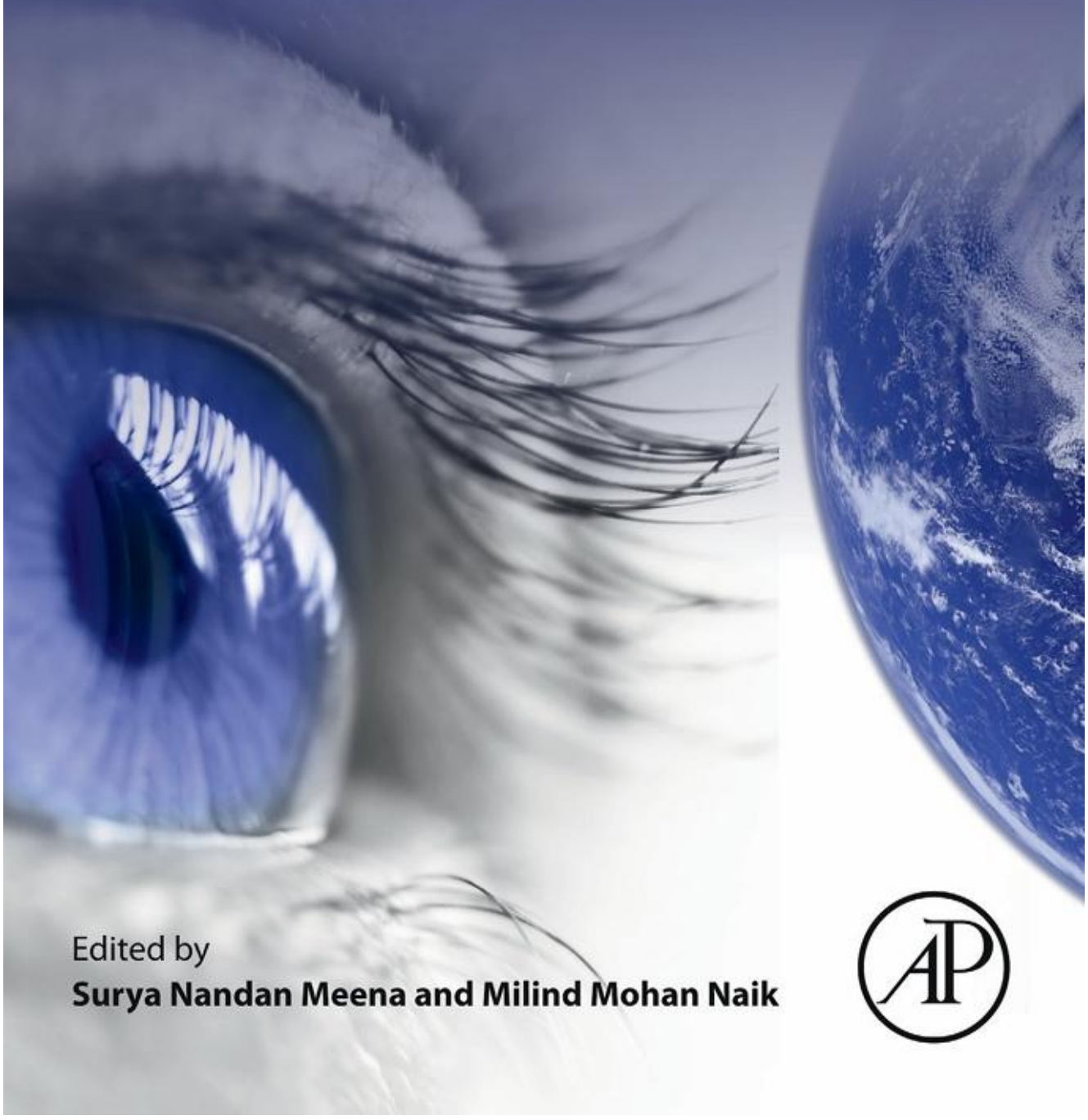
# Advances in Biological Science Research

## A Practical Approach



Edited by
**Surya Nandan Meena and Milind Mohan Naik**

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## A Practical Approach

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# Contents

Chapter 12

# Metagenomics a modern approach to reveal the secrets of unculturable microbes

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## 12.1 Introduction

The most diverse life forms that exist on planet Earth are microorganisms, but still, only 0.1%−1% have been cultivated so far, resulting in creating a great obstacle in understanding the world of microbes. This limitation nowadays has been overcome by the use of data being gathered using metagenomics and single-cell genomic techniques, which bypasses the need for cultivation of microbes in laboratory conditions [1].

The identification of bacterial and archaeal phyla using a small subunit ribosomal RNA database till date has resulted into 89 bacterial and 20 archaeal phyla, which is much less than the expected bacterial phyla of approximately 1500 [2−7]. The lack of data act as an indicator for the incapability of cultivating microorganisms, as the majority of what we have understood so far about microbial life form is based on cultivable organisms. Therefore, the phylogenic information available is being dominated mostly by the Proteobacteria, Actinobacteria, Firmicutes, and Bacteroidetes representing bacteria, with halotolerant and methanogens members of the Euryarchaeota in case of the archaea [3].

The realization of how diverse the untapped microbial community is in any particular environment came from the analysis of RNA (16S rRNA or SSU) genes sequencing directly from various environmental econiches [8]. The outcome of the study revealed that a single cultivable representative was present in less than half of the known microbial phyla [1]. Those phyla that contain exclusively uncultivable microbes are known as Candidate Phyla (CP). This CP is also referred to as microbial dark matter as these microbes account for a large portion of the Earth's biomass as well as biodiversity, but still not

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