Guest editorial

Antarctic microbes, endemism and environmental monitoring

The last decade of Antarctic ecological research has seen a growing awareness of the pre-eminent role played by microscopic life-forms throughout this region of the biosphere. Yet despite much new information, fundamental questions remain about the species diversity and community structure of the Antarctic microflora. There are major deficiencies in our knowledge of all microbial groups, and the information base is especially inadequate for the ice-free and coastal regions increasingly subject to human impacts.

Have the severe environmental conditions of Antarctica selected for an assemblage of endemic microbial species? Micro-organisms are so readily dispersed that a high degree of endemism in any region seems unlikely. Nevertheless, intriguing reports continue to accumulate of new species from a wide range of Antarctic habitats: for example, the unicellular alga *Hemichloris antarctica* which lives beneath the surface of crystalline rocks; the bacteria *Halomonas subglaciescola* and *Flectobacillus glomeratus* which inhabit hypersaline lakes; the yeast *Cryptococcus vischniacii* and the halotolerant rods and cocci such as *Planococcus* (strain A4a) from Dry Valley soils. Surveys of the terrestrial microalgae and cyanobacteria have emphasized a lack of endemism, low species diversity and an absence of some groups (e.g. desmids) at the highest latitudes. However, unlike the determinative bacterial taxonomies, algal taxonomy rests almost entirely upon morphological criteria which may not distinguish important ecological entities. It is difficult to believe, for example, that *Phormidium laminosum* from the frigid glacial streams of the Dry Valleys is genetically identical to the same species in geothermal hot springs.

An exciting new suite of technologies, many based at the molecular biological level, is becoming available to more fully address these questions of genetic diversity. Total DNA hybridization has already been applied to temperate marine microbial assemblages and signals an unprecedented opportunity to assess the genetic distinctiveness of the Antarctic microflora. Ribosomal RNA sequencing and immunochemical assays now offer convincing new tests of similarity between isolates from the Antarctic and elsewhere.

These technologies also have important implications for environmental monitoring. Only a small and often unusual subset of the total microflora readily grows in culture, generating a misleading impression of the ecosystem dominants and community structure. Standard assays may be a poor guide to environmental change. With new methods of gene amplification, nucleic acid probes (e.g. allele-specific oligonucleotides) and the increasing automation of DNA diagnostic procedures it is becoming possible to quantify even minor constituents of the natural community without a culturing requirement; microbial lipid profiling, HPLC assays of pigment signatures, and epifluorescence coupled with image analysis similarly avoid the problems of enrichment.

This new era of biological discovery in Antarctica will still require a strong reliance upon traditional assays, innovative culture techniques and careful microscopy. A combination of these classic microbiological skills and the more recent genetic and biochemical technologies is now a powerful force which promises to yield some of the first adequate monitoring regimes for many Antarctic environments, and new insights into the nature of Antarctic ecology.

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