12	7	-	17	22	15	10	8	7	18	21	18	-
	Krishnagiri	5	16	9	8	-	13	14	10	2	-	8	14	8	6	6	5	9	13	12	-
	Namakkal	7	12	7	4	-	8	10	8	2	-	8	9	9	7	0	5	11	8	4	-
	Salem	4	14	8	6	-	4	18	8	4	-	6	15	8	3	5	4	12	12	6	-
	Tirupur	14	16	19	19	-	15	27	17	10	-	15	25	12	14	9	10	15	15	24	-
Association with place of residence	X^2	28.9					40.79					30.24					28.4				
	Df	42					42					42					42				
	p-value	0.938^{NS}					0.524^{NS}					0.912^{NS}					0.946^{NS}				

NS- Not Significant   df- degree of freedom

D- Daily   **W**- Weekly   **M**- Monthly   **O**- Occasionally   **N**- Never

Table No. XIII shows a significant (P >0.05) no association between place of residence and frequency of high fibre food consumption of the respondents among Fruits. The values are not significant.

TABLE XIV

PLANT EXTRACTS

Criteria	**Parameters**	**Tulsi**					**Hibiscus tea**					**Karpuravalli tea**					**Sangu poo tea**				
		D	**W**	**M**	**O**	**N**	**D**	**W**	**M**	**O**	**N**	**D**	**W**	**M**	**O**	**N**	**D**	**W**	**M**	**O**	**N**
Place of residence	Coimbatore	10	26	14	19	31	4	17	14	17	48	6	17	12	18	47	4	14	8	18	56
	Dharmapuri	9	11	8	7	16	1	8	5	7	30	2	8	0	12	29	1	8	2	7	33
	Erode	5	14	10	10	25	4	10	5	13	32	2	11	4	8	39	4	8	3	8	41
	Krishnagiri	3	10	6	9	11	0	6	4	10	19	1	5	2	11	20	0	4	3	8	24
	Namakkal	2	8	5	5	8	1	5	2	5	15	1	5	1	3	18	3	4	0	2	19
	Salem	4	10	8	4	8	2	4	8	3	17	1	5	9	3	16	2	3	8	4	17
	Tirupur	7	18	13	11	20	2	10	9	9	38	4	10	9	8	37	3	10	4	5	46
Association with place of residence	X^2	36.19					30.336					39.073					46.303				
	Df	42					42					42					42				
	p-value	0.723^{NS}					0.910^{NS}					0.600^{NS}					0.299^{NS}				

NS- Not Significant df- degree of freedom

D- Daily **W**- Weekly **M**- Monthly **O**- Occasionally **N**- Never

Table No. XIV shows a significant ($P > 0.05$) no association between place of residence and frequency of Plant extracts of the respondents. The values are not significant.

3. Impact of nutrition intervention on Knowledge, Attitude and Practice (KAP) Scores of young adults:

Nutrition education provided the opportunity to learn the basic needs of health and nutrition and take the necessary steps to improve the quality in the selection, processing, cooking, and eating pattern of foodstuffs and helps in promoting gut health.

The impact of nutrition education was assessed using pre and post-test questionnaire consisting of 30 multiple choice questions among young adults. Impact evaluation of nutrition intervention on Knowledge, Attitude and Practice of the young adults regarding gut microbiome is presented in Table XV

3.2 Impact of digital health intervention on knowledge about gut microbiome

Change in knowledge of on the Gut microbiome among young adults is given in Table XV

Table XV

CHANGE IN KNOWLEDGE OF ON THE GUT MICROBIOME

Questions	Pre-awareness			Post awareness			Mean difference	't'	p-value
	N	%	M±SD	N	%	M±SD			
4	234	60.9	2.5 ± 0.64	308	80.2	2.7 ± 0.60	0.2	4.4	0.00**
5	184	47.9	2.4 ± 0.61	223	58.1	2.5 ± 0.62	0.1	2.3	0.18*
6	104	27.1	2.3 ± 0.67	236	61.5	2.4 ± 0.69	0.1	3.6	0.00**
7	84	21.9	2.2 ± 0.65	220	57.3	2.4 ± 0.70	0.2	4.7	0.00**
8	83	21.6	2.1 ± 0.73	197	51.3	2.3 ± 0.70	0.2	4.5	0.00**
9	119	31.0	2.0 ± 0.71	263	68.5	2.5 ± 0.6	0.5	9.6	0.00**
10	124	32.3	2.0 ± 0.77	214	55.7	2.3 ± 0.74	0.2	6.5	0.00**
11	187	48.7	2.2 ± 0.85	246	64.1	2.5 ± 0.61	0.3	6.7	0.00**
12	79	20.6	1.8 ± 0.71	192	50.0	2.3 ± 0.76	0.5	8.0	0.00**
13	99	25.8	1.9 ± 0.42	238	62.0	2.4 ± 0.72	0.5	9.5	0.00**
14	41	10.7	1.7 ± 0.65	207	53.9	2.3 ± 0.75	0.6	13.1	0.00**
15	150	39.1	2.1 ± 0.80	80	20.8	2.1 ± 0.54	-	0.2	0.7*
**- Significant at p <0.05 *- Non significant									

Table XV depicted the changes in knowledge among young adults on gut microbiome. The changes in knowledge in question no 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, and 15 in the pre-awareness and post-awareness phases were found to be from 60.9 per cent to 80.2 percent, 47.9 percent to 58.1 percent, 27.1 percent to 61.5 percent, 21.9 to 57.3 percent, 21.6 per cent to 51.3 percent, 31.0 percent to 68.5 percent, 32.3 percent to 55.7 percent, 48.7 per cent to 64.1 percent, 20.6 percent to 50.0 percent, 25.8 to 62.0 percent, 10.7 percent to 53.9 percent, and 39.1 to 20.8 percent respectively. The 't' test results revealed the statistically significant difference between pre-awareness and post-awareness in all the segments of gut microbiome test scores. However, highest level of improvement in gut microbiome test scores was found in post-awareness rather than in pre- awareness.

Statistically significant difference was found at $p \leq 0.05$ and 95% confidence level for the questions 4, 6, 7, 8, 9, 10, 11, 12, 13, 14. Statistically no significant difference was found at $p \leq 0.05$ and 95% confidence level for the questions 5, and 15. It further showed that with the intervention provided to the group there was a significant change in knowledge about the role of Gut microbiome in health. It was encouraging to note that nutrition education had brought a positive effect on the KAP scores.

. A study conducted by (Cresci *et al.,* 2015) finds that Interest in and knowledge of the gut microbiome have increased exponentially in the past decade. The food industry has taken this to full heights; a plethora of "probiotic" or "fermented" food and supplement products populate store shelves, Never before has the discussion of one's bowel habits and GI symptoms been more mainstream.

A study conducted by Dimidi *et al.,* 2019 found that fermented foods that have been tested in at least one randomised controlled trial (RCT) for their gastrointestinal effects were kefir, sauerkraut, natto, and sourdough bread. Despite extensive in vitro studies, there are no RCTs investigating the impact of kombucha, miso, kimchi or tempeh in gastrointestinal health. The most widely investigated fermented food is kefir, with evidence from at least one RCT suggesting beneficial effects in both lactose malabsorption and Helicobacter pylori eradication.

