The interest in microbiology will grow as soon as it is accepted that micro-organisms produce substances beneficial in the therapy of human diseases or for industrial applications. Change as soon as it is accepted that micro-organisms produce substances beneficial in the therapy of human diseases or for industrial applications. The biomass of micro-organisms on our planet is estimated to be much more important than that of plants. Prokaryotes are the basis of every food chain on this planet.

The interest in microbiology will grow as soon as expectations become confirmed that micro-organisms produce substances beneficial in the therapy of human diseases or in industrial applications.
Micro-organisms still dwell where higher organisms cannot survive, not only on the surface, but also deep in the oceans and in the earth

Increasing economic interest in sequencing microbial genomes not only from pathogens but also from other, as yet unknown bacteria. Another indication for the growing interest in microbial genomes are TIGR’s plans to create a comprehensive microbial resource containing the sequence and annotation of each of the completed genomes, as well as associated information about the organisms. They hope to discover new prokaryotes with beneficial properties or devise new medications by analysing the genomes of pathological micro-organisms.

But microbiology itself has already been undergoing very fundamental, almost revolutionary change during the past two decades, notwithstanding the new sequencing techniques. These changes were triggered by new methodologies of studying kinships by means other than comparative morphology and biochemistry. Woese (Woese et al., 1990; Woese, 1994) introduced comparisons of the 16S ribosomal RNA sequences, or corresponding DNA, for establishing phylogenetic trees. The results obtained made it clear that living organisms can be distinguished into three primary ‘kingdoms’ or ‘domains’: the Eucarya, the Bacteria and the Archaea. The separation of prokaryotes into Archaea and Bacteria was a major step forward and has helped to solve numerous classification problems. It clarified properties and compositional differences which had previously been vague or even confused, such as the variety of DNA-binding proteins in chromatin (Li et al., 1998; Bendich and Drlica, 2000).

This new taxonomy now allows microbiologists to progress in the study of micro-organisms in the same way their colleagues did previously with the study of higher organisms, by first selecting representatives of taxa with sufficiently distant kinships. In this manner, the biodiversity gets broadly surveyed. This is exactly the reverse of what has been done in the past with micro-organisms: species belonging to taxa such as Bacillaceae and Enterobacteriaceae were strongly overemphasised because they occur frequently and can be easily cultivated.

Despite today’s anthropocentric trend, many microbiological publications have appeared lately, largely stimulated by a report by the American Academy of Microbiology in 1997 (Staley et al., 1997; Young, 1997). No month passes without some new micro-organisms being discovered, many of them having new, hitherto unknown properties. An example is the discovery of a new form of phototrophy in two widespread aerobic bacteria in surface waters of oceans (Beja et al., 2000; Kolber et al., 2000). One of these recently discovered organisms has a new variant of light-collecting rhodopsin. These bacteria harvest substantial amounts of energy and are supposed to play a very important role as a starter of the food chain that continues with plankton. Micro-organisms have also been found deep under our planet’s surface, where they grow under anaerobic conditions. They seem to be responsible for numerous known and potential biological activities, in particular by living on, and modifying, mineral substrates (Ehrlich, 1996). Indeed, the initial role of micro-organisms as the first inhabitants of our planet was to render the surface of the Earth suitable for the evolution of other life forms yet to come. By using molecular techniques, the ‘new microbiology’ will also give a fresh stimulus to this ‘biogeochemistry’. But many research fields in microbiology, although profiting from the new methods of genetic engineering, still have to be revolutionised in the same way as research on disease-causing prokaryotes has been. In line with the medically-oriented focus of biological research, a large effort is being made to study the mechanisms of infection of human cells by pathogenic bacteria (Niebuhr and Sansonetti, 2000). However, surprisingly little has been published on the essential and beneficial roles of human
intestinal bacteria (Bertschinger, 1997). Realising that there is a huge number of different microbial species that form living communities among themselves and with other animals or plants, the interest in studying these partnerships has greatly increased. Indeed, the non-medical microbiology community has not only studied this symbiotic partnership in ruminants, as can be found in any textbook, but even in protozoa (Görtz and Brüggler, 1998).

The initial role of microorganisms as the first inhabitants of our planet was to render the surface of the Earth suitable for the evolution of other life forms yet to come

Two important symbioses—those of fungi with the roots of plants by forming ‘mycorrhiza’ and those of nitrogen-fixing bacteria with some plant species—have great potential for agricultural applications. These partnerships allow the plants to grow with atmospheric nitrogen in exchange for nutrients for the symbiotic microorganisms. The initial hope of defining all the genes involved in nitrogen fixa-

gene technology. In addition to large-scale DNA sequencing and PCR, ‘biological chips’ (i.e. micro-arrays of DNA or protein-probes) will play an important role in discovering and characterising new potentially useful micro-organisms. These new approaches have also demonstrated that the living cell is not simply a bag of individual genes and their products. Rather, it is the result of a complex network of numerous components in which modifying the amount of one single product can influence many other metabolites—an understanding that could have been reached much earlier. Understanding these networks and the cooperation of a cell’s basic ‘household’ genes is obviously easier using the small and well-known genes of micro-organisms, rather than the human genome.

A suitable ending for this essay might be a quote from Arthur Kornberg, who received the Nobel prize for medicine in 1959 (Kornberg, 1997). He recommended: ‘Increased attention to the microbial world. Neglect of microbial research in recent decades has revealed, through novel and drug-resistant microbial diseases, that we, as animals, are simply guests in a microbial world. Biological and chemical studies of microbes, includ-

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References


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