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**METAGENOMICS: AN APPROACH WILL EXPAND MICROBIAL CAPABILITIES**

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IndiaEmail: [jitmalviya123@gmail.com](mailto:jitmalviya123@gmail.com)**ABSTRACT**

The next challenge was to elucidate the functions of these new phenotypes and determine whether they represented new species, genera, or phyla of prokaryotic life. This challenge spawned various techniques, including metagenomics, the genomic analysis of assemblages of organisms. In a few years, the study of uncultured microorganisms has expanded beyond asking “Who, What, Where, How, When?” to include the difficult question “What are they doing?” The outcomes of the recognition of uncultured microorganisms are worthy of examination. One of these outcomes, metagenomics, is further shaping microbiology. Metagenomics has already opened new avenues of research by enabling unprecedented analyses of genome heterogeneity and evolution in environmental contexts and providing access to far more microbial diversity than has been viewed in the petri dish. This review will explore the origins of metagenomics and examine its recent application to microbial ecology and biotechnology.

**Keywords: Metagenomics, Phenotypes, Genome Analysis,****INTRODUCTION**

Metagenomics is an emerging field in which the power of genomic analysis (the analysis of the entire DNA in an organism) is applied to entire communities of microbes, bypassing the need to isolate and culture individual microbial species. In Greek, “*meta*” means “transcendent” [1]. In its approach and methods, metagenomics transcends individual

genes and genomes, enabling scientists to study all of the genomes in a community as a whole. The tools of classical genomics and microbiology largely rely on isolating individual microbial species in pure cultures—that is, cultures containing only microbes of a particular species. This means that the vast majority of the microbial world has been