3.3 Impact of digital health intervention on attitude towards gut microbiome

Changes in attitude regarding gut microbiome-related concepts

Change in attitude regarding gut microbiome- related concepts among young adults are given in Table XVI

Table XVI

Change in attitude regarding gut microbiome-related concepts

Questions	Pre-awareness			Post awareness			Mean difference	't'	p-value
	N	%	M±SD	N	%	M±SD			
16	218	56.8	1.5 ± 0.67	87	22.7	1.8 ± 0.56	0.3	7.7	0.00**
17	166	43.2	1.8 ± 0.85	113	29.4	1.8 ± 0.66	-	0.1	0.8*
18	101	26.3	1.7 ± 0.44	273	71.1	1.4 ± 0.80	0.3	5.4	0.00**
19	107	27.9	1.9 ± 0.71	219	57	1.6 ± 0.83	0.3	5.1	0.00**
20	85	22.1	2.2 ± 0.68	290	75.5	1.3 ± 0.72	0.5	12.2	0.00**
21	173	45.1	1.8 ± 0.82	284	74.0	1.3 ± 0.67	0.5	7.9	0.00**
22	85	22.1	1.9 ± 0.64	296	77.1	1.2 ± 0.42	0.7	18.7	0.00**
23	79	20.6	1.9 ± 0.62	273	71.1	1.4 ± 0.69	0.5	12.2	0.00**
24	193	50.3	1.7 ± 0.81	284	74.0	1.4 ± 0.73	0.3	5.9	0.00**
25	76	19.8	1.9 ± 0.62	288	75.0	1.3 ± 0.70	0.6	12.4	0.00**
26	71	18.5	2.1 ± 0.69	250	65.1	1.5 ± 0.74	0.6	11.0	0.00**
**- Significant at p <0.05 *- Not significant at p> 0.05									

Table XVI depicted the changes in attitude among young adults regarding gut microbiome- related concepts. The changes in attitude in question no 16, 17, 18, 19, and 20 in the pre-awareness and post-awareness phases were found to be from 56.8 per cent to 22.7 percent, 43.2 percent to 29.4 percent, 26.3 to 71.1 percent, 27.9 to 57 percent, 22.1 per cent to

75.5 percent, 45.1 percent to 74.0 percent, 22.1 per cent to 77.1 percent, 20.6 percent to 71.1 percent, 20.6 to 71.1 percent, 19.8 percent to 75 percent, and 18.5 to 65.1 percent respectively. There is a significant decrease in percentage of question no 16 and 17 shows that the subject's attitude has changed from negative aspects on gut microbiome to positive aspects. The 't' test results revealed the statistically significant difference between pre-awareness and post-awareness in all the segments of gut microbiome test scores. However, highest level of improvement in gut microbiome test scores was found in post-awareness rather than in pre-awareness.

Statistically significant difference was found at $p \leq 0.05$ and 95% confidence level for the questions 16, 18, 19, 20, 21, 22, 23, 24, 25, and 26. Statistically no significant difference was found at $p \leq 0.05$ and 95% confidence level for the question 17. It further showed that with the intervention provided to the group there was a significant change in attitude regarding the general concepts of Gut microbiome.

Similarly in humans, antibiotic therapeutic doses are designed to minimize these effects, but despite these efforts, subsets of the microbiota can shift to that of increased colonization by opportunistic pathogens such as Clostridium difficile and Candida albicans. Noteworthy is that these effects of antibiotic delivery are not limited to oral delivery. Intravenously delivered antibiotics can have an effect on the gut microbiota as they become incorporated into bile and secreted into the intestine via the biliary system (Smith *et al.,* 2002).

In a study conducted by Zimmer *et al* Microbial enrichment has been associated with diets high in fruits, vegetables and fibre compared to a Western diet rich in fat, sugars and animal protein and depleted of fibre. (Zimmer *et al* 2012) analyzed the fecal flora of a large group of healthy volunteers on a strict vegetarian or vegan diet with classical microbiological culture and compared them with age and gender matched subjects consuming an omnivorous diet. The faecal microbiota of vegetarian and vegan subjects showed significantly lower microbial counts of Bifidobacterium, Bacteroides, E. coli and Enterobacteriaceae species and lower stool pH compared with omnivores.

3.4 Impact of digital health intervention on attitude towards gut microbiome

Change in practice regarding lifestyle and gut health

Change in practice regarding lifestyle and gut health among young adults are given in Table XVII

Table XVII

Change in practice regarding lifestyle and gut health

Questions	Pre-awareness			Post awareness			Mean difference	't'	p-value
	N	%	M±SD	N	%	M±SD			
PRACTICE									
27	135	35.2	1.3 ± 0.47	232	60.4	1.6 ± 0.48	0.3	6.9	0.00*
28	165	43.0	1.4 ± 0.49	277	72.1	1.7 ± 0.44	0.3	8.5	0.00*
29	66	17.2	1.1 ± 0.37	222	57.8	1.5 ± 0.49	0.4	12.9	0.00*
30	64	16.7	1.1 ± 0.37	194	50.5	1.5 ± 0.50	0.4	10.9	0.00*
31	203	52.9	1.5 ± 0.49	140	36.5	1.3 ± 0.49	0.2	4.6	0.00*
32	154	40.1	1.4 ± 0.49	248	64.6	1.6 ± 0.47	0.2	7.0	0.00*
33	232	60.4	1.6 ± 0.48	98	25.5	1.2 ± 0.43	0.4	10.4	0.00*
*- Significant at $p < 0.05$									

Table XVII depicted the changes in practice among young adults regarding lifestyle and gut health. The changes in practice in question no 27, 28, 29, 30, 31, 32, and 33 in the pre-awareness and post-awareness phases were found to be from 35.2 per cent to 60.4 percent, 43.0 percent to 72.1 percent, 17.2 to 57.8 percent, 16.7 to 50.5 percent, 52.9 percent to 36.5 percent, 40.1 percent to 64.6 percent and 60.4 percent to 25.5 percent respectively. There is a significant decrease in percentage of question no 16 and 17 shows that the subject's attitude has changed from negative aspects on gut microbiome to positive aspects. The 't' test results revealed the statistically significant difference between pre-awareness and post-awareness in all the segments of gut microbiome test scores. However, highest level of improvement in gut microbiome test scores was found in post-awareness rather than in pre- awareness.

Statistically significant difference was found at $p \leq 0.05$ and 95% confidence level for the seven questions twenty-seven, twenty-eight, twenty-nine, thirty, thirty-one, thirty-two, and thirty-three. It further showed that with the intervention provided to the group there was a significant change in practice among young adults regarding lifestyle and gut health. It was encouraging to note that nutrition education had brought a positive effect on the KAP scores.

In a study of professional rugby players during a regulated environment of preseason training, (Clarke *et al* 2014) demonstrated the impact of exercise and associated dietary changes on the gut microbiota (56). Enhanced gut microbial diversity was significantly higher and positively correlated with increased exercise and dietary protein intake in athletes as compared with size matched (high Body Mass Index – BMI ~30 kg/m2) and age/gender matched (lower BMI

It can be inferred that the nutrition education for the period of one months with the help of the developed nutrition education tools, based on the structured methods of scheduled nutrition education classes to young adults was very effective in imparting and changing the nutrition related Knowledge, Attitude, and Practices of promoting gut health.

3.5 Impact of digital health intervention and dietary modification on food intake of young adults.

Table XVIII

Association between food consumption and Knowledge on Gut microbiome

Food groups		**Pearson's correlations**	**p-value**
Cereals	Knowledge on Gut microbiome	0.8	0.00*
Pulses		0.9	0.00*
Green leafy vegetables		0.98	0.00*
Roots and tubers		0.99	0.00*
Other vegetables		0.97	0.00*
Fruits		0.93	0.00*
**. Correlation is significant at the 0.01 level (2-tailed).			

Table No. XVIII shows a significant (p<0.001) positive correlation between Cereals, Pulses, Green leafy vegetable, Other vegetables, and Fruits consumption and Knowledge status of the respondents, with a Pearson's correlation coefficient ® value of 0.8. The values are significant at 1 percent level of significance.

