

### Migrant DNA in the Bacterial World

Gene Transfer in the Environment.

Edited by S. B. Levy and R. V. Miller.

New York: McGraw-Hill. (1989). 434 pp. \$54.95.

The possibility that cross-species gene transfer acts as a general evolutionary force has enjoyed some interest recently, due in large part to the publication of reports of mechanisms that could facilitate it (e.g., Heinemann and Sprague, *Nature* **340**, 205—209, 1989). Among bacteria, efficient mechanisms for the horizontal spread of DNA have been apparent for many years. The questions, then, that must be addressed are whether these mechanisms operate in natural environments and whether they act on genes relevant to the survivability of the host. The discussion of horizontal genetic flow among bacteria should help to establish criteria for recognizing when horizontal transfer events have occurred and weighing the arguments for and against a general theory of horizontal gene flow,

*Gene Transfer in the Environment* addresses these questions. But these timely issues are only incidental to the purpose of this book, which is written primarily for those involved in releasing genetically altered bacteria into the environment. This book begins with a comprehensive review of transfer mechanisms—conjugation, transduction, and transformation—and gene mobility. In the chapter on conjugation, Ippen-Ihler surveys the large literature on the transfer mechanisms as well as the role of conjugal plasmids in the horizontal spread of antibiotic resistance genes among pathogenic bacteria in hospitals. In the chapter on DNA transformation, Stewart seems to preclude the possibility that most transformation is environmentally important by presenting a dichotomy between what he calls natural transformation (e.g., the high-frequency kind seen with *Haemophilus*) and artificial transformation (e.g., the  $\text{CaCl}_2$ -induced low-frequency kind seen with *Enterobacteriaceae*). This is a curious division, because there appears to be no evidence indicating that either mechanism is actually employed in nature. I did encounter the interesting fact that the steady-state concentrations of DNA in coastal waters range from 0.2–40  $\mu\text{g/l}$ , which does imply many opportunities for DNA spread via transformation.

The remainder of the book discusses bacteria in their natural environments—soil, water, plants, and humans and other mammals. The chapters on bacteria in soil (by Stotsky), in water (by Saye and Miller), and the plants (by Farrand) are highly informative reviews of bacterial ecology and controlled release experiments. They illustrate the difficulty of performing experiments on these systems. The general conclusion seems to be that it is easy to imagine how bacterial genes could spread among soil bacteria and how environmental factors influence that spread, but so far all controlled release experiments have proven

negative—that is, natural bacteria appear to resist the introduction of foreign genes. Some movement of highly promiscuous plasmids into natural flora can be temporarily observed, but they do not persist. In addition, plasmid transfer can be seen in controlled mating experiments when genetically marked donor and recipients are mated in water, soil, or plants. But, in general, natural environments seem to resist the introduction of new bacterial strains. Thus, efforts to replace native nitrogen-fixing bacteria in the field with “improved” laboratory strains have proven negative. The only thoroughly documented examples of natural horizontal spread of genes are seen among the transferable bacterial resistance plasmids growing in farm animals and man; this important subject is covered in two chapters. Though it has been difficult to observe horizontal DNA transfer in other environments, there still seems to be a consensus that genes probably do move horizontally, but these events are sufficiently rare such that, if not fixed by selection, they probably go undetected.

Given that Levy and Miller have tried to assess the problems that will be encountered when genetically engineered bacteria are released into the environment, the book can be judged a success, and it is recommended reading for those planning to release genetically engineered microorganisms. Certainly, anyone involved in regulatory issues will find in this volume an excellent summary of the relevant scientific issues. It is written for scientists; the larger audience of politically concerned laymen would have to work very hard to read this book.

But returning to the question of whether there is any long-term evolutionary significance to horizontal gene spread requires looking to the past, by means of phylogenetic reconstruction based on genetic sequences, where available, paleontological information. Perhaps it would have been fruitful to enlarge the scope of the book by including this approach. The lack of phylogenetic reconstruction is an unfortunate omission, because the authors fail to mention the best example of a plasmid-associated gene, outside of antibiotic resistance, that has experienced horizontal movement (see Yamamoto et al., *J. Bacteriol.* **169**, 1352—1357, 1987).

In addition, if the usual units that are successfully and stably transferred are parts of genes, as opposed to whole plasmids or genes, then the types of approaches described in this book would have overlooked them. Sawyer (*Mol. Biol. Evol.* **6**, 526—538, 1989) has recently presented a case supporting a significant horizontal flow of genetic information within populations of *E. coli*. His work strongly supports the hypothesis that known mechanisms for moving DNA do operate in the environment and that chromosomal DNA is involved. Interestingly, he finds that the average units of transfer are DNA patches of only 100–200 bp. It is granted that, in general, the phylogenetic approach is complex and provides few clear answers. One can pray for rough indications of the extent of horizontal genetic spread. There are a number of reports of whole bacterial genes that have apparently leaped high taxo-

onomic barriers, including the glutamine synthetase gene *Rhizobium*, nitrogen fixation genes, and the genes encoding superoxide dismutase. These are controversial examples, but a brief summary of the arguments would further help the reader decide whether, at the present time, there is evidence of substantial horizontal gene spread among bacteria.

Issues that have already arisen in regard to bacteria can further help clarify the discussion of cross-species gene transfer as a possible general evolutionary force. For example, in response to some of my work (e.g., *J. Mol. Evol.* 26, 16–23, 1987) I have been reproached with the argument that if horizontal gene transfer occurs, it would obliterate taxonomic boundaries. Interestingly, and even ironically, during the initial excitement that followed the discovery of plasmids, Woese and his co-workers were criticized for attempting to reconstruct bacterial phylogeny because, it was argued, the horizontal spread of DNA caused by plasmid movement would so scatter traits that tree-like descent patterns would be lost. Woese did not labor in vain because, despite the known mechanisms for moving DNA about, he obviously succeeded in constructing consistent phylogenetic trees (Fox et al., *Science* 209, 457–463, 1980). But this perennially recurring line of reasoning with which Woese was criticized is fundamentally flawed. The existence of reproductive isolation (i.e., the fact that taxonomic barriers do exist) and the fact that these taxonomic groups can be organized into tree-like patterns of descent does not establish, a priori, the absence of horizontal gene transfer. Evolution favors those with an appropriate balance between genetic variation and genetic stability. If genes or gene segments introduced from other species are viewed as just another source of genetic variability, then cross-species gene transfer could logically exist concomitantly with reproductive isolation and other biological barriers to its employment and sustenance. As is illustrated by the present book, convincing examples are hard to find, and the evolutionary implications of cross-species gene transfer remain an open question.

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