

METAGENOMICS SEQUENCING: “ CURRENT STATUS AND THE ROAD AHEAD ”

By

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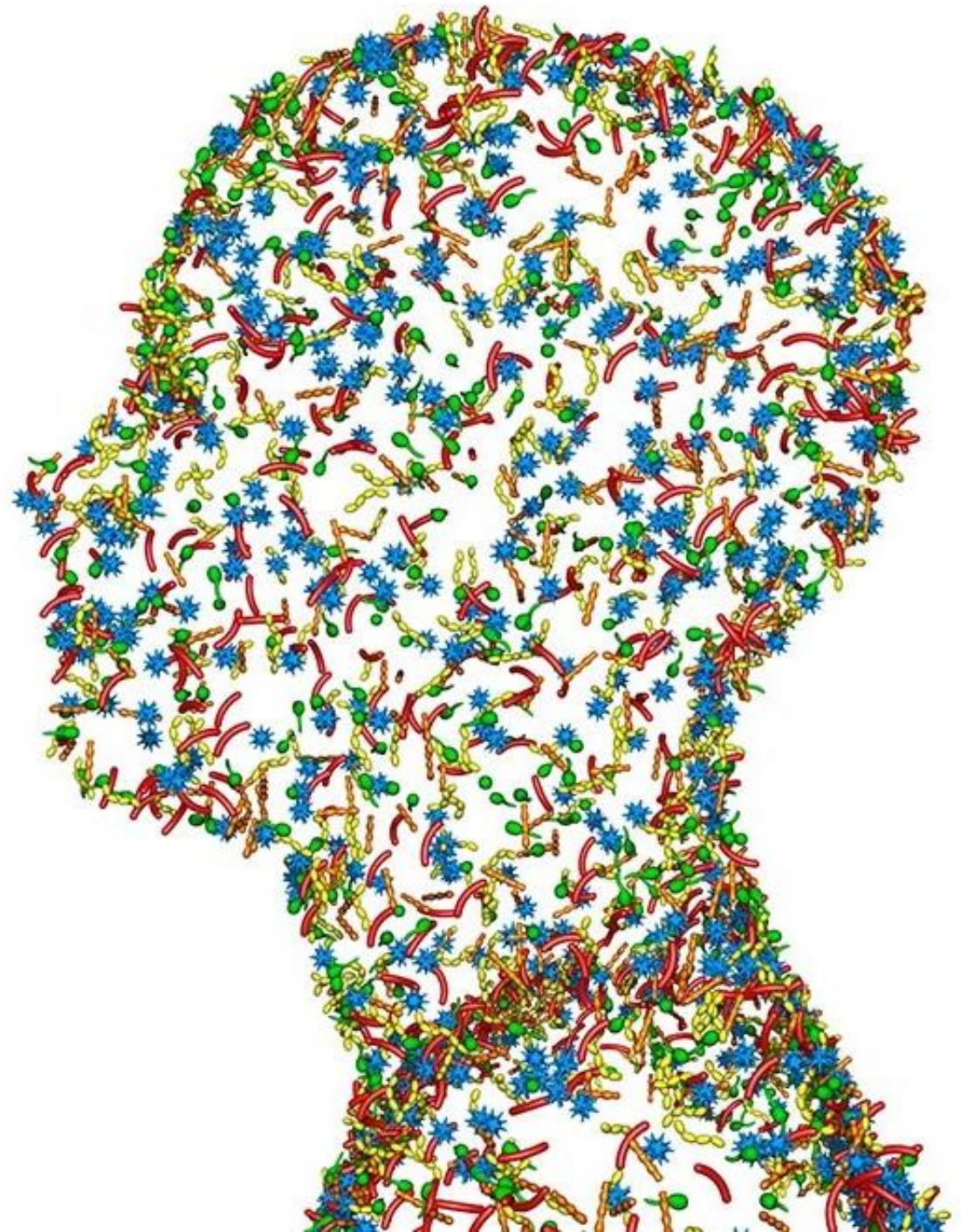
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Dissertation

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Introduction

Metagenomic sequencing is among the new approaches in genomic analysis, which involves the sequencing and analysis of genetic materials obtained from environmental samples without the prior isolation and cultivation of individual species. The method provides an unbiased detection of all microbial groups, resistance, and virulence factors, as well as host biomarkers associated with different disease states. This technique is highly efficient in analyzing unculturable, or previously unknown microbes present in rich microbiota, hence gaining acceptance and opening new avenues in the field of microbial ecology, virology, microbiology, environmental sciences, and biomedical research.