Nutrition and the gut microbiome have been implicated in the etiology of many westernized diseases. However, the role of the gut microbiome in the rising incidences of colorectal cancer (CRC) in countries undergoing dietary and lifestyle transitions. In Zimbabwe, an observational study was recently undertaken to assess the link between CRC risk and dietary changes from traditional to Western during urbanization. Owing to retention of fibre intake in the urban population, the levels of butyrate and butyrogenic bacteria were similar between rural and urban participants, yet the levels of bile acids, indicative of high-fat diet were higher among urban participants. This study demonstrated the potential to prevent a CRC epidemic through retention of traditional high fibre foods, a sustained adjustment of diet that would reverse the pattern of metabolic markers associated with CRC risk (Wilson *et al.,* 2020).

Table XIX

Association between food consumption and Attitude towards Gut microbiome

Food groups		**Pearson's correlations**	**p-value**
Cereals	Attitude towards Gut microbiome	0.81	0.01*
Pulses		0.97	0.00*
Green leafy vegetables		0.97	0.00*
Roots and tubers		0.96	0.00*
Other vegetables		0.96	0.00*
Fruits		0.78	0.02*
**. Correlation is significant at the 0.01 level (2-tailed).			

Table No. XIX shows a significant (p<0.001) positive correlation between Cereals, Pulses, Green leafy vegetable, Other vegetables, and Fruits consumption and Attitude towards Gut microbiome of the respondents, with a Pearson's correlation coefficient ® value of 0.8. The values are significant at 1 percent level of significance.

Accordingly, increased levels of SCFAs were found in vegan, vegetarian, and also omnivore subjects with high-level adherence to the Mediterranean diet, having a remarkable daily intake of plant-based foods, such as fruit vegetables and legumes.[19] In addition, dietary fibre supplementation has been recently demonstrated to select specific groups of fibre-degrading bacteria and to increase SCFA levels with beneficial effects on type 2 diabetes patients.[20] It is well-known that the equilibrium of the gut bacteria is modulated by the dietary components reaching the gut, and the metabolic degradation pathways of several specific classes of macro- and micronutrients have been elucidated. However, the interindividual variability is very high, and in many cases, prolonged dietary exposure is the key factor underpinning the microbiota metabolic capacity (Ercolini *et al.,* 2018).

Table XX

Association between food consumption and Lifestyle practice

Food groups		**Pearson's correlations**	**p-value**
Cereals	Lifestyle Practice	0.78	0.02*
Pulses		0.95	0.00*
Green leafy vegetables		0.95	0.00*
Roots and tubers		0.98	0.00*
Other vegetables		0.93	0.00*
Fruits		0.86	0.00*
**. Correlation is significant at the 0.01 level (2-tailed).			

Table No. XX shows a significant ($p<0.001$) positive correlation between Cereals, Pulses, Green leafy vegetable, Other vegetables, and Fruits consumption and Practices towards Gut microbiome of the respondents, with a Pearson's correlation coefficient ® value of 0.8. The values are significant at 1 percent level of significance.

Study conducted by Conlon *et al.,* 2015 found that the impact of non-dietary lifestyle factors on the gut microbiota has been largely ignored. Smoking and lack of exercise can significantly impact the large bowel (and potentially the microbiota) as they are risk factors for CRC. Indeed, smoking has a significant influence on gut microbiota composition, increasing Bacteroides-Prevotella in individuals with Crohn's Disease (CD) and healthy individuals. Another lifestyle factor, stress, has an impact on colonic motor activity via the gut-brain axis which can alter gut microbiota profiles, including lower numbers of potentially beneficial Lactobacillus.

Summary and Conclusion

V SUMMARY AND CONCLUSION

In the human body, there are trillions of cells in the human microbiota, including bacteria, viruses, and fungi. The gut has the largest population of microorganisms. The skin and genitals are two more frequent habitats. The microbiome, which consists of microbial cells and their genetic material, is live in humans from birth. This connection is essential for good health. The biomass produced by the bacteria living in the gastrointestinal tract is around 4 pounds. Every individual has a unique combination of species. Nutrition, immunity, and effects on the brain and behaviour are all influenced by the microbiota. It has been associated with a multitude of disorders that disrupt the usual balance of microbes.

The microbiome refers to all of the genes located within the microbial cells. A symbiotic association exists between 10 trillion and 100 trillion microbial cells in every human being. As long as the body is healthy, these benefits both the microorganisms and their hosts. According to estimates, the human microbiota may contain approximately 1,000 different types of bacteria.

This symbiotic relationship is beneficial to humans, and the presence of this normal flora includes microorganisms that are so common in the environment that they may be found in almost all animals from the same habitat. These native microbes, on the other hand, include pathogenic bacteria that may overcome the body's defenses that separate them from important organs and systems.

Good bacteria and harmful bacteria in the gut migrate into larger systems and cause GI tract infections. Food poisoning and other gastrointestinal disorders that cause diarrhea and vomiting are examples of these infections. The gut microbiota is 150 times more genetically diverse than the human body, with over 3 million genes. Each person's gut microbiome is unique. It has a significant impact on a person's ability to fight disease, digest food, and even their mood and psychological processes.

Microorganisms have developed alongside humans and are an essential component of life, performing a variety of essential roles. According to research, they have been linked to the following disorders, whether normal or disturbed bacterial populations. Asthma, autism, cancer, celiac disease, colitis, diabetes, eczema, heart disease, malnutrition, multiple sclerosis, and obesity. Energy balance, brain development, and cognitive function are all influenced by gut microorganisms and their genetics. Research is ongoing on exactly how this occurs and ways this relationship can be used for human benefit.

Inflammatory bowel diseases (IBD), such as Crohn's disease and ulcerative colitis, have been linked to bacterial populations in the gastrointestinal system. IBD, obesity, and type 2 diabetes have all been associated with a lack of microbial diversity in the gut. The gut microbiota's health has been connected to metabolic syndrome. These risk factors have been lowered by incorporating prebiotics, probiotics, and other supplements into the diet. The diversity of the microbiota is linked to dietary diversity. Younger adults who eat a wide variety of foods have a more diverse gut microbiota than adults who stick to a distinct dietary pattern.

A total of 384 young adults aged 19-25 years from the west region of Tamilnadu were taken and a study was conducted. For the investigation, appropriate research tools were selected which included a structured food frequency questionnaire, and a pre-and post-intervention questionnaire. Similarly, a pre-and post-intervention questionnaire was used to assess the knowledge level before and after the intervention. The content was a digital health intervention on the Gut microbiome developed. The knowledge was imparted by using digital health intervention as a tool for providing information on the Gut microbiome using WhatsApp, Instagram, and YouTube videos. Finally, impact of digital health intervention was evaluated by administering the post-awareness questionnaire. The data obtained from survey was recorded and further analysis was done using SPSS version 26.0 and Excel 2016. The results obtained from the study are summarized below.

The salient findings of the study:

- Among selected participants, 59.9 percent of the respondents were in the age group of 18-20 years, and the remaining 40.1 percent were in the age group of 21-25 years.
- 64.8 percent of the respondents were female and the remaining 35.2 percent of respondents were male.
- Seventy six percent of respondents were found to be pursuing undergraduate and 18.8 percent pursuing post-graduate and 5.2 percent pursuing Ph.D.
- Majority of the respondents i.e., 26.6 percent belonged to Coimbatore, followed by 17.2 percent Tirupur, 16.7 percent Erode, 13.3 percent, Dharmapuri, 10.2 percent Krishnagiri, 8.9 percent Salem, and 7.3 percent Namakkal.
- Among the selected participants, the majority of the respondents i.e., 53.7 percent belonged to urban areas, while the remaining 46.3 percent of the respondents belonged

to rural areas.

