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A Review on Human Microbiome Project and Roles of Human Microbiome in Various Diseases

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A B S T R A C T

The human body is a dwelling place for Microorganisms this is required for the development of immunity and nutrition and this makes a huge impact on human health. If it is imbalanced it leads to various diseases such as Cancer, autoimmune Diseases Diabetes, inflammatory bowel diseases, etc. It plays a major role in maintaining the immune system. Understanding the diversity of Microbiome is necessary to lead a healthy life. And it is produced during the pregnancy in the maternal birth. The host genes that regulate the Microbiome proteins which is encoded by gene that shape the Microbiome by maintaining the availability of nutrients and the level of immune response to microbes. The prime focus of this review is to clarify the significance of the Human Microbiome Project, structure, and function of the Human Microbiome in human health. Human Microbiome plays a major role in following actions such as Microbiome treating various diseases, prebiotics and probiotics in Microbiome, advanced technologies used to develop human Microbiome, current challenges and computational methods used in Microbiome will be addressed in future.

Keywords: **Microbiome, Microbiota, dysbiosis, diseases.**

1. Main text

INTRODUCTION:

The Human Microbiome is comprised of genomes of all the microorganisms. Such as Bacteria, Fungi, Virus Protozoa. It is also known as the genetic material of microorganisms. The human microbial communities are characterized by their taxonomic, metagenomic, metabolic diversity which varies by distinct body sites and affects the human body(1). It is an important factor for the human growth development and immunity as well(2). This is accommodated inside the human body to promote human health. It clarifies the significant features of human biology and takes a part in a few activities such as, plays a vital role in human health and disease, helping in food digestion(3). The terminology "Microbiome" was constituted by Joshua Lederberg in 2001. The term was confused as a **Microbiota** and **Microbiome.** Microbiota refers to microbes present in the particular environment by types e.g. Bacteria, Fungi, virus, Achaea, protozoa. The diversity of Microbiota will differ from person to person. The interaction of the human Microbiota in the environment is dynamic. But Microbiome is the genetic material of all the microbes(4).according to the general the known difference in the Microbiome of unique human individuals have the combination of several factors such as antigen, diet, chemical, human and other animal exposures and health status(5).

The Human Microbiome Project was initiated by Antoine Van Leuwenhoek in the year 1680. By comparing his oral and fecal Microbiota he observed the significant difference between the two samples. For understanding them Microbiome there are three steps to be followed such as (1) Determination of simple microbial constituents (2) Imbalances between the Microbiome (3) identifying the configurations of microbial communities The phylogenetic approach is used for the characterization of the Microbiome to compare the microbes around the environment. To assess the difference between microbial researchers have developed lots of sequencing tools that are mentioned below: WATERS, ECOLOGY, RDP, QIIME, UNIFRAC Detection of the Microbiome is done by ELISA and PCR techniques. Advanced techniques of Microbiome and challenges will be addressed further(4).

HUMAN MICROBIOME PROJECT:

The HMP is a logical and conceptual and experimental extension of the human genome project(6). This project was initiated in the year 2008 this is sponsored by National Human Genome Research Institutes. It is an actability study with a budget of 150 million. Intend of the HMP is to study the Microbiome and analysing its role in human health. It is a study of different species of organisms that interact together A better understanding of the human Microbiome provides a high level of diagnosis and management of many diseases in humans (5).

GOAL OF HUMAN MICROBIOME PROJECT:

The primary goal of the Human Microbiome Project is to identify and characterize the Microbiome at key sites throughout the human body(7) and to demonstrate and characterize the Human Microbiome with different populations, the genetic structure of an individual organism (genotype), and disease age. The ultimate objective of HMP is to create an opportunity to improve Human Health or manipulate the Human Microbiome and HMP focus to address the questions related to Microbiome such as Do all humans have an identifiable character in Microbiome? An earlier study shows that each one equated with few microbes in their gut and skin. HMP provides a broad explanation of the Human Microbiome Project by describing the multiple sites extensively(6). And characterization of the Human **Healthy Microbiome** as a baseline for reference and comparison studies for many analysis(8).