REVIEW OF LITERATURE

- (Shahbaz Raza, Jungman Kim, Michael J Sadowsky, Tatsuya Unno) The paper reviewed about the advancements in qPCR and next generation sequencing (NGS) technologies have shifted the traditional culture-based MST approaches towards culture independent technologies, where community-based MST is becoming a method of choice.
- (Ayomide Emmanuel Fadiji, Olubukola Oluranti Babalola) In this study, the authors concentrated on beneficial microbes associated with plants using endophytic microbes as a case study. This review presents the general metagenomics and computational methods used in processing plant associated metagenomes with concentration on endophytes.
- (Simon H Ye, Katherine J Siddle, Daniel J Park, Pardis C Sabeti) The authors reviewed current approaches for metagenomic analysis and evaluate the performance of 20 metagenomic classifiers using simulated and experimental datasets. They describe the key metrics used to assess performance, offer a framework for the comparison of additional classifiers, and discuss the future of metagenomic data analysis.
- (Tyler A Joseph, Itsik Pe'er) Here, the authors provide an introduction to whole-metagenome shotgun sequencing studies, a ubiquitous approach for characterizing microbial communities, by reviewing three major research areas in metagenomics: assembly, community profiling, and functional profiling.

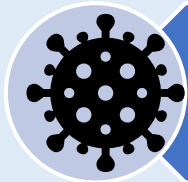
REVIEW OF LITERATURE

- (Asiya Nazir) This paper studies about Metagenomic libraries are, indeed, an essential tool for the discovery of new enzymatic activities, facilitating genetic tracking for all biotechnological applications of interest for the future. This review will explore the origins of metagenomics and examine its recent application to microbial ecology and biotechnology.
- (Alejandra Escobar-Zepeda, Arturo Vera-Ponce de Leon, Alejandro Sanchez-Flores) Here, review is about how the availability of high-throughput sequencing technologies has transformed microbiology and bioinformatics and how to tackle the inherent computational challenges that arise from the DNA sequencing revolution.
- (Jose Antonio, Garrido-Cardenas, Francisco Manzano-Agugliaro) In this article, the authors make a historical review of the metagenomics, analyze and evaluate the different massive sequencing platforms used for metagenomic assays, review the current literature on this subject and advance future problems with which researchers who decide to go deeper in this field could find. In this way, the prior knowledge of the researcher will facilitate the approach of his research.
- (Torsten Thomas, Jack Gilbert, Folker Meyer) This review summarizes the current opinions in metagenomics and provides practical guidance and advice on sample processing, sequencing technology, assembly, binning, annotation, experimental design, statistical analysis, data storage, a

OBJECTIVES



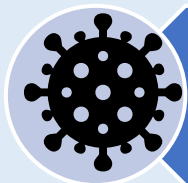
To define and describe the importance of metagenomics.



To provide detailed information regarding the primary factors influencing the metagenomic sequencing market.



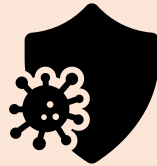
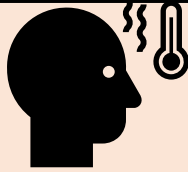
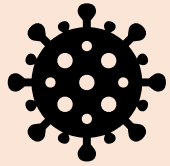
To enlist the drivers, opportunities, restraints and challenges associated with the current use as well as future usage of metagenomics sequencing.



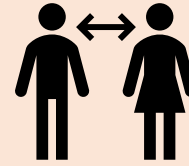
To profile key players in the metagenomic sequencing market and analyse competitively developments were undertaken by major players in the metagenomic sequencing market, which include product launches and enhancements; expansions; partnerships; collaborations and agreements.