- The frequency of consumption of foods from different food groups varied between food among the young adults. The consumption of cereals and millets revealed that rice is the staple food was consumed daily by 89 per cent, while wheat was mostly (80-83%) consumed weekly among young adults irrespective of age. Ragi is a prebiotic, rich source of dietary fibre. Among young adults' millets like ragi, Thinai, Varagu, Samai, Kutharaivali and Cholam were consumed weekly or occasionally.
- The consumption pattern of pulses was not on daily basis among young adults weekly three-to-four-time pattern was observed. The pulses such as Channa dal, green gram dal, Soyabean, Horse gram, Rajmah, Red gram dal, Black gram dal and bengal gram dal were consumed weekly. Fifty to fifty-three per cent of the young adults in all the age groups consumed black gram dhal daily as part of the idly or dosa batter.
- Among the roots and tubers potato, carrot, and radish were consumed once or twice a week followed by an occasional consumption pattern among the adults disregarding the age. The green leafy vegetables such as Agathi, drumstick leaves, Parupu Keerai and Manathakkali Keerai were consumed once a week and sometimes occasionally. Ponangani, fenugreek leaves, and Amaranthus were not preferred by 28 to 34 percent of the adults.
- Other vegetables such as brinjal, beans, drumstick, and ladies' finger were consumed once or twice a week by above 70 per cent of young adults in all age groups. In nearly, 80 per cent of the adults, the consumption of tomatoes was daily.
- But among the young adults only 68 to 70 per cent of them consumed cruciferous vegetables weekly. Plantain flower, and Knol-khol were consumed once in a week by 42.9 per cent and 35.5 per cent respectively.
- Among the fruits, banana consumption a daily (35-35%) consumption was observed. Other fruits such as apple, pomegranate, guava, papaya, sapota, and Seethaphal were consumed once or twice a week 36.9 per cent, 46.6 per cent, 42.9 per cent, 42.9 per cent, 43.4 per cent, 34.8 per cent, and 27.8 per cent respectively.
- Consumption of flesh foods like chicken, mutton, and fish was weekly twice or thrice in most young adults irrespective of their age. Weekly consumption of egg was observed in 63 to 64 per cent of young adults in all age groups. 41 per cent of did not consume organ meat and 21 percent consumed organ meat weekly.
- Among the young adults, 65.1 per cent, and 68.2 per cent in the age group of 18-20

years, and 21-25 years, consumed milk. In 18-20 years, and 21-15 years, most of the milk was consumed as tea or coffee. Thirty four per cent of the young adults consumed panner and cheese by weekly.

- Since the staple food of the Indian population was the cereal-based proportion of cereal consumption pattern of young adults was 99.9% among both men and women. The consumption of cereals was included in the daily meal with the majority preferring rice and wheat. Rice is a staple diet of Tamilnadu, unsurprisingly it is consumed daily by all the study participants.
- Millet's consumption seemed to be less in the study group. Micronutrients rich cereals and millets (Thinai, ragi, Samai, bajra, Varagu, Kutharaivali) are not frequently consumed by the study group.
- There was no significant ($P > 0.05$) association between gender factor and frequency of high fibre food consumption of the respondents was observed.
- Statistically no significant difference was found at p (>0.05) between the place of residence and frequency of high fibre food consumption of the respondents among the food groups of Cereals, Pulses, Green leafy vegetables, Roots and tubers, Other vegetables, and Fruits.
- Statistically no significant difference ($p > 0.05$) between place of residence and frequency of Plant extracts of the respondents of the respondents among
- The change in knowledge among young adults on gut microbiome. The changes in knowledge in question no 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, and 15 in the preawareness and post-awareness phases were found to be from 60.9 per cent to 80.2 percent, 47.9 percent to 58.1 percent, 27.1 percent to 61.5 percent, 21.9 to 57.3 percent, 21.6 per cent to 51.3 percent, 31.0 percent to 68.5 percent, 32.3 percent to 55.7 percent, 48.7 per cent to 64.1 percent, 20.6 percent to 50.0 percent, 25.8 to 62.0 percent, 10.7 percent to 53.9 percent, and 39.1 to 20.8 percent respectively.
- Statistically significant difference was found at $p < 0.05$ and 95% confidence level for the questions 4, 6, 7, 8, 9, 10, 11, 12, 13, 14. Statistically no significant difference was found at $p < 0.05$ and 95% confidence level for the questions 5, and 15. It further showed that with the intervention provided to the group there was a significant change in knowledge about the role of Gut microbiome in health.
- The change in attitude among young adults regarding gut microbiome- related concepts. The changes in attitude in question no 16, 17, 18, 19, and 20 in the pre-awareness and

post-awareness phases were found to be from 56.8 per cent to 22.7 62 percent, 43.2 percent to 29.4 percent, 26.3 to 71.1 percent, 27.9 to 57 percent, 22.1 per cent to 75.5 percent, 45.1 percent to 74.0 percent, 22.1 per cent to 77.1 percent, 20.6 percent to 71.1 percent, 20.6 to 71.1 percent, 19.8 percent to 75 percent, and 18.5 to 65.1 percent respectively. There is a significant decrease in percentage of question no 16 and 17 shows that the subject's attitude has changed from negative aspects on gut microbiome to positive aspects. The 't' test results revealed the statistically significant difference between pre-awareness and postawareness in all the segments of gut microbiome test scores.

- Statistically significant difference was found at $p < 0.05$ and 95% confidence level for the questions 16, 18, 19, 20, 21, 22, 23, 24, 25, and 26. Statistically no significant difference was found at $p < 0.05$ and 95% confidence level for the question 17. It further showed that with the intervention provided to the group there was a significant change in attitude regarding the general concepts of Gut microbiome.
- The change in practice in question no 27, 28, 29, 30, 31, 32, and 33 in the pre-awareness and post-awareness phases were found to be from 35.2 per cent to 60.4 percent, 43.0 percent to 72.1 percent, 17.2 to 57.8 percent, 16.7 to 50.5 percent, 52.9 percent to 36.5 percent, 40.1 percent to 64.6 percent and 60.4 percent to 25.5 percent respectively. There is a significant decrease in percentage of question no 16 and 17 shows that the subject's attitude has changed from negative aspects on gut microbiome to positive aspects. The 't' test results revealed the statistically significant difference between pre-awareness and post-awareness in all the segments of gut microbiome test scores.
- Statistically significant difference was found at $p \leq 0.05$ and 95% confidence level for the seven questions twenty-seven, twenty-eight, twenty-nine, thirty, thirty-one, thirty-two, and thirty-three.
- Significance ($p<0.001$) positive correlation between Cereals, Pulses, Green leafy vegetable, Other vegetables, and Fruits consumption and Knowledge status of the respondents, with a Pearson's correlation coefficient ® value of 0.8. The values are significant at 1 percent level of significance.
- Significance ($p<0.001$) positive correlation between Cereals, Pulses, Green leafy vegetable, Other vegetables, and Fruits consumption and Attitude towards Gut microbiome of the respondents, with a Pearson's correlation coefficient ® value of 0.8. The values are significant at 1 percent level of significance.

- Significance (p<0.001) positive correlation between Cereals, Pulses, Green leafy vegetable, Other vegetables, and Fruits consumption and Practices towards Gut microbiome of the respondents, with a Pearson's correlation coefficient ® value of 0.8. The values are significant at 1 percent level of significance.

Conclusion

The study, thus concluded that digital health intervention as a tool for communication on Gut microbiome among young women proposed positive changes in different knowledge areas the group with the intervention. An increase in knowledge was found in almost all the fields like general information on the Gut microbiome, the role of the gut microbiome in health, the role of fermented foods in gut health, gut microbiome-related concepts, antibiotics, and gut health, Prebiotics and gut health, life-style and gut health. Without providing knowledge on the Gut microbiome, the knowledge level of the young adults remained similar except for some areas of knowledge on the Gut micro biome. Nutrition education brings positive change in the consumption pattern among young adults. Prebiotic and dietary fibre consumption was lesser among young adults before the intervention. Post intervention increase their prebiotic and dietary fibre consumption. The study participants increase their number of servings of fruits and vegetables in their regular diet and also the millets consumption was increased. In the beginning, Plant extracts are not widely consumed by young adults. After the intervention for a period of one month, found a gradual increase in plant extracts consumption. This showed the importance and need for education to be imparted to young adults.

