

book discuss aspects of glial cell-axonal interactions during development and repair. The discussion of the potential use of cultured glial cells to repair demyelinated lesions and to support the regeneration of traumatic CNS injuries is an interesting inclusion in the book, which, if possible, will revolutionise modern medicine. Invertebrates have for a long time represented a fruitful paradigm for the identification of regulatory genes that play roles in mammalian development and the

final chapter in the book gives an interesting overview of glial cell development in the insect nervous system.

In conclusion, 'Glial Cell Development' gives an excellent overview of a broad range of topics in modern glial cell research and the book is valuable for researchers working in the field as well as for newcomers, students and others with interest in neurobiology.

Niels Aagaard

**YAC Protocols. Methods in Molecular Biology, vol. 54.** Edited by D. Markie. The Humana Press; Totowa, 1995. x+378 pp. \$69.50 (pb). ISBN 0-896-03313-9

Laboratory or methods manuals are almost always useful publications: often they are the result of didactic efforts of their authors, enacted to finding a way to focus and verify their own protocols, otherwise frequently ill-defined. Of course they are (or are meant to be) of great help to colleagues in the field who desire to enrich their experimental tools with a novel technique. They could also represent, if and when the methodological details are accompanied by appropriate overviews, an advantageous observatory to newcomers to the field.

In order to meet all these plausible goals, a book of this sort requires *inter alia* a panel of authors and/or an editor who both share the awareness of the above scopes and possess the competence to present concisely the underlying theory and precisely the various protocols in question.

'YAC Protocols', volume 54 of the successful series 'Methods in Molecular Biology', gets close to responding fully to the aforementioned criteria. It is timely, since it appears almost 10 years after the publication in *Science* of the epochal YAC paper by Burke, Carle and Olson; 10 years in which the yeast artificial chromosomes (YAC) have contributed remarkably to the advancement of the various genome projects. Yet, it has been reliably stated that the YACs may have made their time at least as megacloning vectors, and are likely to yield the way to other cloning systems, possibly of prokaryotic origin, such as the PAC (phage P1-based artificial chromosomes) and the BAC (factor F-based artificial chromosomes), the main reason being the substantially unresolved problem of 'co-cloning' and this is an issue deserving some reflection.

Co-cloning is also known as 'chimerism'. It consists in the undesired apposition within the same YAC of fragments derived from unlinked regions of the genome under study: it is an inconvenience which could seriously mislead mapping and sequencing efforts. Admitted from the very beginning of the YAC technique, co-cloning has been unfortunately minimised by the original YAC apostles, who claimed it could be kept well below 10%; even if later acknowledged to be more conspicuous, it was deemed as marginally important, easy to be spotted and eventually eliminated in subsequent years (also through the use of recombinant deficient hosts). Yet, at the conclusion of the first 5 year phase (mapping) of the Human Genome Project, reliable commentators have issued a rather severe sentence of the future of the YACs, and this is so just because of the chimerism,

now recognised to affect 50–60% of most of the generally available YAC libraries.

In front of all this, it is frankly a bit disappointing to see that a book on YAC protocols devotes only a few pages to the detection of chimerism (Chapter 11 deals with this problem and is one of the shortest), and neglects any discussion on the two distinguishable causes of co-cloning (co-ligation of different restriction fragments *in vitro*, and recombination between different constructs taken up *in vivo* by the same host cell), as well as on the possible remedies (dephosphorylation of the genomic fragments rather than of the chromosomal arms, or at least a ratio of dephosphorylated vector to phosphorylated insert higher than ten, as recommended in Chapter 1; and finally the use of a transformation ratio DNA/spheroplasted cells lower than here suggested, which turns out to be close to, if not higher than, ten, as well as the adoption of recombination defective strains as hosts, as already mentioned). This is an omission which seems to amount to considering co-cloning as unavoidable, a sort of 'original sin', which probably is not deserved.

On the positive side, it should be noticed that the various chapters are loaded with useful tips and information; if one wanders through the notes one has the chance of stumbling happily into real treasure chests of illuminating and curious details, of the nature one, in less competitive years and fields, used to learn by chatting with friendly colleagues in front of a beer during breaks at a meeting.

Thus, the chapters on the transfer of YAC into novel hosts, be they different yeast strains or mammalian cells, represent very instructive reading for those who intend to use the yeast artificial chromosomes as vector to dissect other more or less complex genomes, or for those who strive to exploit the YAC as intermediates of more ambitious constructs, such as the MAC (Mammalian Artificial Chromosome), probably likely to be used for manipulative rather than for analytical purposes. Not only for them, somehow broader surveys of the chromosome features, such as telomeres, and in particular centromeres and DNA replication origins (admittedly much simpler in yeast than in higher eukaryotes), would have contributed to a better and broader overview of the field of artificial chromosomes as the last addition to the synthetic approach to the study of life.

Vittorio Sgaramella

**Guidebook to the Small GTPases.** Edited by M. Zerial and L.A. Huber. A Sambrook and Tooze publication at Oxford University Press; Oxford, 1995. xix+476 pp. £29.50 (pb). ISBN 0-19-859944-7

This book puts together information on the small GTPases, a family of proteins where our knowledge has exploded in recent years. With the discovery of the regulatory role of the Ras protein, governed by its binding alternatively to GTP and GDP, and the discovery of a large number of homologous proteins with similar characteristics, a fruitful field of research has developed, leading to improved understanding of the regulatory proteins of several biological processes. The common biochemistry of these proteins, and the lack of homology of several proteins regulating or being regulated by similar structures are fascinating challenges for the interested molecular biologist, and much of the focus in the field today is on unraveling the mechanisms by which the small GTPases affect the activities of other proteins.

These characteristics makes it possible to use information from one

biological system to the other – provided you get access to it. This is one aspect of the uses of this book.

In this guidebook, information on the GTPases themselves, the proteins that activate and inactivate them as well as their effectors (or presumed effectors) is given. They are organized in logical sections, where a common format has been attempted for each entry: After a brief summary, information on nucleotide sequence (gene), amino acid sequence (protein), posttranslational modifications, localization, interacting components (activators, inactivators, substrates) and functional studies (and references) is presented. Each protein is presented with one to two pages, with tabular material, drawings as well as the occasional picture presenting primary data. Needless to say, not all proteins have all information, and ironically, the mamma-