

Agron. Sustain. Dev, Mohammad Saghir Khan, Almas Zaidi and Parvaze A. Wani. Department of Agricultural Microbiology, Faculty of Agricultural Sciences, Aligarh Muslim University, Aligarh U.P., 202002, India E-mail: khanms17@rediffmail.com.

**Role of phosphate-solubilizing microorganisms in sustainable agriculture - A review.(2006)**

Compared with the other major nutrients, phosphorus is by far the least mobile and available to plants in most soil conditions. Although phosphorus is abundant in soils in both organic and inorganic forms, it is frequently a major or even the prime limiting factor for plant growth. The bioavailability of soil inorganic phosphorus in the rhizosphere varies considerably with plant species, nutritional status of soil and ambient soil conditions. To circumvent phosphorus deficiency, phosphate-solubilizing microorganisms (PSM) could play an important role in supplying phosphate to plants in a more environmentally-friendly and sustainable manner. The solubilization of phosphatic compounds by naturally abundant PSM is very common under in vitro conditions; the performance of PSM in situ has been contradictory. The variability in the performance has thus greatly hampered the large-scale application of PSM in sustainable agriculture. Numerous reasons have been suggested for this, but none of them have been conclusively investigated. Despite the variations in their performance, PSM are widely applied in agronomic practices in order to increase the productivity of crops while maintaining the health of soils. This review presents the results of studies on the utilization of PSM for direct application in agriculture under a wide range of agro-ecological conditions with a view to fostering sustainable agricultural intensification in developing countries of the tropics and subtropics.

# MICROBIAL DIVERSITY AND SUSTAINABILITY

Tony O'Donnell

Department of Agricultural and Environmental Sciences,

University of Newcastle upon Tyne

NE1 7RU

## Introduction

Microorganisms play an integral and often unique role in the functioning of ecosystems and in maintaining a sustainable biosphere. Indeed, the role of microorganisms in maintaining the dynamic equilibrium and integrity of the biosphere is so critical that the continued existence of life is dependent upon the sustained, microbially-mediated transformation of matter in both terrestrial and aquatic environments. That almost all biological processes in the environment, either directly or indirectly, involve microorganisms is often overlooked with the potential benefits of regulating, optimizing and exploiting microbial activity largely unexplored (Zedan, 1993). Thus, it is now generally accepted that the extent of microbial diversity has not been adequately characterised and that there is an immense mismatch between our knowledge of that diversity and its importance in both ecosystem processes and economic development (Zedan, 1993).

## Quantifying Microbial Diversity

Unlike macroecologists, microbial ecologists working on natural communities are faced with quite unique challenges posed by, for instance: (i) the very large number of individuals per sample (*e.g.* more than 10<sup>9</sup> 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 (*e.g.* more than 10<sup>4</sup> species per gram of soil (Klug and Tiedje, 1994); and (iii) the difficulty of defining a microbial species (Goodfellow and O'Donnell, 1993; Claridge and Boddy, 1994) or some other unit that encompasses the appropriate level of diversity (O'Donnell *et al.*, 1994). 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 populations. Scale effects, both temporal and spatial, are not only of fundamental importance in the quantification of biodiversity, but pose basic questions for microbial ecology the resolution of which could lead to the 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 are substituted for the

classical eukaryotic species. The structure of such curves would be particularly important in predicting the location of 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' (e.g. 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).

Temporal 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. 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 can these data be used as quantitative indices of sustainability. Advances in the analysis and quantification of microbial diversity will undoubtedly require extensive, collaborative, interdisciplinary studies.

In addition to the development of new procedures, the efficacy and importance of 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, readily analysed properties of the microbial community. Estimates based on phenotypic, and to a lesser extent chemical techniques, are likely to reflect the physico-chemical environment and as such may be influenced by community composition and function at a particular site, at a given time. Thus, sampling and collecting procedures need to be standardised temporally. Analysis of microbial communities using rRNA sequences is likely to be less sensitive to variability in the physico-chemical environment providing the methodology can be improved and the bias in nucleic acid extraction and amplification procedures removed (Embley and Stackebrandt, 1994).

Although significant steps have been taken over the last few years, the required technology remains 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 existing methods and human resources, a re-assessment of the 'species' as the basic unit of microbial diversity, and the introduction of new methodologies, significant progress in the quantification of microbial diversity can be expected.

## **Conclusions and Assessment**

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 pounds. 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-makers 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, we are limited by our inability to quantify microbial diversity. This makes it difficult to indicate what needs to be conserved in order to support our biotechnology industries and to understand fully the interactions between organisms responsible for maintaining a functional ecosystem.

## References

- Claridge, M. and Boddy, L. (1994) Species recognition systems in insects and fungi, pp.261-74 in Hawksworth, D. (ed.) *The Identification and Characterization of Pest Organisms*, Wallingford: CAB International.
- Embley, T. and Stackebrandt, E. (1994) The use of 16S ribosomal RNA sequences in microbial ecology. In Pickup, R., Saunders, J. and Codd, G. (eds.) *Ecological Approaches to Environmental Microbiology*, Oxford: Chapman and Hall.
- Goodfellow, M. and O'Donnell, A. (1993) Roots of bacterial systematics, pp.3- 55 in Goodfellow, M. and O'Donnell, A. (eds.) *Handbook of New Bacterial Systematics*, London: Academic Press.
- Klug, M. and Tiedje, J. (1994) Response of microbial communities to changing environmental conditions: chemical and physiological approaches, pp.371-78 in R. Guerrero, R. and C. Pedros-Alio, C. (eds.) *Trends in Microbial Ecology*, Barcelona: Spanish Society for Microbiology.
- O'Donnell, A., Goodfellow, M. and Hawksworth, D. (1994) Theoretical and practical aspects of the quantification of biodiversity among microorganisms, *Phil. Trans. Royal Soc. B* (In press).
- Torsvik, V., Salte, K., Sorheim, R. and Goksoyr, J. (1990a) Comparison of phenotypic diversity and DNA heterogeneity in a population of soil bacteria, *Appl. Environ. Microbiol.* 56, 776-781.

Torsvik, V., Goksoyr, J. & Daae, F. (1990b) High diversity of DNA of soil bacteria, *Appl. Environ. Microbiol.* 56, 782-787.

Zedan, H. (1993) The economic value of microbial diversity, *BioTechnology* 43, 178-185.

**(Courtesy:** Article Published in ‘The UK Strategy for Sustainable Agriculture: A Critical Analysis’ – Martin Whitby and Neil Ward (eds); Centre for Rural Economy Report , Department of Agricultural Economics and Food Marketing, University of Newcastle upon Tyne; 1994)