Future Recommendations:

- Characterization of key members of the healthy gut community and interpretation of the large metagenomic datasets.
- Future study using fecal sample analysis for more accurate results.
- Future studies aim to identify the taxonomic diversity of the microbiota using the different Next generation sequencing -based methods used for metagenomic studies.

Bibliography

BIBLIOGRAPHY

Adak, A., & Khan, M. R. (2019). An insight into gut microbiota and its functionalities. *Cellular and molecular life sciences : CMLS*, *76*(3), 473–493. https://doi.org/10.1007/s00018-018-2943-4.

Akbari E, Asemi Z, Daneshvar Kakhaki R, Bahmani F, Kouchaki E, Tamtaji OR et al (2016) Efect of probiotic supplementation on cognitive function and metabolic status in Alzheimer's disease: a randomized, double-blind and controlled trial. Front Aging Neurosci 8:256. https://doi.org/10.3389/fnagi.2016.00256.

Al Khodor, S., & Shatat, I. F. (2017). Gut microbiome and kidney disease: a bidirectional relationship. *Pediatric nephrology (Berlin, Germany)*, *32*(6), 921–931. https://doi.org/10.1007/s00467-016-3392-7.

Alissa, E. M., & Ferns, G. A. (2017). Dietary fruits and vegetables and cardiovascular diseases risk. *Critical reviews in food science and nutrition*, *57*(9), 1950–1962. https://doi.org/10.1080/10408398.2015.1040487.

Andreas NJ, Kampmann B, Mehring Le-Doare K (2015) Human breast milk: a review on its composition and bioactivity. Early Hum Dev 91:629–635.

Arboleya, S., Bottacini, F., O'Connell-Motherway, M., Ryan, C. A., Ross, R. P., van Sinderen, D., & Stanton, C. (2018). Gene-trait matching across the Bifidobacterium longum pan-genome reveals considerable diversity in carbohydrate catabolism among human infant strains. *BMC genomics*, *19*(1), 33. https://doi.org/10.1186/s12864-017-4388-9.

Askarova, S., Umbayev, B., Masoud, A. R., Kaiyrlykyzy, A., Safarova, Y., Tsoy, A., Olzhayev, F., & Kushugulova, A. (2020). The Links Between the Gut Microbiome, Aging, Modern Lifestyle and Alzheimer's Disease. *Frontiers in cellular and infection microbiology*, *10*, 104. https://doi.org/10.3389/fcimb.2020.00104.

Bäckhed, F.; Roswall, J.; Peng, Y.; Feng, Q.; Jia, H.; Kovatcheva-Datchary, P.; Li, Y.; Xia, Y.; Xie, H.; Zhong, H.; et al. Dynamics and stabilisation of the human gut microbiome during the first year of life. Cell Host Microbe 2015.

Bagdasarian N, Rao K, Malani PN (2015) Diagnosis and treatment of Clostridium difcile in adults: a systematic review. JAMA 313(4):398–408. https://doi.org/10.1001/jama.2014.17103.

Baldwin, J., Collins, B., Wolf, P. G., Martinez, K., Shen, W., Chuang, C. C., Zhong, W., Cooney, P., Cockrell, C., Chang, E., Gaskins, H. R., & McIntosh, M. K. (2016). Table grape consumption reduces adiposity and markers of hepatic lipogenesis and alters gut microbiota in butter fat-fed mice. *The Journal of nutritional biochemistry*, *27*, 123–135. https://doi.org/10.1016/j.jnutbio.2015.08.027.

Barko, P. C., McMichael, M. A., Swanson, K. S., & Williams, D. A. (2018). The

Gastrointestinal Microbiome: A Review. *Journal of veterinary internal medicine*, *32*(1), 9–25. https://doi.org/10.1111/jvim.14875.

Bindels LB, Delzenne NM, Cani PD, Walter J. Towards a more comprehensive concept for prebiotics. Nat Rev Gastroenterol Hepatol 2015; 12(5):303-10; PMID:25824997; http:// dx.doi.org/10.1038/nrgastro.2015.47.

Bunesova V, Lacroix C, Schwab C. Fucosyllactose and L-fucose utilization of infant Bifidobacterium longum and Bifidobacterium kashiwanohense. *BMC Microbiol*. 2016;16(1):248. Published 2016 Oct 26. doi:10.1186/s12866-016-0867-4.

Bunesova, V., Lacroix, C., & Schwab, C. (2016). Fucosyllactose and L-fucose utilization of infant Bifidobacterium longum and Bifidobacterium kashiwanohense. BMC Microbiology, 16(1), 248. https://doi.org/10.1186/s12866-016-0867-4.

Bunesova, V., Lacroix, C., & Schwab, C. (2018). Mucin cross-feeding of infant Bifidobacteria and Eubacterium hallii. Microbial Ecology, 75(1), 228–238. https://doi. org/10.1007/s00248-017-1037-4.

Byndloss MX, Olsan EE, Rivera-Chávez F, et al. Microbiota-activated PPAR-γ signaling inhibits dysbiotic Enterobacteriaceae expansion. Science 2017;357:570-5. doi:10.1126/science. aam9949.

Charbonneau MR, Blanton LV, DiGiulio DB, Relman DA, Lebrilla CB, Mills DA, Gordon JI (2016) A microbial perspective of human developmental biology.

Clarke, S. F., Murphy, E. F., O'Sullivan, O., Lucey, A. J., Humphreys, M., Hogan, A., Hayes, P., O'Reilly, M., Jeffery, I. B., Wood-Martin, R., Kerins, D. M., Quigley, E., Ross, R. P., O'Toole, P. W., Molloy, M. G., Falvey, E., Shanahan, F., & Cotter, P. D. (2014). Exercise and associated dietary extremes impact on gut microbial diversity. *Gut*, *63*(12), 1913–1920. https://doi.org/10.1136/gutjnl-2013-306541.

Conlon, M. A., & Bird, A. R. (2014). The impact of diet and lifestyle on gut microbiota and human health. *Nutrients*, *7*(1), 17–44. https://doi.org/10.3390/nu7010017.

Cresci, G. A., & Bawden, E. (2015). Gut Microbiome: What We Do and Don't Know. *Nutrition in clinical practice: official publication of the American Society for Parenteral and Enteral Nutrition*, *30*(6), 734–746. https://doi.org/10.1177/0884533615609899.

Cronin, P., Joyce, S. A., O'Toole, P. W., & O'Connor, E. M. (2021). Dietary Fibre Modulates the Gut Microbiota. *Nutrients*, *13*(5), 1655. https://doi.org/10.3390/nu13051655.

Deehan, E. C., & Walter, J. (2016). The Fibre Gap and the Disappearing Gut Microbiome: Implications for Human Nutrition. *Trends in endocrinology and metabolism: TEM*, *27*(5), 239–242. https://doi.org/10.1016/j.tem.2016.03.001.

Deehan, E. C., Duar, R. M., Armet, A. M., Perez-Muñoz, M. E., Jin, M., & Walter, J. (2017). Modulation of the Gastrointestinal Microbiome with Nondigestible Fermentable Carbohydrates To Improve Human Health. *Microbiology spectrum*, *5*(5), 10.1128/microbiolspec.BAD-0019-2017. https://doi.org/10.1128/microbiolspec.BAD-0019-2017.

