OPEN ACCESS Freely available online

Applied Microbiology: Open Access

Short Communication

The Applications of Metagenomics in Microorganisms

Bangaru Naidu Thaddi*

Department of Biotechnology, GITAM Deemed to be University, Visakhapatnam, India

DESCRIPTION

Metagenomics-controlled molecular technologies are increasingly being used to study the human microbiota. Several large-scale research are in underway with the goal of producing reference data sets such as genetic catalogues, microbiological species, and entire genetic sequences of species that move to various bodily areas. Traditional culture methods for identifying microbes, on the other hand, are severely constrained. Progress has been achieved in the study of the human intestine microbiome recognise to the use of molecular biologic technology in the field of intestinal microbiology, particularly metagenomic sequencing using next-generation sequencing technology. Metagenomics can be used to investigate the variety and dysbiosis of the intestinal microbiome, as well as its relationship to health and disease. Functional Metagenomics can also uncover functional genes, microbial pathways, antibiotic resistance genes, functional dysbiosis of the gut microbiome, and interactions and co-evolution between the microbiota and the host, although significant limits remain. The goal of this study is to highlight how metagenomics may be used to investigate the potential of increasing the human gut microbiota.

Microorganisms such as archaea, bacteria, viruses, and eukaryotes live in the human gastrointestinal system (midgut). Bacteria make up the majority of microorganisms in the gastrointestinal system, with a density of roughly 1011-1013 cells per gramme of faeces, and the colon colonises 90% of all germs. The gut microbiota is a neglected endocrine organ that protects the host from harmful microbes, modulates the immune system, and regulates metabolic processes [1,2]. Handelsman and Rodan originally defined metagenomics in 1998, and it has now become another DNA sequencing tool for researching complicated gut microbial ecosystems. Its purpose is to generate a random sequence of the complete DNA taken from the sample to list all of the genes from the community. Several next-generation sequencing techniques have been developed in recent years to make it easier to analyse huge numbers of microorganisms in a variety of settings and parts of the human body, including the gut. Both 16S rDNA sequence analysis and metagenomics were utilised to explore uncultivated gut microbial communities. The previous research has focused on the sequencing of the 16S rRNA gene, which is found in all bacteria, and provides a number of new links between the composition of the gut microbiota and disease [3].

The natural history phase, which identifies the living parts, is usually the first step in explaining and comprehending the function of a biotope. Microorganisms were originally addressed by 16S rRNA ribotyping, which offers qualitative and quantitative outlines of species composition and has been frequently employed to examine human microbial communities due to the limitations of traditional microbiology methodologies. This research revealed that the migratory bacterial file in the gastrointestinal system is restricted to a small percentage (20%) of the population and demonstrates qualitative and quantitative inter-individual variation, with some species being common to most people [4]. The human intestinal microbiome has also been researched. With roughly 160 bacterial species per individual, the average human gut microbiome has been well documented. Furthermore, on average, the individual microbiome is stable throughout time. Jeremiah and colleagues discovered that 60% of their individual microbiota and abnormalities were present in the faecal microbiota of 37 patients in the United States using low-error 16S ribosomal RNA amplicon sequencing and full-genome sequencing methods to classify the bacterial strain composition in the faecal microbiota. The species miraculously survived for five years. The human gut may have three enterotypes, characterized by the relative prevalence of certain organism groups: Privotella, Ruminococcus, and bactericidal species, according to an in-depth profile of metagenomic datasets collected from the faecal metagenomes of healthy individuals [5].

Further investigations on the functional metagenomics of the human gut microbiome have been concentrated in recent years due to quickly increasing computational technologies critical to the analysis of metagenomic data and prior surveys on marine and other environmental bacteria. Genes from a wide range of bacteria are produced in *Escherichia coli* (*E. coli*), which is a typical host for functional metagenomics. Other species, such as Streptomyces, Bacillus subtilis, and Lactococcus lactis, can also be utilised to enhance gram-positive bacterial DNA heterogeneity [6]. Interactions between gut microorganisms and

Correspondence to: Bangaru Naidu Thaddi, Department of Biotechnology, GITAM Deemed to be University, Visakhapatnam, India, E-mail: Bdrbangarunaidu@gmail.com

Received: 13-Jul-2022, Manuscript No. AMOA-22-16990; **Editor assigned:** 15-Jul-2022, Pre QC No. AMOA-22-16990 (PQ); **Reviewed:** 02-Aug-2022, QC No. AMOA-22-16990; **Revised:** 10-Aug-2022, Manuscript No. AMOA-22-16990 (R); Published: 19-Aug-2022, DOI: 10.35284/2471-9315.22.8.255

Citation: Thaddi BN (2022) The Applications of Metagenomics in Microorganisms. Appli Microbiol Open Access. 8.255.

the host can also be detected through metagenomics. The putative mechanisms of interaction between gut bacteria and the host, on the other hand, remain unknown. Intestinal microbial pathways and *E. coli* metagenomic clones have been shown to influence intestinal mucosal proliferation by activating the nuclear factor-B pathway in epithelial cells using high-throughput screening approaches. Proteins produced by Gram-positive bacteria and surface-exposed proteins in the human gut microbiota have recently been found to play a role in immune regulation using functional metagenomics [7].

Although the approach is more difficult, metagenomics based on shotgun sequencing should be more appropriate. It has already generated an unparalleled and comprehensive sequence of data, which is continually being improved and evaluated with better bioinformatics techniques, resulting in high biological significance. A few years ago, large-scale metagenomic techniques were created to study human microbes, particularly the digestive tract. These initiatives were originally established to give reference knowledge in terms of species, genes, and functions that characterise the human gut microflora and other places, among other goals.

In conclusion, metagenomics can disclose new genes and microbial pathways, as well as detect functional dysbiosis, in addition to detecting the diversity of the human gut microbiome. The use of metagenomics to elucidate the mechanisms and correlations between the human intestinal microbiota and illnesses has enormous promise. Metagenomics, on the other hand, contains flaws and can be improved. The use of metagenomic technology to the microbiota of the human gut is still in its early phases. Nevertheless, it has long been used in various environments, including as mud and the sea. As a result of the success of using metagenomic technology to explore these settings, more research into the human gut microbiome will be conducted. In addition, the human gut contains eukaryotes and viruses in addition to bacteria. Few studies of eukaryotes and viruses have been conducted using the metagenomics approach to date, therefore future investigations of the human gut microbiome using the metagenomics approach are both promising and urgently needed.

REFERENCES

1. Weinstock GM. Genomic approaches to studying the human microbiota. Nature. 2012; 489(7415):250-256.
2. Ley RE, Turnbaugh PJ, Klein S, Gordon JI. Human gut microbes associated with obesity. nature. 2006; 444(7122):1022-1023
3. Shendure J, Ji H. Next-generation DNA sequencing. Nat Biotechnol. 2008; 26(10):1135-45.
4. Blaser M, Bork P, Fraser C, Knight R, Wang J. The microbiome explored: Recent insights and future challenges. Nat Rev Microbiol. 2013;11(3):213-217.
5. Faith JJ, Guruge JL, Charbonneau M, Subramanian S, Seedorf H, Goodman AL, et al. The long-term stability of the human gut microbiota. Sci. 2013; 341(6141):1237439.
6. Handelsman J. Metagenomics: Application of genomics to uncultured microorganisms. Microbiol Mol Biol Rev. 2004; 68(4): 669-685.
7. Verberkmoes NC, Russell AL, Shah M, Godzik A, Rosenquist M, Halfvarson J, et al. Shotgun metaproteomics of the human distal gut microbiota. ISME J. 2009; 3(2):179-189.