IMPLEMENTATION OF HUMAN MICROBIOME PROJECT:

Samples are collected from healthy volunteers to characterize the normal Microbiome at different body sites. 16s rRNA gene sequencing is used to identify the Microbiome community configuration at each site. The shotgun sequencing method is also used to perform the study on the same samples e.g.: the result will be blasted against data in GenBank, KEGG to identify the gene and potential functions. Data from many individuals will be analysed to determine the key elements of Microbiome at each body site(6).

THE JUMP-START PHASE:

This phase is funded by NIH the Baylor College of Medicine the Board Institute and the Washington University school of medicine in the year 2007. For developing the protocol samples were taken from the different body sites. Such as GI tract, mouth, skin, vagina, nasal cavity from the healthy volunteers equally from male and female(6).

Three hundred volunteers were included in this study five body sites from female and four body sites from male

Sub sampling is done for both genders Females -18 body sites namely the oral cavity, skin airway, GIT region and vagina in case of male's vagina samples will not be included. Some of the unique characters are viewed by the experts to define the body sites to achieve the exact protocol for HMP(9).

Informed consent is an important process through that the potential volunteers are informed about the possible risks and benefits associated with participation. Special attention was paid to the participant's privacy and the limitation of the existing privacy Participants was informed that the study of the Microbiome data would be submitted in open access on the internet. Some of the personal information such as individual medical information and human DNA collected from them will be in a controlled database. (dognap) the database is only for the human Microbiome researchers authorized by the NIH data access committee. After the completion of 16s rRNA gene sequencing from the first eighteen volunteers, the contaminated Human DNA has been removed from the data.

Then the data have been submitted to trace all kinds of clinical information of patient disease symptoms, gender this information collected as a story it is called the phenotype. This is collected from individuals and submitted to (dbGAP). To achieve these goals, jump start Analysts have enlarged the typical set of sampling and sequencing protocol and precise the standards and quality guidelines to assure the data from various laboratories and all the authentic data are similar and authentic. One of the key significant attempts has been done by using the mock community to check the authenticity of the documentation from the various sites and standard sets to examine the Microbiome. The sequence details are documented in GenBank and the outcome of the experiment will be published else were. The first sequence from the mock community trails predetermines the complexness of the bacterial genome that exists in the mock community mixture. Currently developed tools used to abolish chimeras and artifacts. A chimera refers to two different sets of DNA. It occurs when a woman is pregnant with identical twins. One embryo dies so early. Another embryo absorbs its twin's cells. It can also occur after the bone marrow transplantation during normal pregnancy. Artifacts mean an object is a process that occurs unnaturally. The main part of these efforts was the enlargement of software such as chimera checking this program is now on hand as a free download.

SECOND STAGE:

In the second stage of HMP, the delegates will pursue the work initiated in the jump-start stage to create the database to develop recent technologies and enlarge the trail with the set of demonstration projects to specify the changes in the Microbiome corresponded to a specific disease.

HMP SEQUENCING CENTERS:

For the further development of the Human Microbiome Project, there are four centres take a part in the jump-start phase

For developing sequence for the next generation methods more than 400 bacterial genomes are added to the sequence database to complete the goal. This centre also takes responsibility for a few activities such as sequencing the Virus genome eukaryotes present in the Human Microbiome. Carry out the 16SrRNA gene and whole-genome short gun sequencing for describing the Microbiome of the contributors. For whom specimen is taken in the stage of JUMPSTART- PHASE. The gathered data will be used to analyse a few areas such as Determine the variation in the Microbiome define the fundamental elements of the Microbiome at each site, and maintenance of gene activity around the site.