Dimidi, E., Cox, S. R., Rossi, M., & Whelan, K. (2019). Fermented Foods: Definitions and Characteristics, Impact on the Gut Microbiota and Effects on Gastrointestinal Health and Disease. *Nutrients*, *11*(8), 1806. https://doi.org/10.3390/nu11081806.

Dowd, A. J., Jackson, C., Tang, K., Nielsen, D., Clarkin, D. H., & Culos-Reed, S. N. (2018). MyHealthyGut: development of a theory-based self-regulatory app to effectively manage celiac disease. *mHealth*, *4*, 19. https://doi.org/10.21037/mhealth.2018.05.05.

Edwards, S. M., Cunningham, S. A., Dunlop, A. L., & Corwin, E. J. (2017). The Maternal Gut Microbiome During Pregnancy. *MCN. The American journal of maternal child nursing*, *42*(6), 310–317. https://doi.org/10.1097/NMC.0000000000000372.

Enam, F., & Mansell, T. J. (2019). Prebiotics: tools to manipulate the gut microbiome and metabolome. *Journal of industrial microbiology & biotechnology*, *46*(9-10), 1445–1459. https://doi.org/10.1007/s10295-019-02203-4.

Ercolini, D., & Fogliano, V. (2018). Food Design To Feed the Human Gut Microbiota. *Journal of agricultural and food chemistry*, *66*(15), 3754–3758. https://doi.org/10.1021/acs.jafc.8b00456.

Fardet, Anthony. (2017). Chapter 16: New concepts and paradigms for the protective effects of plant-based food components in relation to food complexity. 10.1016/B978-0-12-803968-7.00016-2.

Ferreira-Lazarte, A., Gallego-Lobillo, P., Moreno, F. J., Villamiel, M., & Hernandez-Hernandez, O. (2019). In Vitro Digestibility of Galactooligosaccharides: Effect of the Structural Features on Their Intestinal Degradation. *Journal of agricultural and food chemistry*, *67*(16), 4662–4670. https://doi.org/10.1021/acs.jafc.9b00417.

Ferreira-Lazarte, A., Gallego-Lobillo, P., Moreno, F. J., Villamiel, M., & Hernandez Hernandez, O. (2019). In vitro digestibility of galactooligosaccharides: Effect of the structural features on their intestinal degradation. Journal of Agricultural and Food Chemistry, 67(16), 4662–4670. https://doi.org/10.1021/acs.jafc.9b00417.

Gibson, G. R., Probert, H. M., Loo, J. V., Rastall, R. A., & Roberfroid, M. B. (2004). Dietary modulation of the human colonic microbiota: updating the concept of prebiotics. *Nutrition research reviews*, *17*(2), 259–275. https://doi.org/10.1079/NRR200479. .

Gómez, B., Gullón, B., Yáñez, R., Schols, H., & Alonso, J. L. (2016). Prebiotic potential of pectins and pectic oligosaccharides derived from lemon peel wastes and sugar beet pulp: A comparative evaluation. Journal of Functional Foods, 20, 108–121. https://doi.org/10.1016/j.jff.2015.10.029.

Holscher H. D. (2017). Dietary fiber and prebiotics and the gastrointestinal microbiota. *Gut microbes*, *8*(2), 172–184. https://doi.org/10.1080/19490976.2017.1290756.

Kim, Moo Jung & Moon, Youyoun & Tou, Janet & Mou, Beiquan & Waterland, Nicole. (2016). Nutritional Value, Bioactive Compounds and Health Benefits of Lettuce (Lactuca sativa L.). Journal of Food Composition and Analysis. In Press. 10.1016/j.jfca.2016.03.004.

Koh, A., De Vadder, F., Kovatcheva-Datchary, P., & Bäckhed, F. (2016). From Dietary Fibre to Host Physiology: Short-Chain Fatty Acids as Key Bacterial Metabolites. *Cell*, *165*(6), 1332–1345. https://doi.org/10.1016/j.cell.2016.05.041.

Kok, C. R., Gomez Quintero, D. F., Niyirora, C., Rose, D., Li, A., & Hutkins, R. (2019). An *In Vitro* Enrichment Strategy for Formulating Synergistic Synbiotics. *Applied and environmental microbiology*, *85*(16), e01073-19. https://doi.org/10.1128/AEM.01073-19.

Kowalski, K., and Mulak, A. (2019). Brain-gut-microbiota axis in Alzheimer's disease. J. Neurogastroenterol. Motil. 25, 48–60. doi: 10.5056/jnm18087.

Kumbhare, S. V., Francis-Lyon, P. A., Kachru, D., Uday, T., Irudayanathan, C., Muthukumar, K. M., Ricchetti, R. R., Singh-Rambiritch, S., Ugalde, J., Dulai, P. S., Almonacid, D. E., & Sinha, R. (2022). Digital Therapeutics Care Utilizing Genetic and Gut Microbiome Signals for the Management of Functional Gastrointestinal Disorders: Results From a Preliminary Retrospective Study. *Frontiers in microbiology*, *13*, 826916. https://doi.org/10.3389/fmicb.2022.826916.

Lagier JC, Khelaifa S, Alou MT, Ndongo S, Dione N, Hugon P et al (2016) Culture of previously uncultured members of the human gut microbiota by culturomics. Nat Microbiol 1:16203. https://doi.org/10.1038/nmicrobiol.2016.203.

Liu R. H. (2004). Potential synergy of phytochemicals in cancer prevention: mechanism of action. *The Journal of nutrition*, *134*(12 Suppl), 3479S–3485S. https://doi.org/10.1093/jn/134.12.3479S.
Long SL, Gahan CGM, Joyce SA. Interactions between gut bacteria and bile in health and disease. Mol Aspects Med 2017;56:54-65. doi:10.1016/ j.mam.2017.06.002.

Lovegrove, A., Edwards, C. H., De Noni, I., Patel, H., El, S. N., Grassby, T., Zielke, C., Ulmius, M., Nilsson, L., Butterworth, P. J., Ellis, P. R., & Shewry, P. R. (2017). Role of polysaccharides in food, digestion, and health. *Critical reviews in food science and nutrition*, *57*(2), 237–253. https://doi.org/10.1080/10408398.2014.939263.
Lupton, D. (2017). Digital Health: Critical and Cross-Disciplinary Perspectives.

Majid, A., & Priyadarshini C G, P. (2020). Millet derived bioactive peptides: A review on their functional properties and health benefits. *Critical reviews in food science and nutrition*, *60*(19), 3342–3351. https://doi.org/10.1080/10408398.2019.1686342.

Makki, K., Deehan, E. C., Walter, J., & Bäckhed, F. (2018). The Impact of Dietary Fibre on Gut Microbiota in Host Health and Disease. *Cell host & microbe*, *23*(6), 705–715. https://doi.org/10.1016/j.chom.2018.05.012.

Markowiak, P., & Śliżewska, K. (2017). Effects of Probiotics, Prebiotics, and Synbiotics on Human Health. *Nutrients*, *9*(9), 1021. https://doi.org/10.3390/nu9091021.

Meskó B, Drobni Z, Bényei É, Gergely B, Győrffy Z. Digital health is a cultural transformation of traditional healthcare. *Mhealth*. 2017;3:38. Published 2017 Sep 14. doi:10.21037/mhealth.2017.08.07.

Mills, S., Stanton, C., Lane, J. A., Smith, G. J., & Ross, R. P. (2019). Precision Nutrition and the Microbiome, Part I: Current State of the Science. *Nutrients*, *11*(4), 923. https://doi.org/10.3390/nu11040923.

Mohajeri, M. H., Brummer, R., Rastall, R. A., Weersma, R. K., Harmsen, H., Faas, M., & Eggersdorfer, M. (2018). The role of the microbiome for human health: from basic science to clinical applications. *European journal of nutrition*, *57*(Suppl 1), 1–14. https://doi.org/10.1007/s00394-018-1703-4.