Methodology

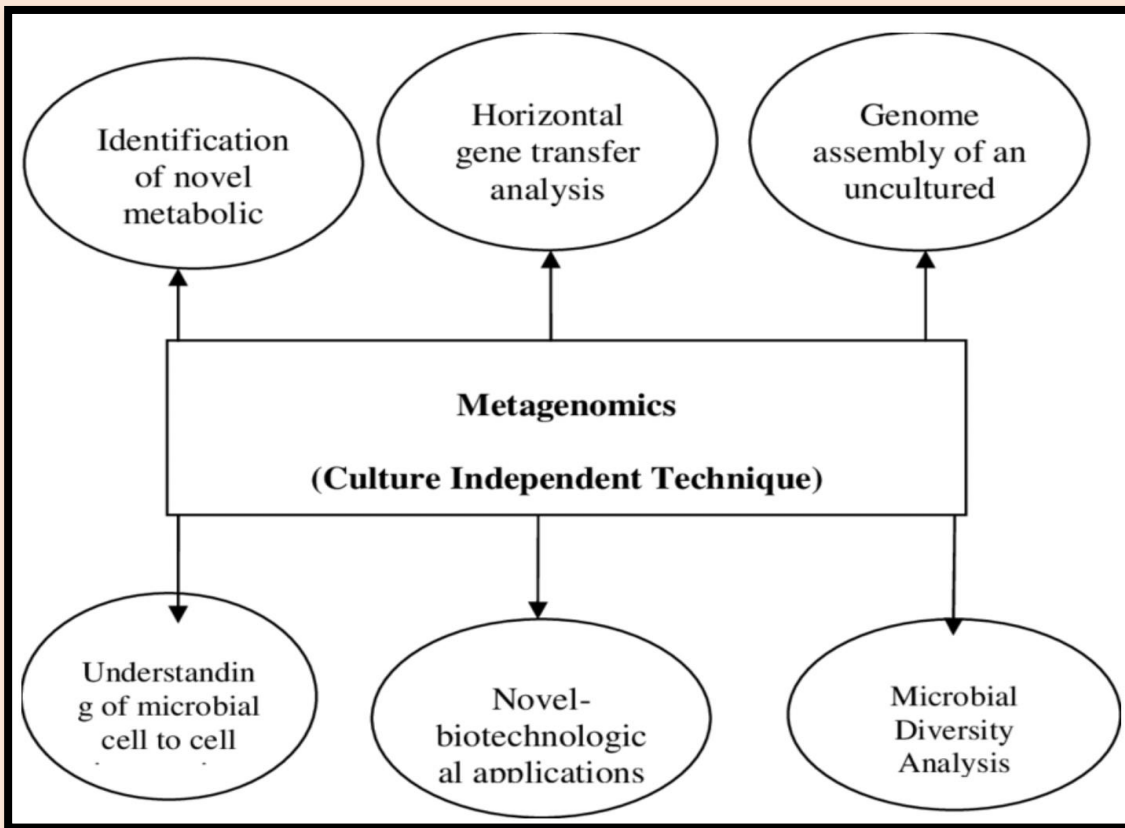
- The data was collected through extensive secondary research. The research study involved extensive secondary sources, directories, and databases such as D&B Hoovers, Bloomberg Business, and Factiva along with government databases to identify and collect information useful for this technology-based, market-oriented and commercial study of the metagenomic sequencing market. Secondary sources referred to for this research study include publications from organisations such as the World Health Organisation (WHO), Institute of Bioinformatics and applied biotechnology (IBAB), National Institutes of Health (NIH), Joint Genome Institute (JGI), National Human Genome Research Institute (NHGRI), National Center for Biotechnology Information (NCBI), Personalized Medicine Partnership for Cancer (PMPC), Association For Clinical Genomic Science (ACGS), and Department of Biotechnology (DBT).
- Study design: Descriptive cross-sectional study



