

Short Communication

Microbial Diversity Conservation: A Cornerstone for Primary and Secondary Production

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The microbial world is the largest unexplored reservoir of biodiversity on the earth. It is an important frontier in biology under intensive investigations. The exploration of microbial diversity has been spurred by the fact that microbes are essential for life since they perform numerous functions essential for the biosphere that include nutrient recycling and environmental detoxification. The management and exploitation of microbial diversity has an important role in sustainable development with the industrial and commercial application of microbial diversity worth millions of rupees. Given the heterogeneity of natural environments and the enormous potential of microorganisms to provide novel pharmaceuticals, fine chemicals and new technologies, the biotechnology industry has a vast, largely untapped resource for the discovery of new chemicals and novel processes. However, despite the obvious economic value of microbial diversity, microorganisms have been largely ignored in debates on the conservation and management of global diversity. There is, therefore, an urgent need to persuade policy-maker to be more concerned about the conservation, management and exploitation of microbial diversity. There are a number of reasons why the conservation of microbial diversity has not received the same attention as plants and animals. For example, microorganisms are invisible, less familiar and perceived primarily as agents of disease. With respect to the role of microorganisms in sustainable development, little is known about the potential contribution of microbial diversity to the national economy, to wealth creation and to improvements in the quality of life. An appreciation of these factors might be one way of changing government and public perception of microorganisms by showing that the sustainable use of microbial diversity has positive economic value. This would help justify the costs involved in conserving microbial diversity, but equally provide a useful indicator of the costs of inaction. In terms of the scientific rationale needed to underpin policy, quantification of microbial diversity has been limited. This makes it difficult to indicate what needs to be conserved in order to support the biotechnology industries and to understand fully the interactions between organisms responsible for maintaining a functional ecosystem.

Key words: Plant diversity, microbial diversity, nutrient recycling, ecosystem functioning.

INTRODUCTION

The microorganisms play an integral and often unique role in the functioning of the ecosystems and in maintaining a sustainable biosphere and productivity. The loss of biodiversity and their ability to provide ecological services to humans has now become a central theme in ecology. A number of major experiments have recently shown that declining plant diversity may impair such

ecosystem properties as plant biomass, primary production and nutrient retention (Tilman et al., 1996; Hooper and Vitousek, 1999). Presently, the relationship between biodiversity and ecosystem functioning in ecological and environmental sciences has emerged as a central issue. However, few experiments have directly tested the consequences of changing the diversity of ecosystem components other than plants (Naeem et al., 1994; Mikola and Setälä, 1996; Van der Heijden et al., 1998).

Recently, Naeem et al. (1994, 2000) simultaneously

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manipulated the diversity of primary producers (algae) and decomposers (bacteria) in aquatic microorganisms and found complex interactive effects of algal and bacterial diversity on algal and bacterial biomass production. Both algal and bacterial diversity had significant effects on the number of the carbon source used by bacteria, suggesting nutrient cycling associated with microbial exploitation of organic carbon source as the link between bacterial diversity and algal production. Several explanations are possible (Morin, 2000) but the theory is sorely lacking. Because producers and decomposers are two key functional groups that form the basis of all ecosystems (Harte and Kinzig, 1993), interactions between producer diversity and decomposer diversity might have major consequences on the functioning of ecosystems. Thus, it is now generally accepted that the extent of microbial diversity has not been adequately characterized and that there is an immense mismatch between the knowledge of that diversity and its importance in both ecosystem process and economic development (Zedan, 1993). Soil quality has been defined as the capacity of the soil to function within ecosystem boundaries to sustain biological productivity, maintained environmental quality, and promote plant and animal health (Doran and Parkin, 1994; Staben et al., 1997). Nutrient immobilization by decomposers and competition for inorganic nutrients between plants and decomposers are known to occur, but at equilibrium, the two functional groups must be limited by different factors in order to allow their consistence and ecosystem persistence.

ANALYSIS OF MICROBIAL DIVERSITY

The dissimilar macro-ecologists and microbial ecologists working on natural communities were faced with quite unique challenges posted by, for instance: (i) the large number of individuals per samples (for example, more than 109 organisms per gram of soil (Torsvik et al., 1990a, b); (ii) the problem of differentiating between different populations and the very high diversity at a relatively small scale (more than 104 species per gram of soil) (Klug and Tiedje, 1994); and (iii) the difficulty of defining a microbial species or some other unit that encompasses the appropriate level of diversity for bio- management of diseases (Singh et al., 2008 a, b). The immediate challenge facing microbial ecologists is how best to quantify microbial diversity in natural environments. Estimates of the microbial diversity must accommodate the spatial and temporal variability in microbial population. Scale effects, both temporal and spatial, are not only of fundamental importance in the quantification of biodiversity, but present basic questions for microbial ecology, the resolution of which could lead to development of fundamental theories and hypotheses as to how microbial communities are structured in space

and time, how they respond to environmental pressures and how diversity is connected to function (Klug and Tiedje, 1994).