Morrison, D. J., & Preston, T. (2016). Formation of short chain fatty acids by the gut microbiota and their impact on human metabolism. *Gut microbes*, *7*(3), 189–200. https://doi.org/10.1080/19490976.2015.1134082.

Ndeh, D., Rogowski, A., Cartmell, A., Luis, A. S., Baslé, A., Gray, J., Venditto, I., Briggs, J., Zhang, X., Labourel, A., Terrapon, N., Buffetto, F., Nepogodiev, S., Xiao, Y., Field, R. A., Zhu, Y., O'Neill, M. A., Urbanowicz, B. R., York, W. S., Davies, G. J., … Gilbert, H. J. (2017). Corrigendum: Complex pectin metabolism by gut bacteria reveals novel catalytic functions. *Nature*, *548*(7669), 612. https://doi.org/10.1038/nature23659.

Oak SJ, Jha R (2018) The efects of probiotics in lactose intolerance: a systematic review. Crit Rev Food Sci Nutr. https://doi. org/10.1080/10408398.2018.1425977.

Oliphant, K., & Allen-Vercoe, E. (2019). Macronutrient metabolism by the human gut microbiome: major fermentation by-products and their impact on host health. *Microbiome*, *7*(1), 91. https://doi.org/10.1186/s40168-019-0704-8.

Pluta, R., Ułamek-Kozioł, M., Januszewski, S., & Czuczwar, S. J. (2020). Gut microbiota and pro/prebiotics in Alzheimer's disease. *Aging*, *12*(6), 5539–5550. https://doi.org/10.18632/aging.102930Pluta, R., Ułamek-Kozioł, M., Januszewski, S., & Czuczwar, S. J. (2020). Gut microbiota and pro/prebiotics in Alzheimer's disease. *Aging*, *12*(6), 5539–5550. https://doi.org/10.18632/aging.102930.

Rooks MG, Garrett WS (2016) Gut microbiota, metabolites and host immunity. Nat Rev

Immunol 16(6):341–352. https:// doi.org/10.1038/nri.2016.42.

Rossen NG, MacDonald JK, de Vries EM, D'Haens GR, de Vos WM, Zoetendal EG et al (2015) Fecal microbiota transplantation as novel therapy in gastroenterology: a systematic review. World J Gastroenterol 21(17):5359–5371. https://doi.org/10.3748/wjg. v21.i17.5359.

Samtiya M, Aluko RE, Dhewa T, Moreno-Rojas JM. Potential Health Benefits of Plant Food-Derived Bioactive Components: An Overview. *Foods*. 2021;10(4):839. Published 2021 Apr 12. doi:10.3390/foods10040839.

Santha, Agnes. (2018). Deborah Lupton: Digital Health. Critical and Cross-Disciplinary Perspectives. Acta Universitatis Sapientiae, Social Analysis. 8. 109-112. 10.2478/aussoc-2018-0007.

Sarkar A, Lehto SM, Harty S, Dinan TG, Cryan JF, Burnet PW (2016) Psychobiotics and the manipulation of bacteria–gut–brain signals. Trends Neurosci 39(11):763–781.

Saville, B. A., & Saville, S. (2018). Xylooligosaccharidesand arabinoxylanoligosaccharides and their application as prebiotics. Applied Food Biotechnology, 5(3), 121–130. https://doi.org/10.22037/afb.v%vi%i.20212.

Schwab, C., Ruscheweyh, H. J., Bunesova, V., Pham, V. T., Beerenwinkel, N., & Lacroix, C. (2017). Trophic interactions of infant Bifidobacteria and Eubacterium hallii during Lfucose and fucosyllactose degradation. Frontiers in Microbiology, 8, 95. https://doi. org/10.3389/fmicb.2017.00095.

Schwiertz, A. (2016). Microbiota of the human body. New York: Springer119–142 https:// doi.org//10.1007/978-3-319-31248-4.

Sharma, S., & Tripathi, P. (2019). Gut microbiome and type 2 diabetes: where we are and where to go?. *The Journal of nutritional biochemistry*, *63*, 101–108. https://doi.org/10.1016/j.jnutbio.2018.10.003.

Shi, N., Li, N., Duan, X., & Niu, H. (2017). Interaction between the gut microbiome and mucosal immune system. *Military Medical Research*, *4*, 14. https://doi.org/10.1186/s40779-017-0122-9.

Sidhu, M., & van der Poorten, D. (2017). The gut microbiome. *Australian family physician*, *46*(4), 206–211.

Singh, B., Singh, J. P., Kaur, A., & Singh, N. (2016). Bioactive compounds in banana and their associated health benefits - A review. *Food Chemistry*, *206*, 1–11. https://doi.org/10.1016/j.foodchem.2016.03.033.

Smith, D. L., Harris, A. D., Johnson, J. A., Silbergeld, E. K., & Morris, J. G., Jr (2002). Animal antibiotic use has an early but important impact on the emergence of antibiotic resistance in human commensal bacteria. *Proceedings of the National Academy of Sciences of the United States of America*, *99*(9), 6434–6439. https://doi.org/10.1073/pnas.082188899.

Stephen, A.M., Champ, M.M., Cloran, S.J., Fleith, M., van Lieshout, L., Mejborn, H., and Burley, V.J. (2017). Dietary fibre in Europe: current state of knowledge on definitions, sources, recommendations, intakes and relationships to health. Nutr. Res. Rev. 30, 149–190.

Takumi, T., Yoshihiro, K., Toshio, T., & Yasuhiro, K. (2018). 1-Kestose, the smallest fructooligosaccharide component, which efficiently stimulates Faecalibacterium prausnitzii as well as Bifidobacteria in humans. Foods, 7(9), 140. https://doi.org/10. 3390/foods7090140.

Tandon, D., Haque, M. M., Gote, M., Jain, M., Bhaduri, A., Dubey, A. K., & Mande, S. S. (2019). A prospective randomized, double-blind, placebo-controlled, dose-response relationship study to investigate efficacy of fructo-oligosaccharides (FOS) on human gut microflora. Scientific Reports, 9(1), 5473. https://doi.org/10.1038/s41598-019- 41837-3.

Umu, Ö., Rudi, K., & Diep, D. B. (2017). Modulation of the gut microbiota by prebiotic fibres and bacteriocins. *Microbial ecology in health and disease*, *28*(1), 1348886. https://doi.org/10.1080/16512235.2017.1348886.

Vayena, E., Haeusermann, T., Adjekum, A., & Blasimme, A. (2018). Digital health: meeting the ethical and policy challenges. *Swiss medical weekly*, *148*, w14571. https://doi.org/10.4414/smw.2018.14571.

Wang, Shumin & Xiao, Yue & Tian, Fengwei & Zhao, Jianxin & Zhang, Hao & Zhai, Qixiao & Chen, Wei. (2020). Rational use of prebiotics for gut microbiota alterations: Specific bacterial phylotypes and related mechanisms. Journal of Functional Foods. 66. 103838. 10.1016/j.jff.2020.103838.

Williams S, Chen L, Savignac HM, Tzortzis G, Anthony DC, Burnet PW (2016) Neonatal prebiotic (BGOS) supplementation increases the levels of synaptophysin, GluN2A-subunits and BDNF proteins in the adult rat hippocampus. Synapse 70(3):121–124. https://doi.org/10.1002/syn.21880.

Xu, D. P., Li, Y., Meng, X., Zhou, T., Zhou, Y., Zheng, J., Zhang, J. J., & Li, H. B. (2017). Natural Antioxidants in Foods and Medicinal Plants: Extraction, Assessment and Resources. *International journal of molecular sciences*, *18*(1), 96. https://doi.org/10.3390/ijms18010096

Yin, A. L., Hachuel, D., Pollak, J. P., Scherl, E. J., & Estrin, D. (2019). Digital Health Apps in the Clinical Care of Inflammatory Bowel Disease: Scoping Review. *Journal of medical Internet research*, *21*(8), e14630. https://doi.org/10.2196/14630.

