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| Book Name: | [Microbiology and Biotechnology Research: An Overview](https://www.bookpi.org/bookstore/product/microbiology-and-biotechnology-research-an-overview-vol-1/) |
| Manuscript Number: | **Ms\_BPR\_4622** |
| Title of the Manuscript:  | **Metagenomics: a modern-day tool for exploring the diverse microbial communities of East Kolkata Wetland** |
| Type of the Article | **BOOK CHAPTER** |

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| PART 1: Comments |
|  | Reviewer’s comment**Artificial Intelligence (AI) generated or assisted review comments are strictly prohibited during peer review.** | Author’s Feedback *(Please correct the manuscript and highlight that part in the manuscript. It is mandatory that authors should write his/her feedback here)* |
| **Please write a few sentences regarding the importance of this manuscript for the scientific community. A minimum of 3-4 sentences may be required for this part.** | The interaction of society with the environment has led to the development of crisis phenomena in the biosphere, which necessitates the consistent implementation of sustainable environmental management. Only under this condition can a balance be achieved in the interaction between humans and nature, and the proper use of the natural basis for the development of productive forces be ensured.The importance of wetlands is confirmed by the fourth Strategic Plan of the Ramsar Convention for 2016-2024.Thanks to the recent development of sequencing machines capable of rapidly (and inexpensively) sequencing huge amounts of DNA, it is now practical to sequence DNA extracted from complex microbial ecosystems, similar to a soil sample. Several different approaches are used, but all depend on the first step of extracting the microbial DNA from the sample (and separating it from the much more complex DNA of any eukaryotes that may be present).The DNA encoding the small subunit (16S) ribosome of both bacteria and archaea contains some highly conserved regions; that is, regions of identical or nearly identical sequence. By using primers that target these regions, it is possible to obtain enough material by PCR to sequence the entire 16S rRNA gene.By comparing the different sequences to a database of sequences from known organisms, it is possible to estimate how many different types of microbes are present. Because of the significant genetic diversity found between ‘strains’ of the same species, closely related (>97% identity) 16S rDNA sequences are assigned to the same ‘phylotype’ because we cannot be sure whether they belong to separate species or two strains of the same species. In either case, a collection of 16S rDNA sequences can be organised to form a phylogenetic tree to show patterns of relatedness.Another way metagenomics can be used is to find new functions in a host (e.g. *E. coli*) if it can express the new gene with which it has been transformed. For example, screening a library of E. coli clones for their ability to resist an antibiotic could reveal genes involved in antibiotic resistance - a worrying development in recent years.Thus, investigations of diverse microbial communities, including ecosystems such as wetlands, are relevant for understanding the important place of microbial organisms in the nutrient cycle and their participation in the regulation and stability of biocenosis.The content of the manuscript and the results of a detailed study of wetland microbiosinosis of East Kolkata wetlands brings together the interests and background for discussion of a wide range of scientific community. |  |
| **Is the title of the article suitable?****(If not please suggest an alternative title)** | The title of the manuscript reflects the chosen focus of the study and is appropriate for this manuscript. |  |
| Is the abstract of the article comprehensive? Do you suggest the addition (or deletion) of some points in this section? Please write your suggestions here. | The abstract of the article is quite informative and briefly describes all stages of the conducted research, its results and conclusions. |  |
| **Is the manuscript scientifically, correct? Please write here.**  | The manuscript is logical and competently structured. The characteristics and importance of wetlands, their microbial diversity, and the significance and role of metagenomics in the study of microbiosynosis of the studied biotopes are described in an accessible and professional manner. An important aspect of the manuscript is the interpretation of the studies for the prospective application of metagenomics in the study of wetland microbial ecology. |  |
| **Are the references sufficient and recent? If you have suggestions of additional references, please mention them in the review form.****-** | The literature used in writing the manuscript is quite actual. |  |
| Is the language/English quality of the article suitable for scholarly communications? | The language and its quality meet the requirements of the article's design and are adapted for scientific communication. |  |
| Optional/General comments | An interesting manuscript, I liked it. It contains important facts and challenges for the environmental problems identified by the scientists-authors. |  |

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| **PART 2:**  |
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|  | **Reviewer’s comment** | **Author’s comment** *(if agreed with reviewer, correct the manuscript and highlight that part in the manuscript. It is mandatory that authors should write his/her feedback here)* |
| **Are there ethical issues in this manuscript?**  | *(If yes, Kindly please write down the ethical issues here in details)* |  |

**Reviewer details:**

**Seniuk Igor, National University of Pharmacy, Ukraine**