DISCUSSIONS



IMPORTANCE OF METAGENOMICS



Market Segmentation

WORKFLOW	PRODUCT & SERVICE	TECHNOLOGY	APPLICATION	REGION
Sample processing & library preparation	Reagents	16S rRNA Sequencing	Drug Discovery	North America (US & Canada)
Sequencing	Instruments	Shotgun Metagenomic sequencing	Clinical Diagnostics	Europe (Germany, UK, France, & ROE)
Data Processing & Analysis	Services	Whole-genome Sequencing & De Novo assembly	Soil Microbiome applications	Asia Pacific (Japan, China, India, & ROAPAC)
	Analysis & Data	Metatranscriptomics	Industrial Applications	Latin America
			Ecological & environmental applications	Middle East & Africa
			Other Applications	

INFLUENCING FACTORS

By Product & Service Segment

Based on products & services, the market is segmented into reagents & consumables, instruments, services, and analysis & data interpretation solutions. According to various studies and papers, the reagents & consumables segment has the largest market share. Factors such as the development and commercialization of high-quality reagents and kits and the continuous requirement of sequencing reagents by end-users are expected to drive the growth of this segment in the market.

By Technology

Based on technology, the market is segmented into 16S rRNA sequencing, shotgun metagenomic sequencing, whole-genome sequencing & de novo assembly, and meta-transcriptomics. According to various studies and papers, the 16S rRNA sequencing segment has the largest market share. The high accuracy and affordability offered by 16S rRNA sequencing, advancements in bioinformatics solutions, and the growing number of metagenomic research activities to identify and classify various bacterial strains are the major factors driving the growth of the 16S rRNA sequencing market.

By Application

Based on applications, the market is segmented into drug discovery, clinical diagnostics, soil microbiome applications, industrial applications, ecological & environmental applications, veterinary applications, and other applications. According to various studies and papers, the drug discovery segment has the largest share of the market. The large share of this segment can be attributed to the increasing research activities for novel drug discovery and growing collaborations between market players, academic institutions, and pharmaceutical companies for drug development.

By Region

According to various studies and papers, North America has the largest share of the market. Factors such as the increasing applications of metagenomics in diagnostics and genomics research, the availability of research funding, and the development of NGS data analysis solutions are driving the growth of the market in North America.

Drivers, Opportunities, Restraints and Challenges

DRIVERS • Technological innovation in NGS platforms. • Initiatives and funding from government & private bodies for large-scale sequencing projects. • Declining costs of genome sequencing. • Significant applications of metagenomics in various fields.	RESTRAINTS • End-user budget constraints in developing countries.
CHALLENGES • Challenges associated with metagenomic NGS	OPPORTUNITIES • NGS Data analysis using big data.

Key players operating in the Metagenomics Market

S. No.	Key Players
1.	Illumina, Inc. (US)
2.	Thermo Fisher Scientific, Inc. (US)
3.	Qiagen N.V. (Netherlands)
4.	PerkinElmer, Inc. (US)
5.	Oxford Nanopore Technologies (UK)
6.	Pacific Biosciences (US)
7.	BGI group (China)
8.	Psomagen, Inc. (South Korea)
9.	Eurofins Scientific (Luxembourg)
10.	Zymo Research Corporation (US)

STRATEGIC OVERVIEW

The key strategies adopted by the top players in this market include product launches, expansions, partnerships, collaborations, agreements, and acquisitions.

Company Name	New Product Launches	Collaborations	Partnership
Illumina, Inc. (US)	Launched the TruSight Software Suite, a turn-key data analysis solution to accelerate and facilitate the adoption of whole-genome sequencing for the identification of genetic diseases.	Entered into a collaboration agreement with Roche to accelerate the availability of distributable NGS- based IVD tests on Illumina's diagnostic (Dx) sequencing systems.	Entered a 15- year partnership with QIAGEN to broaden the availability and use of NGS-based IVD kits, including companion diagnostics, for patient management.
Thermo Fisher Scientific, Inc. (US)	Launched ion torrent carrier seq ECS kit, an NGS- based solution for expanded carrier screening research.	Collaboration with AstraZeneca to codevelop NGS- based companion diagnostics.	Partnership with First Genetics JCS to develop NGS-based diagnostics in Russia.
Qiagen N.V. (Netherlands)	Launched QIAcube connect a next-generation automation solution for sample processing in research labs.	Collaboration with INOVIO expanded to develop NGS companion diagnostics for INOVIO'S VGZ- 3100 for advanced cervical dysplasia.	Partnership with Verogen to offer solutions for human identification, including NGS.
Oxford Nanopore Technologies (UK)	Launched PromethION 24 and PromethION48. They offers high throughput, long-read, real-time, direct nanopore sequencing data.		
Pacific Biosciences of California, Inc. (US)	Launched the sequel II system. The system includes the new SMRT Cell 8M, as well as chemistry instrument control software, and the SMRT Link software package.		