Zhao, L., Zhang, F., Ding, X., Wu, G., Lam, Y. Y., Wang, X., Fu, H., Xue, X., Lu, C., Ma, J., Yu, L., Xu, C., Ren, Z., Xu, Y., Xu, S., Shen, H., Zhu, X., Shi, Y., Shen, Q., Dong, W., … Zhang, C. (2018). Gut bacteria selectively promoted by dietary fibres alleviate type 2 diabetes. *Science (New York, N.Y.)*, *359*(6380), 1151–1156. https://doi.org/10.1126/science.aao5774.

Zimmer, J., Lange, B., Frick, J. S., Sauer, H., Zimmermann, K., Schwiertz, A., Rusch, K., Klosterhalfen, S., & Enck, P. (2012). A vegan or vegetarian diet substantially alters the human colonic faecal microbiota. *European journal of clinical nutrition*, *66*(1), 53–60. https://doi.org/10.1038/ejcn.2011.141.

Web reference

Tamil Nadu Population Sex Ratio in Tamil Nadu Literacy rate data 2011-2022 (census2011.co.in)

Appendix

APPENDIX I

QUESTIONNAIRE LINK

Consumption pattern of Prebiotics and Plant extracts

https://forms.gle/9eVpvBZCQEu6Ptbr5

KAP Questionnaire

Pre-intervention KAP Questionnaire

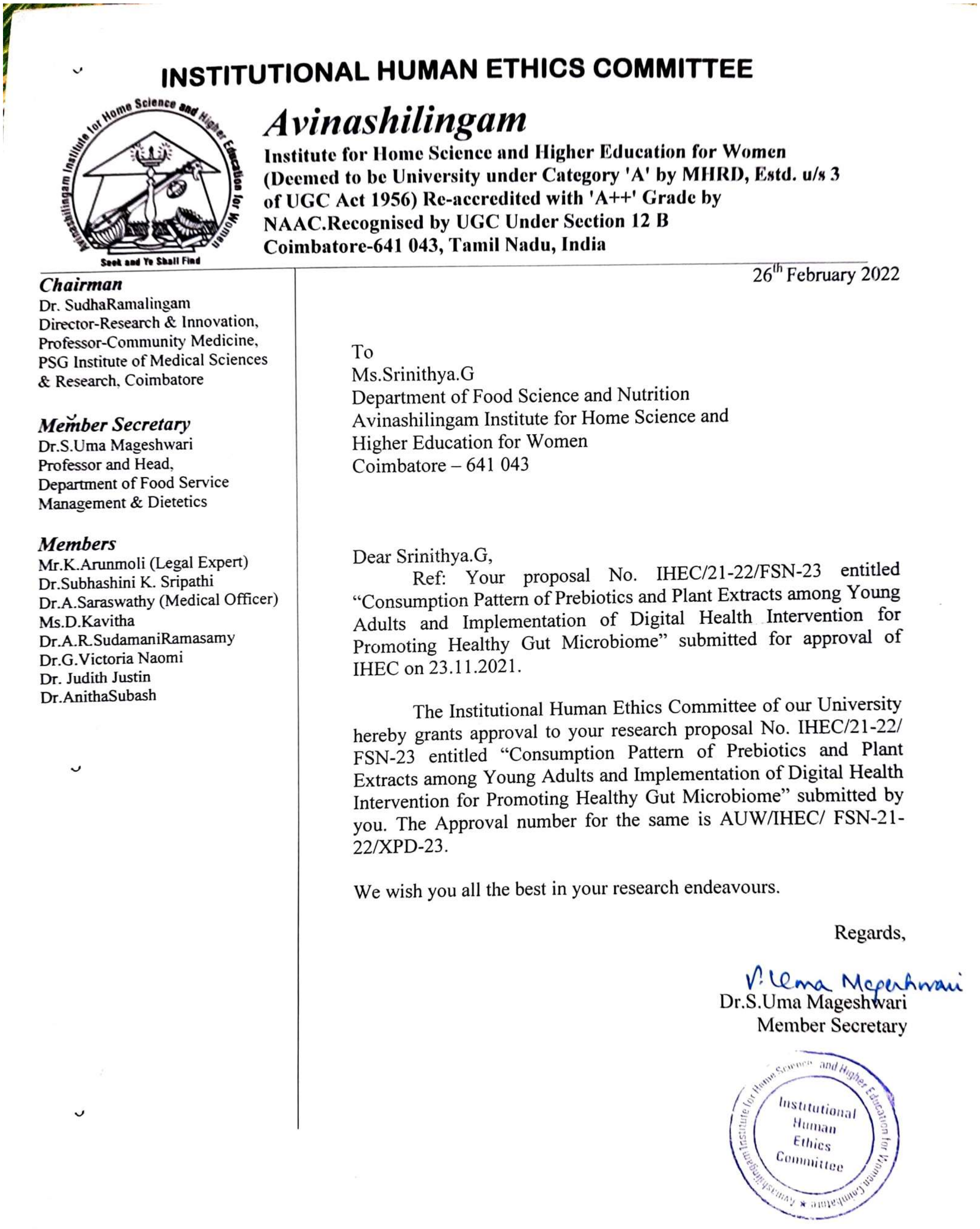
https://forms.gle/w4yy1QYB23ySwJGf8

Post-Intervention KAP Questionnaire

https://forms.gle/sXGfbYzjM7gLs8RA9

APPENDIX II

ETHICAL COMMITTEE CLEARANCE CERTIFICATE



INSTITUTIONAL HUMAN ETHICS COMMITTEE

Avinashilingam

Institute for Home Science and Higher Education for Women
(Deemed to be University under Category 'A' by MHRD, Estd. u/s 3
of UGC Act 1956) Re-accredited with 'A++' Grade by
NAAC.Recognised by UGC Under Section 12 B
Coimbatore-641 043, Tamil Nadu, India

Chairman
Dr. SudhaRamalingam
Director-Research & Innovation,
Professor-Community Medicine,
PSG Institute of Medical Sciences
& Research, Coimbatore

Member Secretary
Dr.S.Uma Mageshwari
Professor and Head,
Department of Food Service
Management & Dietetics

Members
Mr.K.Arunmoli (Legal Expert)
Dr.Subhashini K. Sripathi
Dr.A.Saraswathy (Medical Officer)
Ms.D.Kavitha
Dr.A.R.SudamaniRamasamy
Dr.G.Victoria Naomi
Dr. Judith Justin
Dr.AnithaSubash

26th February 2022

To
Ms.Srinithya.G
Department of Food Science and Nutrition
Avinashilingam Institute for Home Science and
Higher Education for Women
Coimbatore – 641 043

Dear Srinithya.G,

Ref: Your proposal No. IHEC/21-22/FSN-23 entitled "Consumption Pattern of Prebiotics and Plant Extracts among Young Adults and Implementation of Digital Health Intervention for Promoting Healthy Gut Microbiome" submitted for approval of IHEC on 23.11.2021.

The Institutional Human Ethics Committee of our University hereby grants approval to your research proposal No. IHEC/21-22/ FSN-23 entitled "Consumption Pattern of Prebiotics and Plant Extracts among Young Adults and Implementation of Digital Health Intervention for Promoting Healthy Gut Microbiome" submitted by you. The Approval number for the same is AUW/IHEC/ FSN-21-22/XPD-23.

We wish you all the best in your research endeavours.

Regards,

V. Uma Mageshwari
Dr.S.Uma Mageshwari
Member Secretary

Institutional
Human
Ethics
Committee