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Research Article

Metagenomics: Rejuvenating Oral Medicine: Concepts Recultured- A Meta-Analysis Research

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Abstract

Background: Metagenomics is the study of genetic material which has been directly taken from environmental samples. It is also known as environmental genomics, ecogenomics or community genomics. The initial molecular work in this field was done by Norman R. Pace and colleagues, they used PCR to explore the diversity of ribosomal RNA sequences. The knowledge that was gathered from these explorative studies led Pace to propose the idea of cloning DNA directly from environmental samples in the early 1985. Metagenomics as said can be a powerful tool to view the microbial world and its hidden diversity of microscopic life. Metagenomics offers immense potential to understand the entire world of living creatures around us. Since DNA sequencing shows a fall, when compared to metagenomics, which now allows microbial ecology to be investigated at a much larger scale and detail than before.

Aim of the Study: To assess the significance of metagenomics in identification and diagnosis of oral microbiota.

Research Question: Is Metagenomics actually significant in various microbe related pathological arenas of Oral Medicine?

Materials and Methods: With the Medline database taken as a source for authenticated scientific research data, articles were selected having undergone randomized control trial. Out of these, articles (studies) were chosen which met the criterion for Meta-Analysis.

Results and Conclusion: After analysing the results, we can conclude that our study is highly significant and metagenomics plays a significant role in identification of oral microbiota.

Keywords: Metagenomics; Oral Medicine; Meta-Analysis Research

Introduction

As we all are aware of the fact that composition of the oral microbiome in both healthy and diseased individuals is complex and dynamic. In search for etiological agents of infection in dentistry traditional approaches are just not sufficient. In such a scenario, Metagenomics can be a boon for the study of complex oral microbiome.

Metagenomics, as mentioned is the study of metagenomes, genetic material recovered directly from environmental samples. It is also known as Ecogenomics, Environmental Genomics, Community Genomics. The first person who studied organisms directly from pond water and his own teeth was Anton van Leeuwenhoek. The early molecular study and work in this field was done by Norman R Pace (1985 - 1991) [1,2]. Three scientists, namely, Jo Handelsman, Robert Goodman, Jon Clardy gave the term metagenomics for the first time. Recently, Kevin Chen and Lior Pachter defined metagenomics as "the application of modern genomics technique without the need for isolation and lab cultivation of individual species".

These clones are either sequenced randomly or based on specific traits such as antibiotic production. Screening of these clones are done for phylogenetic markers like 16SrRNA or any other conserved genes using multiplex PCR (136) or by the process of hybridization [3,4].

Aim of the Study

To assess the significance of metagenomics in identification and diagnosis of oral microbiota.

Research Question

Is Metagenomics actually significant in various microbe related pathological arenas of Oral Medicine?

Materials and Methods

Various studies and researches have documented the significance of metagenomics in identification and diagnosis of oral microbiota. With this fact in mind, a literature based meta-analysis was carried out to fulfil the aim of this study. With the Cochrane and other scientifically assisted databases like Medline and Medno database taken as a source for authenticated scientific research data, 35 study articles have undergone Randomized Control Trial out of which 18 articles were finally selected based on the criterion of Meta-analysis.

Result

The statistical analysis was determined in the form of forest plot. Interpreting the graph there is odds ratio and standard deviation values for each article. The central line shows what is called as null hypothesis or median line. Towards the left of the midline depicts the standard deviation values of all studies selected for meta-analysis and towards the right side of midline depicts the p values of the studies. The over all probability value (p value) is obtained in form of diamond. Since the diamond is on the right side of median line it shows that study is significant and with p-value of 0.0001, thus suggesting that our article is highly significant with sensitivity and specificity. So, finally interpreting the result we can say that Metagenomics plays a significant role in identification and diagnosis of oral microbiota.