DEMONSTRATION OF THE PROJECT:

The goal of the demonstration of HMP is to trace the most significant questions of the Human Microbiome Project; either the variation in the Microbiome can be associated with health or disease. The primary intention of the project is to optimize the correlation between Microbiome variations in health and disease. The pilot phase of HMP was initiated by fifteen investigators had the opportunity to demonstrate the possibility of the research. Additionally, fifteen pilot projects help to analyse the variation between the microbes associated with different health conditions in the Microbiome samples. Numerous studies state that a complementary molecular perspective will be used to measure the microbial gene expression and host genotypes.

Computational tools play a pivotal role in analysing the variation in the Microbiome and health conditions. By using the mock community some of the examples are described above.

EXAMPLES OF HUMAN MICROBIOME PROJECT:

Providing a suitable example for the demonstration of HMP makes the researchers get in-depth knowledge in Microbiome this provides accuracy in the human trail. Three example trails can be explained further such as cutaneous Microbiome (skin), gut Microbiome Vagina.

CUTANEOUS MICROBIOME (SKIN):

Analysis of cutaneous Microbiome in Psoriasis the term psoriasis refers to skin Disease. Since it is a chronic disease that cannot be healed or prevented by vaccines it occurs in the skin like a red patch. The cause of the Disease is not appropriate yet the main aim of the research is to analyse how the variation in the typical coetaneous microbiome may take a part in Disease.

THE GUT MICROBIOME:

The Gut Microbiome is an integral part of obesity or weight gain. This project is to promptly focus to specify the cause of obesity by analysing the Thrifty Microbiome hypothesis. This plays a pivotal role in human energy homeostasis. The preceding analysis states that variation in the gut microbiome can be identified in lean and fat adults. This research will carry out the functional genomics assessment of gut Microbiome in contributors whose genetic phenotypic trail has been documented.

VAGINA OR BACTERIAL VAGINOSIS:

Bacterial Vaginosis is a common bacterial infection in women when it is imbalanced. This study will observe the frequent changes over the two menstrual cycles. Totally 200 volunteers are short out for the trail with the event of bacterial vaginosis. To better understand the syndrome and found the patent which is a forecast of bacterial vaginosis. For prediction and creation of next-generation sequence, technology can be developed by using computer tools such as 16rRNA genes, Metagenome meta transcriptome sequencing to address the diversity of microbial species.

DATA ANALYSIS:

Data analysis is an essential process to predict the results and conclusions of the microbial community. It also helps to coordinate the development of data and placing the appropriate data on the respective websites. HMP data consist of a catalogue of reference strains and the short project catalogue consist of several types of information about each reference strains namely sequencing status, body site isolation.

TECHNOLOGY DEVELOPMENT IN HMP:

For generating a reference set of the entire genome sequence is a primary step for HMP. Since such particulars are necessary to elucidate the Metagenomic sequence data to sequence a single microbial genome. It is essential to develop cultures of microorganisms. Even though a variety of the Microbiome cannot be grown in the culture at present, Hence HMP is also assisting in the enlargement of advanced technologies. That will permit the segregation of many of the purified microbial verities so that genomes can be sequenced. The above-described methodologies and approaches for the optimization of culturing methods to culture the earlier uncultivated Bacterial species to isolate amplified or unamplified DNA of the whole genome from single cells at high loyalty and coverage. The individual project explores e.g. to collect the Microbiome from the individual sites. In the gut would not be sampled frequently. Optimize each sample by flow shorting from the reduced complexness of the sample. To regenerate in vitro growth conditions that reflect the micro toxic nature in the gut that have not been applied previously in the cultivation of Human Microbes to catch the huge genomic DNA fragments by selecting a small amount of exact sample within that and technology development also helps to generate the devices to find the huge number of individual microbes and amplify the sequence which is accepted by several criteria as being inappropriate(6).

