

BOOK REVIEWS

Microbial Evolution. Gene Establishment, Survival, and Exchange. Robert V. Miller and Martin J. Day (eds). ASM Press, Washington DC, 2004. 374 pp. Price: US \$99.

Evolution is a fascinating subject. More so, because its study is no longer an esoteric or simply intellectually satisfying pursuit, but has all the ramifications of a thoroughly practical discipline. Microbes have been around for almost four billion years, astoundingly older (almost 3 billion years) than plants and animals and consequently have a substantially more chequered evolutionary history than most other forms of life. The study of the evolution of microbes has the potential to answer some of most contentious issues – consequences of the introduction of genetically engineered microbes (GEM or GMO) in the environment. This follows from the fact that forces which drove evolution of earliest genes and genomes, very likely drive the evolution of genomes today.

The book under review has been divided into four sections, each comprising 4–8 chapters written by acknowledged experts in the field. The thoughtfulness of the editors is evident right from the beginning as Section I entitled ‘Intracellular mechanisms for generating diversity’, is devoted to mechanisms that underlie the generation of diversity among bacteria without resorting to any unnecessary introductory chapters. For many years, bacterial evolution was thought of as a process whereby a population of cells would, over a period of time, accumulate sufficient genetic variants so that, on a shift in environmental conditions, at least one of these variants would contain a suitable combination of mutations to allow it to compete successfully in the new environment. The selected strain would then act as the progenitor of the next population, and this evolutionary process would be repeated. The paradox however is how effective this process would be, given the low rates of mutation, fidelity of replicative polymerases, and the myriads of DNA-damage surveillance and repair enzymes. Nonetheless, it is now clear that bacteria have the ability to generate more genetic diversity than is predicted from the spontaneous mutation frequency. It is in this context that besides mutation, RecA-dependent generation of genetic diversity (homologous recombination), non-homologous recombination, gene duplication and gene loading have been discussed. Addi-

tionally, the synthesis of low-fidelity DNA polymerases, which are inducible in response to environmental stresses, can introduce high genetic variation. The process of homologous recombination and the creation of genetic diversity go hand in hand. The current models suggest that homologous recombination occurs more often than previously thought. Also, our understanding of the range of DNA elements and the mechanisms which underlie non-homologous recombination amongst bacteria, has grown substantially. The discovery of the genomic islands and integrons has further increased the repertoire of DNA elements which take part in non-homologous recombination. The sequencing of a larger number of microbial genomes and the study of comparative genomics has revealed that these elements are involved in horizontal gene transfer to a degree much more than originally thought. All these aspects have been discussed in various chapters under this section (chapters 1–3). Analysis of the current databases shows that large proportions of genes of an organism are related to genes in distantly related species, indicating that all known life forms share a common pool of highly conserved genetic information, shaped to a considerable extent by the duplication and divergence of DNA sequences predating the prokaryotic–eukaryotic divide. The role of gene duplication in evolution, especially in the development of complex metabolic pathways, has also been reviewed under this section (chapter 4). Though bereft of any concrete experimental evidence as yet, the possible role of multiple chromosomes in generating sequence diversity has also been speculated (chapter 5).

Section II (Intercellular mechanisms for gene movement) is mainly devoted to the mechanisms that underlie horizontal gene transfer, viz. conjugation (chapter 7), conjugative and mobilizable transposons (chapter 8), bacteriophage-mediated transduction (chapter 9) and transformation (chapter 10). Each chapter is a lucid blend of fundamental and state-of-the-art knowledge about these subjects. All authors agree that these phenomena have played an important role in the evolution of microbes. Among these, transduction seems to head the list as Robert V. Miller (Oklahoma State University), who is also one of the editors, would make us believe because (i) bacteriophages are the primary components of all natural ecosystems as are their hosts, the bacteria; (ii) all groups of

bacteria are known to be infected by some phages; (iii) transduction has been shown to occur in terrestrial environments (soils and plant surfaces), aquatic environments (lakes, oceans, marine sediments, rivers and natural biofilms) and inside eukaryotic organisms, and (iv) both chromosomal and plasmid DNA can be transduced with equal efficiencies. Martin J. Day (Cardiff University), the other editor, however, puts up a similar case for transformation, albeit a bit feebly (chapter 10). The origin of the conjugative transposons and mobilizable transposons has also been debated. It is evident that the authors have scrupulously refrained from drawing inferences that may seem too chivalrous.

Section III is entitled, ‘Mechanisms for gene establishment and survival’. Classically, mutations were supposed to arise during growth, spontaneously. However, this classical theory is being challenged. The controversial process called ‘adaptive’ mutagenesis, has been of considerable interest. The result of the mechanisms which underlie this process is the production of mutations in non-dividing or stationary-phase bacteria subjected to non-lethal selective pressure, such as nutrient-limited environment. Stationary-phase-induced or adaptive mutagenesis has been shown to occur in a variety of different organisms. The subject of adaptive mutation (chapter 12), its mechanisms and regulation, and its role in evolution forms an exceedingly interesting part of the section. Several areas, which are just beginning to be understood from the perspective of their role in bacterial evolution, have also been discussed. For example, bacterial biofilms have been used as a platform to study bacterial adaptation and evolution. The microbial diversity, both phenotypic and genetic, in the biofilm population is far greater than that in the planktonic phase. In such structured communities, the potential for gene transfer is much higher due to the population densities. This indicates that the fundamental forces that drive evolution are an integral part of biofilms (chapter 13). The exploration of biofilms from the evolutionary perspective has exciting potential. In the same vein, the spatially segregated deep subsurface microbial communities have been evolving independently for long periods of time. Their slow growth and/or dormancy could affect microbial evolution as strongly as spatial segregation apparently does. Their study may reveal new paradigms of evolution (chapter 14). Intercellular signalling (quorum sensing) is

the hallmark of microbial communities. Such intercellular signalling is mediated by *N*-acyl-L-homoserine lactones (AHL), furanosyl borate diester (AI-2), 3-hydroxy palmitic acid methyl ester and signalling peptides. These allow bacteria to speciate further with the evolution of new behaviours that exploit the benefits of multicellularity (chapter 15).