Spatial effects include an assessment of the relationship between community composition and scale. This is analogous to the area-species curve in macroecology but would require that appropriate measures of microbial diversity be substituted for the classical eukaryotic species. The structure of such curves would be particularly important in predicting the location of the undiscovered diversity and would provide insight into how microbial diversity changes relative to the environment. Such studies could be extended to include an evaluation of biodiversity in 'comparable' (for example, the same soil type or similar vegetation cover) but geographically isolated habitats thereby providing information on microbial dispersal, evolution and selection (Klug and Tiedje, 1994). Chronological shifts in microbial diversity are brought about by changes in the environment of the microorganisms and may be induced by the organisms or imposed on the community from outside (Singh and Srivastava, 1984). A prerequisite to the quantification of diversity in natural samples is an understanding of the magnitude and level at which such changes operate. There is a need to know which taxonomic rank is most susceptible to change, what are the implications for estimates of microbial diversity at a given site, and whether the data can be used as quantitative indices of sustainability. Advances in the analysis and quantification of microbial diversity will undoubtedly require extensive, collaborative and interdisciplinary studies.

In addition to the development of new procedures, the efficacy and importance of the existing techniques will need to be re-evaluated, and protocols developed to enable extrapolative approaches to be used in sites where limited resources preclude intensive studies. Biodiversity estimates will need to be based on stable and readily analyzed properties of the microbial community. Estimates based on phenotypic, and to a lesser extent chemical techniques, are likely to reflect the physio-chemical environment and as such may be influenced by community composition and function at a particular site at a given time. Thus, sample and collecting procedures need to be standardized temporally. Analysis of microbial communities using ribosomal ribonucleic acid (rRNA) sequences is likely to be less sensitive to variability in the physio-chemical environment provided the methodology can be improved and the basis in nucleic acid extraction and implication procedures removed (Embley and Stackebrandt, 1994).

Although significant steps have been taken over the last few years, the required technology is still in its infancy and is as yet unable to provide the tools necessary to quantify microbial diversity in anything but the simplest of natural habitats. Nevertheless, with an awareness of the limitations of the existing methods and

human resources, a reassessment of the 'species' as the basic unit of microbial diversity, and the introduction of new methodology, significant progress in the quantification of microbial diversity can be expected.

Positive effects of plants species diversity on ecosystem process have been attributed to two classes of mechanism: functional niche complementarity and selection of extreme trait values. In both cases, biodiversity provide a range of phenotypic trait variation. The same two classes of mechanism operate with microbial diversity. Greater productivity of systems containing a greater diversity of both producers and decomposers is predicted by the increased likelihood that each functional group contains a species that is highly efficient in using resources. The importance of microbial diversity in sustainable development was shown by the serendipitous discovery of penicillium by Alexander Fleming and subsequent research efforts led to development of several other bioactives which has revolutionized the treatment of infectious diseases. Another emphasis of discovery of *Thermus aquaticus* by Thomas Brock, the source of thermostable deoxyribonucleic acid (DNA) polymerase used in polymerase chain reaction (PCR) had changed the face of modern biology.

In the area of plant microbe interaction and sustainable plant development, the rhizosphere competent bacteria most probably resulted from along co evolution with plants, and the soil acted as a reservoir of these microbes. The signaling compounds produced by plants may act either as attractants or repellants of bacterial populations. The greenhouse and field experiments showed that VAM inoculation controlled the incidence of plant diseases (Chandra and Kehri, 2006).

CONCLUSIONS

The role of microorganisms in maintaining the dynamic equilibrium and integrity of the biosphere is important because the existence of life is dependent upon the sustained, microbial-mediated transformation of matter in both terrestrial and aquatic environments. Presently, simple ecosystem plants and microbes are linked through recycling of different material. The ecosystem considers a diversity of plant organic compounds and a diversity of microbial species. Nutrient recycling efficiency from organic compounds to decomposers is then the key parameter that controls the ecosystems processes such as primary and secondary productivity and producer and decomposer biomass. The ecosystem predicts that microbial diversity has a positive effect on nutrient recycling efficiency and the ecosystem processes through either greater intensity of microbial exploitation of

organic compounds of functional niche complementary, much like in plants. Microbial niche breadth and overlap should not affect ecosystem processes unless they increase the number of organic compounds that are decomposed.

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