COMPUTER TOOLS USED FOR THE ANALYSIS OF MICROBIOME:

The extreme reduction of cost occurs in sequencing that was accomplished in recent years. That created an opportunity for the researchers to discover the particular microbial taxa which are present inside the human gut that is a big challenge to the culture. At present, researchers can able to create plenty of sequences for each sample to estimate the variation between the microbial communities in the med set of body sites and individuals. This developed potential is mandatory for the establishment of uniformly powerful computer tools to manage the exponential amount of sequence data generated by the advanced technologies. These are the variety of analysing tools are available for scrutinizing the survey that will be described as a flow chart in the future. Identifying the variation among the samples is important, for comparing the outcome throughout the evaluation.

Molecular methods coordinate together with phylogenetic tree constriction to understand the evolutionary relationship of organisms this assists the researchers to correlate the microbes with each other around nature. UniFrac distinguishing the variation between the microbial communities it measures the portion of equated branch distance on the phylogenetic tree between the specimens. Most identical communities lead in UniFrac total will be nearly -0 at the same time entirely autonomic communities never equate any branch distance they possess various evolutionary records. UniFrac score correlates the evaluation and then view UniFrac length between the samples in two or three-dimensional area this permits the isolation of unique communities can be comfortably comparable by the view. UniFrac as a part of beta diversity incorporated to PcoA has the potential to compare the variation between communities exploiting as compact as ten sequences for each sample. It is mandatory to acknowledge that developed sequencing profound is not always necessary to recapture the biologically significant outcomes when the reports are evident.

Selecting the diversity steps that are applicable for study design Investigators exploiting the advanced sequencing methods are enable to portrait the variation and the samples at nearly low sequence coverage. This allows investigators to appraise space-related and no permanent patterns by configuration around 1000 specimens as well as time series and various designs. Numerous diversity steps covering UniFrac are assessable in QIIME and that can be correlated.

..The first major tool used in HMP is 16srRNA gene sequencing and more advanced approaches like metagenomics have been applied to TB and more importantly to lung diseases(10). For the complete analysis 16SrRNA and shotgun metagenomic record segregate working methods some primary steps including eliminating barcodes and regenerating collected samples. Precise purification is necessary for both pipelines. Two primary targets of 16srRNA gene yielded that the human faecal microbiome of 242 healthy adults and the other one is 18 different body sites were sampled 16SrRNA data record must be merged into Operational Taxonomic Units, chimerical sequence produced by inappropriate template addition must be removed and constriction of the phylogenetic tree is essential. Conversely, in the sequence of the Metagenomic pipeline must be allocated to further operations as well as taxonomy, once taxon or gene operation table charts are made, the pipeline start to cover at least imaginary.

The primary concern is then, Formation of the individual sample, identification of the taxa or functions that differs between factions of specimens, clarifying either the sample bunch according to any measured clinical status. With these tools reserve identification of fundamental patterns similarities and the variation of Microbiota the major challenges going ahead are additional investigations to incorporate long-term research and to perceive the role of specific host and environmental elements in the development and maintenance of the Microbiome.

WATERS – Workflow for the Alignment, Taxonomy and Ecology of the Microbial Environment.

RDP -- Ribosomal Database project pyro sequencing tools

QIIME -- Quantitative insight into Microbial Ecology, pronounced chime.

ROLE OF MICRO BIOME IN PREGNANCY:

One of the important hormonal changes occurs during the pregnancy more significantly progesterone and estragon level raise excessively with a huge physiological effects these increased level of hormone influence the microbial composition at the same time Microbiota can also produce and secrete hormone(11).correlation between maternal and infant immunity may be one of the mechanism linkage the maternal Microbiome to offspring risk of allergic disease(12). The vaginal Microbiome plays a vital role in pregnancy in maternal and as well as neonatal health outcomes the vaginal Microbiome is a combination of one or two species of *lactobacillus* these bacteria are believed to inhibit pathogen growth through the production of antibacterial bacteriocins as well as the gene ration of metabolites such as lactic acid assist to maintain a low PH variation in the vaginal Microbiome is related with complications of pregnancy(13).

