

COMMENTARY

REVELATIONS RECURRING

by Bernard Dixon

If I were opposed in principle to the deliberate release of genetically modified organisms (GMOs) into the environment (which I am not), I would build my case not on hazards supposedly inherent in the recombination of diverse fragments of DNA, nor on the artificiality of gene splicing, nor on the presumptuousness of humans "playing God," nor on the added impetus biotechnology allegedly gives to the growing polarisation of the planet into the rich North and the impoverished South, nor even on the question of whether we really need better bio-control agents or novel plants with built-in herbicide resistance. I would focus instead on one simple question: is our knowledge of natural gene transmission sufficiently comprehensive to adopt as the baseline against which to assess the consequences, perhaps distant in space and time, of today's release of GMOs?

Consider, for example, the paper entitled "Attachment and replication of *Pseudomonas aeruginosa* bacteriophages under conditions simulating aquatic environments," which has just been published in the *Journal of General Microbiology* (137:661, 1991). It comes from Tyler A. Kokjohn, Gary S. Saylor, and Robert V. Miller, working at three U.S. centers—Argonne National Laboratory, Argonne, Ill.; Loyola University of Chicago, Maywood, Ill.; and the University of Tennessee in Knoxville. By publishing evidence that could be crucially important in assessing both the performance and safety of GMOs in the environment, Kokjohn and his colleagues have at the same time provided a telling reminder of just how restricted has been our knowledge of microbial populations in the biosphere—and indeed how incomplete that knowledge may still be.

The trigger for the investigation by Kokjohn *et al* was another piece of research which exposed the shaky foundations of textbook lore concerning the terrestrial biosphere. In August 1989, Oivind Bergh and co-workers at the University of Bergen in Norway reported that the load of bacteriophages in natural waters was no less than three to seven orders of magnitude higher than was supposed until that time (*Nature* 340:429, 1989). Transmission electron microscopy of samples from the North Atlantic, Chesapeake Bay, and other locations showed the presence of up to 10^8 bacterial viruses per ml of water. At a stroke, that discovery killed stone dead the conventional wisdom, retailed in countless reviews and research papers, that bacteriophage infection of suspended bacteria in natural-water systems must be an extremely rare event.

It has taken rather longer for two further implications of the Bergen work to be widely accepted—that virus infection is important in the ecological control of planktonic microbes, and that phages may mediate genetic exchange between bacteria in aquatic environments. Tyler Kokjohn and his collaborators have now made those implications compelling. They have found that when cells of the common aquatic bacterium *P. aeruginosa* are physiologically

competent to allow phage growth, neither the attachment nor the replication of either temperate or virulent phages are impaired at cell densities equal to or lower than those found in natural waters.

Kokjohn *et al* also cite work by Lita Proctor and Jed Fuhrman at the State University of New York at Stony Brook and the University of California, Los Angeles. Last year, writing in *Nature* (343:60, 1990), they reported high counts of phages, together with bacteria and cyanobacteria in the final irreversible stage of lytic infection, in the eastern Caribbean. This immediately modified our understanding of the death of cyanobacteria and heterotrophic bacteria. In view of the low estimates of phages in the sea, discredited by the Bergen group, marine biologists had hitherto attributed this bacterial mortality to grazing by protozoa.

From this and other recent evidence, together with their own findings, Kokjohn and colleagues conclude that phages are important effectors of microbial ecology in aquatic ecosystems, and that they exist in dynamic equilibrium with their hosts. "Thus the potential of bacterial viruses to control both the density and genetic diversity of natural populations of their hosts must be considered in the modelling of aquatic systems. In addition, consideration of phage-host interactions is essential in the evaluation of potential risk associated with the environmental release of genetically engineered microorganisms, as well as in the evaluation of the effectiveness of any released organism in carrying out its desired environmental function."

One scarcely needs to draw a detailed diagram to emphasise the significance of this newly realistic picture of microbial life in the biosphere. In less than two years, we have learned that bacterial viruses are vastly commoner in water than was previously imagined, and that they probably have extensive interactions with aquatic bacteria. Clearly, this new knowledge extends our vision of the machinery available for the horizontal movement of genes in nature. And that, in turn, alters our perspective on the possible onward journeys of stretches of DNA ferried into GMOs and then disseminated into the environment.

What is at issue here is not, of course, the revelation of any concrete hazard associated with the release of GMOs. Nevertheless, the work of Kokjohn and his associates reinforces the need for caution in the assessment of such releases. Think of other recent reports that have dramatically altered our knowledge of microbial ecology—Patrick Trieu-Cuot's finding of natural gene transfer between Gram positive and Gram negative bacteria (*J. Bacteriology* 170:4388, 1988), Phillippe Mazodier and Charles Thompson's description of conjugation between *Escherichia coli* and *Streptomyces* (*Bio/Technology* 7:398, 1989), and Jack Heinemann and George Sprague's report on conjugal transfer of DNA from *E. coli* to yeast (*Nature* 340:205, 1989). How many more revelations are yet to come?