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Short Communication

Environmental Microbiology Genomics

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SHORT COMMUNICATION

The difficulty to culture the overwhelming majority of microorganisms, as well as the finding that laboratory produced bacteria rarely function in the wild, limit the use of natural microbial diversity in biotechnology. To realise the potential of microbial biotechnology, it is now obvious that a better understanding of the community structure, function, and evolution of bacteria in their natural habitats is essential. Microbiologists are using genomics and related high-throughput technologies on both cultured microorganisms and environmental samples to solve these new challenges [1]. Together with the biotechnology afforded by this research, this endeavour will lead to fresh perspectives on ecosystems and biological function. Although bacteria and their viruses is only a small portion of the massive interwoven web of life that makes up the global ecosystem, they account for the vast bulk of it in terms of numbers [2].

The diversity of settings in which they dwell, the tactics they adopt to survive and expand, and the substrates they modify in that service result in a plethora of forms and functions that we are only beginning to comprehend. The growth and death of microbe subpopulations in response to environmental change, as well as their invasion into new niches, can cause significant changes in the balance of a local ecosystem and interfere with human operations, with consequences ranging from oil line corrosion to increased prevalence and introduction of new pathogenic strains. Contribution to major geochemical cycles, ability to buffer environmental change through bioremediation, and the prospect of a plethora of novel activities for energy conversion, catalysis, and natural product synthesis are all positive elements of microbial populations [3].

High-throughput sequencing and developments in DNA cloning and amplification technologies, together with genomic techniques, are allowing for complete assessments of the composition and dynamics of microbial communities that are mostly un-culturable. This new science, known as'metagenomics,' offers new insights into the capacities of microbes to collaborate and compete for survival in a variety of contexts. Ecological dynamics, the creation of new kinds of biological systems, and the identification of new functionalities that could be utilised for biotechnological and therapeutic purposes are all being revealed by genomic investigations into the diversity of ambient bacteria. This science enables the unification of microbial ecology, environment, and gene function, as well as the associated experimental and bioinformatics hurdles that must be solved to achieve this goal [4,5].

The identification of constituent organisms greatly aids efforts to comprehend the biological content of environments, the nature of generated ecologies, and their significance in regional and global geochemistry. Traditional microscopic and culturing techniques have a considerably narrower ability to explore this variety than modern approaches enabled by genomic technologies [6]. According to current estimates, only about 1% of microbial species can grow in isolation under typical laboratory settings [7]. Instead, sequencing and other techniques for detecting DNA from environmental samples can provide a much more detailed picture of the creatures in a community, as well as their placement in their ecological roles. Phylogenetic marker genes, which come from the universality of specific processes such as transcription and translation, substantially contribute in the identification and classification of both well-known and unknown organisms. Although genes for RNA subunits of the ribosome, most commonly the small subunit (16S rRNA gene), can be used to identify bacterial lineages, the most commonly used phylogenetic markers are genes for RNA subunits of the ribosome. These have been used in numerous studies to determine the presence and relative abundance of taxonomic groups within environmental samples [8].

These studies sequenced rRNA genes directly, scanned rRNA genes in large-insert clones produced from environmental materials using PCR amplification, or sequenced the 16S rRNA gene and subsequently computed the results. New species, clades, and divisions have been discovered, driving future research toward a more balanced understanding of the tree of life. In addition, these studies have revealed that the diversity of different communities can range from a few

to thousands of species. Beyond initial surveys, temporal and spatial examinations of microbial population structure are essential because they will allow for community composition comparison analyses, revealing the relationship between ecology and the conditions that favour one population structure over another. As a result, we expect that less time-consuming approaches to detecting the presence of organisms in environmental samples, such as those based on the hybridization of probes to the 16S rRNA gene, would be valuable as researchers try to characterise populations more quickly, possibly even in the field [9,10]. The separation of a probe in the latter method enables for the detection of considerably more types. Furthermore, several taxonomic specificity probes can be utilised, allowing for quick categorization and possibly quantification of the organisms present in a sample. However, one disadvantage of probe-based approaches is that they are confined to the discovery of known groups and will miss the existence of truly unique organisms. These methods may be most effective if an initial survey has provided a better understanding of the organisms believed to be there, allowing for the creation of tailored probes.

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