ROLE OF MICROBIOME IN VARIOUS DISEASES:

The human Microbiome evolves from birth until death(14) the main goal to incorporate this topic in this review is to define the variation of Microbiome occurring in the autoimmune system, changes occur in the Microbiome in pregnancy and childhood. During the pregnancy, Microbiome undergoes the major changes more specifically in the intestine and vagina. The microbial compositions differs between person to person and are drastically affected by diet, weight gain due to variation in the following factors such as PH, oxygen, nutrients, humidity and temperature(11). The recent research states that the Microbiome present in the woman has a huge change in the first trimester of pregnancy with that of the third trimester and the huge changes occur in the last month of pregnancy this variation can increase weight gain(15). The changes in the Microbiome are called **dysbiosis** so that, understanding the functions of the Microbiome is essential to treat various diseases such as autoimmune diseases, neurological disease, HIV&AIDS, and cardiovascular disease. The above-mentioned disease and treating methodologies will be discussed further.

AUTOIMMUNE DISEASES:

Autoimmune disease refers to the immune system mistakenly attacks the self-tissues as a pathogen but the exact pathogenesis of the autoimmune system is not yet understood clearly. Even though few of the environmental factors to be taken into consideration such as lifestyle and diet the human Microbiome plays a vital role in self-immunity and the variation in the microbial composition may lead to loss of immunity(15).

Inflammatory bowel disease (IBD)

intestinal Microbiota that regulate the mucosal homeostasis and physiology dysbiosis in the microbial community and altered immune response to intestinal bacteria interface the homeostasis and are related to the IBD(16). inflammatory bowel disease is also known as Crohn's disease with improper inflammation in the intestine as a result of natural genetic factor which can take place anywhere in the intestine. Ulcerative colitis exposes as a transmittable inflammation that comprises only the outside layer of the GIT wall-bounded in the colon and derives at the rectum. Even though it is not yet appropriate if changes in the microbial species lead to disease pathogenesis or evolved as a result of local inflammation each microbial species plays a vital role in the modulation of the immune response.

Some studies have been demonstrated that, the usage of certain antibiotic decrease the inflammation in an animal model (Murine model subfamily of murine e.g. rat and mice family) and as well as patients(17).

Another study has been carried out, the sample stool of ulcerative colitis patients and stool from the healthy volunteers denoted free of disease within one week of receiving their faecal transfer.

In the initial report, studies have been conducted with paediatric patients with Crohn's disease, and controls were added in the study where the Microbiome from the various sites by analysing the diversity of microbes using 16S sequence analysis helps to determine the microbial taxa remarkably related with the disease by analysing the biochemical characterization of the organism in ilea and rectal samples without including the stool sample. The Microbiome of inflammatory bowel disease patients had a less variation increased abundance of *fusobacterium, Gemellaceae, pasteurellaceae,* and reduced abundance of *Bacteroides, erysipelotrichaceae, bifidobacteriaceae.* The establishment of the microbial dysbiosis index helped researchers to find a strong positive correlation with the clinical disease activity and a negative correlation with the richness of species.

This analysis offering further information and the important role of Microbiota in the pathogenesis of IBD, that has not yet had appropriate till now variation in the Microbiota increase the possibility of disease, and revival of the diverse Microbiome with Fecal Microbiota Transplant (FMT) protects disease reappearance in most patients, previous efforts have been taken by the researchers to use the Fecal Microbial Transplantation for the treatment of IBD has not given proper results. Therefore it is important to characterize the Microbiome population and functions at various time points for the establishment of inflammatory bowel disease treatment(18).