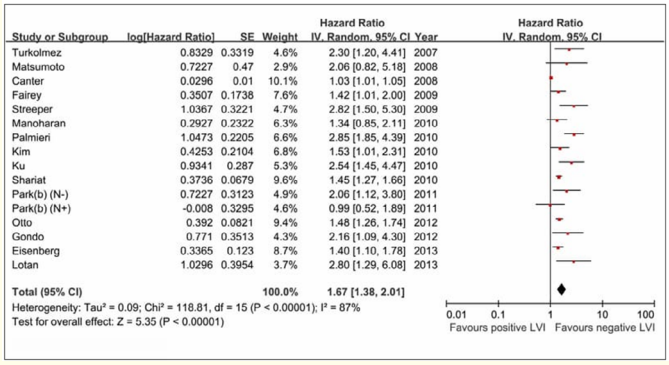


Figure 1

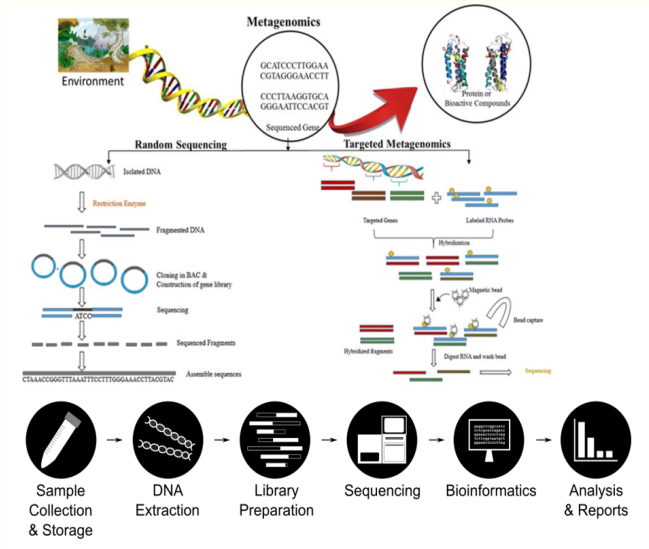
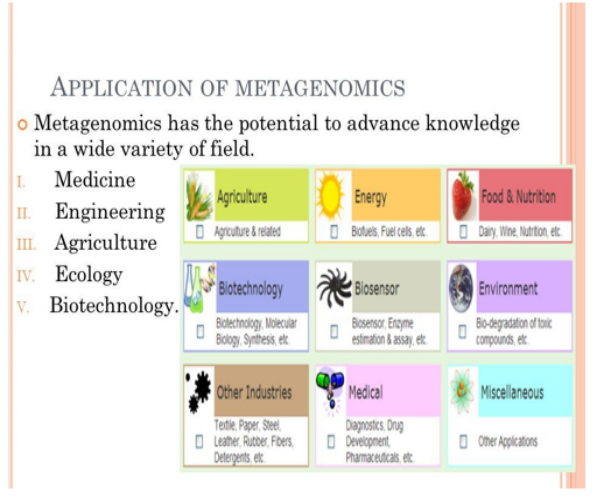


Figure 2



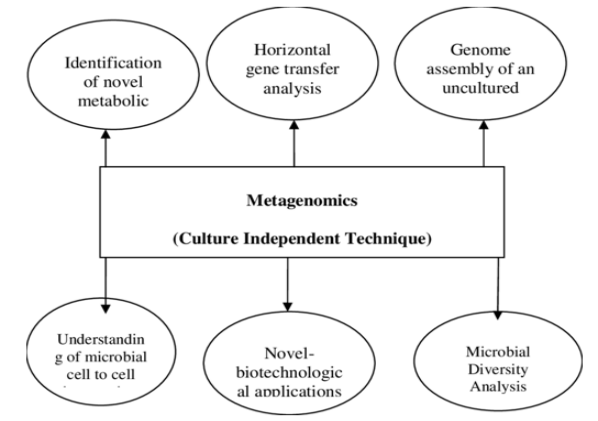


Figure 3

Discussion

Metagenomics is a new field of research which aims to explain non-cultured microbes [5]. Non-cultured microbes are nearly present in most of the environments of earth in major amounts. It is really critical to directly access the genetic content of entire communities of organisms without the help of any tool. In such cases, metagenomics is gradually proving itself as an important tool [6]. It comprises of construction and screening of metagenomics DNA libraries [6] which helps in isolating new enzymes and certain drugs of industrial importance as well. Recently metagenomes of extreme environments have also been used as sources of novel bio-catalyst [7].

Steps to metagenomics are as follows:

1. DNA fragments are extracted from the environment directly and cloned into the plasmid vector.
2. Library preparation is done, wherein a library is kept in record that comprises of environmental DNA fragments.
3. The next step is amplification of DNA fragments by the process of polymerase chain reaction (PCR).
4. A nucleotide sequence is generated (which is considerably stable) that depicts the diversity of microbes.
5. Nucleotides are then sequenced and analysed in a microbial host.
6. It is then screened for a specific function such as production of new enzyme or a drug of importance.

Application of metagenomics

1. To evaluate the outcome of age, diet and pathologic states (example- obesity, cancer) on the gut microbiome of humans living in different contrasting environmental conditions.
2. Inspection of primable DNA remains [8].
3. Studying the level of antibiotic resistance in soil microbes.
4. Analysing library profiles [9] can be done quickly with improved bioinformatics. Improving the ad bioinformatics will quicken analysis for library profiling.
5. Clinical diagnostic metagenomics brings the promise of an assumption free one-size-fits-all workflow [10]. This could be applied to any sample to detect any kind of pathogen. Knowing the fast development of tools targeted for pathogen identification, and likely future improvements and cost-effectiveness of sequencing, combined with commoditization of laboratory [11] and informatics workflows will start to compete with the plethora of methods currently in use in the diagnostic laboratory, while also delivering additional useful information (example: genomic epidemiology, antimicrobial resistance, virulence) [12,13]. Summing up, it is appropriate to say that metagenomics will play an important role in the clinical laboratory and diagnosis in the near future.

Conclusion

The way microbiologists' approach to many problems has been now totally transformed by metagenomics. Redefining the concept

of a genome [14,15] it has also accelerated the rate of gene discovery. Applications of metagenomics to biotechnology has an endless potential [16]. Gone is the time when microbiology used to rely on analysis by diverse methods, the future is now metagenomics. Microbiology has long relied on diverse methods for analysis, and metagenomics can provide the tools to balance the abundance of knowledge attained from culturing with an understanding of the uncultured majority of microbial life [17,18].

As the study has already demonstrated the association of Metagenomics and Clinical Diagnostics [19] hence, we can conclude that Metagenomics is a significant and potent tool [20] in identification and diagnosis of all microorganisms in a clinical sample including uncultivable, rare and novel pathogens [21,22]. Thus, summarizing our study it can be said that Metagenomics has potential to revolutionize Clinical Diagnostics.

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