Although bacteria have existed for almost four billion years, pathogens originated relatively recently. Thus the mechanisms that lead to the origin of pathogenic lifestyle of bacteria, provide important clues to evolution of disease-causing microbes and pathogenicity per se. An elegant description of pathogenicity islands, type-three secretion systems, horizontal gene transfer, and evolution of highly pathogenic *Escherichia coli* O157:H7 is provided in chapter 16. This chapter also discusses how loss of DNA contributes towards pathogen evolution, as exemplified by genome decay and pseudogene formation in *Mycobacterium leprae*. The genomic decay in vertically transmitted bacteria has been described with respect to *Buchnera aphidicola*, which resides in specialized cells called mycetocytes in the aphid body cavity (chapter 17). *Buchnera* cells never encounter any environment apart from the aphid. A discussion of the genomic decay in other bacteria which form obligate associations (parasitic or symbiotic) with animal host as exemplified by *Vibrio harveyi* and chlamydiae (pathogenic and the recently discovered in association with free-living amoebae), would have been an interesting incorporation.

Entitled a bit curiously – ‘Mechanisms for detecting genomic diversity’, section IV explores the role of horizontal gene transfer in generating genomic diversity and genomic differentiation (chapter 19), prokaryotic genome evolution as inferred from comparative genomics involving genome-wide analyses (chapter 20), and molecular basis of defining a bacterial species, including a critical assessment of the use of rRNA (or rDNA) as the molecular chronometer (chapter 21). Interestingly, the last chapter (chapters 6, 11, 18 and 21) in each of the four sections, contributed by the editors themselves, is a well-rounded critique of each section. These chapters, with a judicious mix of philosophy, are indeed inspiring.

As usual, coming from ASM, this book is a compilation of state-of-the-art knowledge on the subject of bacterial evolution. Undoubtedly, it is a feast to the connoisseurs

of microbial evolution. A hallmark of the book is that each chapter brings into focus the areas that need to be explored further. These would serve to guide prospective researchers. Since the book avoids the heavy bibliography-laden-reviews style, it would be equally useful to students of general microbiology, microbial genetics and evolutionary biology, who are interested in gaining basic understanding and insights into bacterial evolution. The questions at the end of each chapter are sharp and thought-provoking. The highly pruned references and suggested reading will be extremely helpful to both experts and non-experts. This book is a must for those interested in microbial evolution.

J. S. VIRDI

*Microbial Pathogenicity Laboratory,
Department of Microbiology,
University of Delhi South Campus,
Benito Juarez Road,
New Delhi 110 021, India
e-mail: viridi_dusc@rediffmail.com*

The Greying of India – Population Ageing in the Context of Asia. Rajagopal Dhar Chakraborti. Sage Publications India Pvt Ltd, B-42, Panchsheel Enclave, New Delhi 110 017. 2004. 467 pp. Price: Rs 880.

The Greying of India by Rajagopal Dhar Chakraborti is a suitable and appropriate title for the current-day demographic scenario of India in particular, and Asia in general. The transition from highest fertility of about six births during 1950s to around two per woman in 2005 and side by side, the transition in the average life expectancy from low to the highest in the continent is attracting scholars to ponder over the reasons for the same and the consequences of these changes. As an outcome of this demographic transition, the numbers of those living beyond the age of 60 are rising considerably. This alarming rise in the elderly population though not an unexpected trend; is one, the country is not prepared to face yet. Under such circumstances the current book not only attracts sociologists and social demographers but also poses a challenge to the policy makers. This book is Dhar's second of its kind after *Ageing of Asia* (2002).

The book brings out the rapid growth of the older population in Asia and the reasons for the same. Impact of ageing on economy, status of the aged and steps to be taken by the countries to make ageing graceful are also dealt with.

To quote, ‘Less developed countries have enormous potential for population growth at older ages as the large cohorts currently in the younger age groups reach adulthood later’. ‘Gerontological transition, explains that population momentum is a major cause behind the swelling of the number of tomorrow's aged in Asian countries.’

So far, ageing was not a serious problem in India or Asia because it was the family, that shouldered all the responsibilities of the elderly. However, of late, with low fertility rates and smaller family sizes, caring for the elders is becoming a real problem. Older people are regarded as economically unproductive. ‘They excel in experience, patience, and wisdom, the younger are noted for energy, enterprise, enthusiasm, the capacity to learn new things, to adapt themselves, to innovate.’ Thus changing age structure will come in the way of economic development. Population ageing will contribute towards more health expenditure and comes in the way of capital formation, as elders depend more on their saving rather than earning.

The author brings in the impact of ageing on politics; how older voters can influence the political agenda of the country, not only by voting but also by bringing about laws favourable to them. This may even result in inter-generational conflict. If the non-marketable services in the family are not available, private institutions and nursing homes for the aged will be needed.

One full chapter is dedicated to the status of the aged; specifically it refers to India for which data are available. Based on the data the author provides hints on what will be the status of elderly in future in the country. Rural elders outnumber urban elders; dependency of elders is more in rural areas where females, specially single and widowed, will be more compared to single male. More and more elderly are now living without their children and are still working for their livelihood. Prevalence of chronic diseases among the aged is high and much higher in urban areas. These issues are highlighted scientifically for the first time. There are reasons to believe that the incidence of low levels of well-being among the aged in Asia, particularly for India, is proved with the currently available data. However, the data do not support the idea