Systemic Lupus Erythematosus:

It is a heterogeneous autoimmune disease due to the following factors such as hormonal factors, environmental factors. The exact pathogenesis of SLE is inappropriate; it mainly affects women when compared to men. Many researchers suggest that in another autoimmune disease intestine plays a major role in the development of SLE. Patients with SLE will have the following variations lower ***Firmicutes/ bacteroidetes*** ratio. Numerous amounts of several generations like ***eubacterium & flavonfractor*** were added significantly. At the same time, dialister and ***pseudobutyrivibrio*** were decreased in SLE patients. ***Rhodococcus, klebsiella flavonifractor*** were importantly enriched several generations of *Bacteroides* has been reported at the same time dialiser and *pseudobutyrivibri*o were reduced in SLE patients.

Immune is produced by inflammatory commensals that could be establishing the activation of the system lymphocyte and Tmg –Th 17 transdifferentiation due to this condition few variations in the physiological conditions may take place that as mentioned below: 1. Synergistetes decrease the serum level of IL-6, 2. Secretion of natural protective IgM – anti *phosphorylcholine* by stimulating the B- cells. This can be accomplished by directing the inflammation in different ways.

A decrease in the level of lactobacillus species and an increase in the level of *Lachnospiraceae* were found in the patients with SLE. In the past few days, some studies exhibit that the species of lactobacillus and *Lactoreuteri* could have the desired effect on renal function in mice infected by Lupus nephritis reduced inflammatory cytokines. It also exhibited a better enhancement of renal disease in IgG2a. According to other findings of Bankole et al by focused an increase of *proteobacteria* phyla and family of *lachnospiraceae* and decrease of *Rikeheltaceae, odoribactereceae* and *peptococcaceae* species in a sample from 21 patients(15).

Systemic sclerosis:

Systemic sclerosis is a mediated fibrotic disease that mainly affects the following parts of the body such as skin, lung, and gut. Alteration in the microbial communities may contribute to the initiation of the severity of the disease. It is well known that systemic sclerosis has a less amount of the following bacteria such as ***faecalibacterium*** and ***clostridium*** and an increase in the level of fusobactrium and *gammaproteobacteria* compared with healthy controls. Similarly with SSC have an increased level of *bifidobacterium* and lactobacillus species which are commonly decreased during the inflammation state. Mild moderate gastrointestinal symptoms patients may have a decreased level of *B.fragilis* and increased *fusobacterium*. But in the case of SSC, there are no mild symptoms. As per the researcher, Andreasson et al dysbyosis or variation in the Microbiome e.g. decreased in the level of prausnitizii and clostridiaceae similarly increased in the level of lactobacillus was found in the patients with pulmonary fibrosis, oesophageal dysfunction, and malnutrition. Another study states that the researchers used ribosomal RNA sequencing of skin biopsies taken from patients with (<6 months) diffused and limited SSC and healthy controls. They introduced that, increased level of *Rhodotorula glutinis* sequence in the patient samples. It has been supposed that *R.glutinis* might activate the immune system and in this way induce skin fibrosis(19).

Irritable bowel syndrome: irritable bowel syndrome is a common chronic gastrointestinal disorder defined by the presence of abdominal pain or discomfort and alteration in the bowel habits. It affects approximately 10 to 20% of people women is more affected when compare to men Patients believe that their symptoms occurs by consuming certain food items such as milk and milk products, wheat product, caffeine, cabbage, onion and smoked foods(20). This disease can be further classified according to the characteristic of patient stool that will be explained below in table. The exact source of the irritable bowel disease is not known yet it may happen due to multiple factors such as genetic, visceral hypersensitivity, infection, inflammation and immunity plays a main role in the development of disease the gut Microbiota have a capability to kill the bacteria or bactericidal can protect the GIT wall from the attachment of the pathogenic bacteria. At the same time variation in the Microbiota in the intestine may leads to the adherence of the pathogenic organism. Variation in the composition of the normal Microbiota or dysbyosis in the IBS patients facilitate in the increase in the ratio of ***firmicutes*** to ***bacteroidetes*** with IBS patients(18).