Competitive Scenario

This segment studies the growth strategies adopted by market players in the last three years. Several players in this market have adopted various strategies to expand their global presence and increase their market share. Product launches, expansions and acquisitions are a few major strategies adopted by market players to grow in the metagenomic sequencing market.

Product Launches

Month & Year	Company Name	Product Name	Product Type
April 2019	Pacific Biosciences of California, Inc. (US)	Sequel 2 system	System
June 2019	BGI Genomics (China)	BGI-Xome	Services
February 2020	Thermo fisher scientific, Inc. (US)	Ion-Torrent Carrier Seq ECS Kit	Kits
July 2020	Illumina, Inc. (US)	TruSight Software Suite	Software
October 2020	QIAGEN N.V. (Netherlands)	QIAseq Human Exome TR Insights Solution	Kits and software

Deals

Year and Month	Development Type	Company 1	Company 2
2020 June	Acquisition	Illumina, Inc. (US)	BlueBee (Netherlands)
2021 January	Collaboration	Illumina, Inc. (US)	Helix opco llc (US)
2021 January	Collaboration	Oxford Nanopore Technologies, Ltd. (UK)	NVIDIA (US)
2021 July	Strategic Alliance	QIAGEN N.V. (Netherlands)	Sysmex Corporation (Japan)
2021 September	Collaboration	Thermo Fisher Scientific, Inc. (US)	AstraZeneca (UK)

CONCLUSION

- Metagenomics is one of the fastest developing research areas. The requirement is to study the human microbiome as a whole ecosystem for a better understanding of the relation between microbiota and host health or disease. For this reason, powerful methodologies are required to globally analyse these ecosystems, with metagenomic approaches being key for further analysis of the human microbiome.
- In the future, this kind of approach i.e., metagenomics would identify biomarkers of well-being that correspond to a general and more balanced microbiota. In addition, metagenomics can also provide us with a better understanding of the relationship between us and our microbiome and the role of this interaction with health.
- Metagenomic next-generation sequencing (mNGS) for pathogen detection is becoming increasingly available as a method to identify pathogens in cases of suspected infection. mNGS analyses the nucleic acid content of patient samples with high-throughput sequencing technologies to detect and characterize microorganism DNA or RNA. This can lead to an improved ability to diagnose patients, although there remain concerns regarding contamination and detection of non-clinically significant organisms.
- The development of improved DNA isolation methods, cloning strategies, and screening techniques allowed the assessment and exploitation of microbial assemblages from extreme and inhospitable environments, such as solfataric hot springs, hypersaline basins, and ice. With the launch of next-generation sequencing techniques, more and increasingly complex environmental sequence data sets were produced, which in turn led to the development of various bioinformatics tools for the analysis and comparison of these data sets concerning taxonomic and metabolic diversity.
- In recent years, studies of the gene expression and protein production of microbial communities emerged to complement DNA-based metagenomic analyses. Meta-transcriptomics and meta-proteomics are approaches that have the potential to allow us to understand the functional dynamics of microbial communities. In combination with metagenome DNA analysis, these approaches offer significant promise to advance the measurement and prediction of the in situ microbial responses, activities, and productivity of microbial consortia. In addition, analyses of the thereby-generated comprehensive data sets have an unprecedented potential to shed light on ecosystem functions of microbial communities and evolutionary processes.



THANK YOU