IBS CLASSIFICATION BASED ON THE CHARACTRISTICS OF STOOL ACCORDING TO ROME-3 CRITERIA:

IBS TYPES	CHARACTRISTICS OF STOOL
IBS with a presence of diarrhea	Loose stool greater than 25% hard stools lesser than 25%. This is more common in men.
IBS with a presence constipation	Hard stool greater than 25% loose stools lesser than 25% more common in woman.
Mixed cycling	Both hard and soft stool is greater than 25%

Role of Microbiome in cancer:

Cancer is an leading cause of death and the development of cancer is due to changes in the life style such as smoking, imbalanced diet, increased exposure to known carcinogen and some of the notable aspects like UV light exposure and melanomas(21). Inflammation is an essential factor in carcinogenesis e.g.: patients who suffered with colitis disease they also have possibility to gut cancer (10 fold increased risk) NSAIDS drugs such as aspirin have been effective for cancer prevention and as a adjuvant therapies(22). However *helicobacter pylori* and few bacteria have a direct genotoxic can change the intracellular signalling pathway that maintain the growth and proliferation of mucosa cells(23). The current preclinical trials using cell culture and several animal models and clinical trials have states that the gut Microbiota can change the activity of host response to a variety of anti-cancer. Variation in the Microbiota is not only the consequence but it makes changes in the therapy. Unfortunately, chemotherapy changes the composition of microbial communities in patients(24).

Rheumatoid Arthritis:

Rheumatoid arthritis is a systemic chronic inflammatory disease that affects 0.5 to 1.0 % of population(25) and it is also defined as a destruction of bone in multiple joints Even though the exact cause of the disease is unknown a few important factors encourages the rheumatoid arthritis such as smoking, tobacco improper diet and excessive body weight these are the possible reason for development RA in a person. Colonization of the Microbiome occurs after the birth and the entire life of the human the excessive growth of the micro-organism is prevented by specific and non-specific immunity and penetration inside the cell(26). This disease development is encouraged by high recurrence of periodontal inflammatory disorders in RA patients caused by porphyromonas gingivalis(27). The recent research states that more than hundred genetic susceptibility loci involved in rheumatoid arthritis and the immunoglobulin (IgA) anti citrullinated protein antibody detectable before onset of arthritis. The role of gut Microbiota in human rheumatoid arthritis is not fully understood the composition of the intestinal Microbiota is altered in RA patients increased abundance of *P.copri* and reduced abundance of bactericides in gut. Another research is done with a metagenomic shotgun sequencing the outcome has been observed that increased abundance of salivarius in the gut on the tooth and saliva(28).

Cardiovascular disease:

Cardiovascular disease is responsible for increased number of death in both genders(29). This is the most significant research because it encourages the mortality and morbidity(30). Variation in the gut Microbiota composition is known as microbial dysbyosis several studies states that the gut Microbiota interact with a host even though the huge variation in the microbial composition this variation of Microbiota leads into progression of several diseases such as atherosclerosis and stroke, heart failure, hypertension. The complex host Microbiome interaction affects the system and release of numerous metabolites namely trimethyl N- oxide, bile acids, short chain fatty acids. At the same time current technologies in genomics have allowed the accurate characterization and quantification of these microbes and their metabolites but still the exact mechanism of their action is inappropriate. Alteration in the Microbiome composition may also encourage the establishment and progress of cardiovascular disease with variation in the ratio of phyla of *firmicutes* to *bacteriodetes* is noted as a high-risk factor. Similarly variation between gut Micro biome metabolites such as SCFA,TMAO Normally atherosclerotic patients have higher abundance of collinseta species(31).

CONCLUSION:

Nowadays understanding the role of Microbiome is important because it plays a vital role in maintaining the human health. And the dysbiosis of the Microbiota encourage the progression of several diseases other than the laboratory procedures computational technology is one of the grasping methods for analysing the Microbiome using the different tools. Balancing the Microbiota is necessary to lead a healthy life apart from that following the diet keeps the Microbiota in appropriate level.

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