
Book Reviews

Mechanism of Transcription. Cold Spring Harbor Symposium on Quantitative Biology Volume LXIII. Cold Spring Harbor Press. 1999. 679 pages. Cloth \$258 ISBN 0 87969 550 1. Paper \$110 ISBN 0 87969 552 8.

This, the 63rd Cold Spring Harbor Symposium Volume, appears almost thirty years after the last Symposium devoted solely to transcription and forty years after the discovery of RNA polymerase by Samuel Weiss and Lenny Gladstone. The book is indeed dedicated to Sam's memory; pleasingly, because his contribution to molecular biology has in the past been considerably underestimated. The volume contains 67 articles arranged into eight sections, the first four of which deal with basic topics: initiation, activation, RNA polymerase structure and elongation/termination. Twelve of the thirty-nine studies described in these sections use prokaryotic materials (and two, archaeal), reflecting the major contributions which can still be made using these more tractable organisms when investigating fundamental and highly conserved processes. I wonder whether the relevant research funding bodies in the United Kingdom (and elsewhere) distribute grants proportionately. The final four sections concentrate solely on eukaryotes, dealing with repression mechanisms; chromosome structure and transcription; remodelling of the chromatin (by non-covalent mechanisms); and regulatory complexes and pathways.

This collection of papers by many of the best groups working on transcription throughout the world will clearly be very valuable to academic and industrial researchers in the field, as well as to teachers of final year undergraduates and first year postgraduates in molecular genetics, biochemistry, developmental biology and related subjects. The book is the more valuable because so many of the articles are really reviews. It is nevertheless inevitable that, because our insights into transcription and its regulation are still developing rapidly, this volume will not for long be the last word on most topics.

Those considering buying the book for themselves can get a detailed grasp of its contents by reading

Losick's excellent closing summary. I shall only mention some features which I found particularly useful or striking. (For brevity, papers are referred to only by first author's name.) Solid structural information, accumulated by various approaches (e.g. Darst, Burley, Kornberg, Chedin) is allowing fascinatingly detailed models to be proposed: e.g. by Darst, regarding CRP-stimulation of *E. coli* RNA polymerase at type II promoters; daringly (and characteristically stimulatingly) by Ebright for initiation and elongation complexes and even termination mechanisms, in prokaryotes and eukaryotes; for details of eukaryotic pol II and pol III initiation processes (e.g. Tsai, Reinberg, Kumar, Kornberg, Davidson); and for T7 RNA polymerase action (Cheetham), incidentally adding another nail to the coffin of a once fashionable elongation model. (When is an inchworm not an inchworm? When it's a red herring.) Archaeal transcription (Bell) is interesting intrinsically and as a model for eukaryotic systems. Reviews on general transcription factors (e.g. Reinberg, Tsai, Coin, Kumar) and on core promoter elements (e.g. Smale, Burke) make eukaryotic initiation begin to seem comprehensible even to this ancient prokaryotologist, although the existence of systems such as SAGA (Steger, Kotani, Winston) and TRF (Naar) as alternatives, respectively, to TFIID and its TBP component further complicate the overall picture. Recent work on rRNA transcription in *E. coli* (Gourse) may have solved the long-standing problems of growth-rate and stringent control, resurrecting Maaloe's venerable model implicating NTP concentration as the central regulator. Powerful evidence for activation simply by recruitment is provided through the bold construction of chimaeric *E. coli* activators and polymerase subunits (Dove): many other papers deal with the numerous targets for such activation (and indeed for repression) in eukaryotic systems. There are excellent reviews of bacterial sigma factor structure and function (Gross) and of sigma⁵⁴-holoenzyme activation by NtrC, whose ATP-dependent role in promoter-opening (Rombel) might be compared with the role of helicase components of TFIID in eukaryotes (Coin). The extraordinary

repetitive CTD domain of the largest pol II subunit, whose phosphorylation by TFIIF (Coin) or P-TEFs (Peng, Garber) regulates the switch from initiation to elongation, now appears also to play a vital role in processing of pol II transcripts (McCracken). There are stimulating updates on the mechanisms of elongation and termination in *E. coli* (Korzheva) and on anti-termination, especially for λ Q protein (Roberts) and HIV1-Tat (Garber), the latter's mechanism echoing that of λ N (Greenblatt). There is an explosion of new information on the importance, for initiation, repression and activation of eukaryotic transcription, of chromatin structure and its modification by the acetylation or phosphorylation state of histones (e.g. Mizzen, Struhl, Grunstein, Steger) or by non-covalent remodelling of nucleosomes (e.g. Peterson, Schnitzler, Winston). Long range activation (e.g. Bell, Fernandez) or silencing (e.g. Cockell, Wade) may even involve additional effects of three-dimensional effects of three-dimensional organization of the nucleus. Finally, I liked the refreshing speculations suggesting that repressors (with or without the aid of histone-like proteins) might maintain accessibility of (some) promoters in the nucleoid of *E. coli* (Adhya). Such ideas may help to bridge gulfs between the pro- and eukaryotic worlds.

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The Genetics of Cattle. Edited by R. Fries and A. Rubinsky. CABI Publishing, 1999.
 ISBN 0 85199 258 7. 710 pages.

Any purchaser of this book would know why we kept cattle, but a visitor from outer space (or perhaps from our inner cities) would be hard pressed to do so from reading the chapter titles. Included among the chapters are the domestication of cattle, the genetics of hair colour, of behaviour, of reproduction, of development and BSE. There are none on the genetics of lactation or milk production, or on the genetics of growth or meat production. The nearest to appear to fit that bill are more specialised chapters on the genetics of meat quality and the molecular genetics of milk production (primarily protein composition). In fact the genetics of milk production appears as part of the chapter on the improvement of dairy cattle, and that on meat production in one on the improvement of beef cattle. But these comprehensive chapters are of similar length to others dealing with specialised topics; such that more space is taken up on the genetics of cattle behaviour, on which little is known, than on the genetics of milk yield, on which there has been, and continues to be, extensive research particularly at the

quantitative level. An opportunity to provide a comprehensive review of the genetics of cattle has been missed.

Presumably this reflects the belief of the editors that cattle improvements by traditional means of selecting animals on their own and relatives' performance for the traits of interest will soon be replaced by molecular genetic methods or other manipulations. For example there are chapters on marker assisted selection and reproductive techniques, including cloning and transgenics. There is not, however, any discussion of the technology used for genetic evaluation of the animals to be selected (or cloned) based on records available, nor on the genetics or genetic analysis of herd life or feed intake.

On the positive side, this multi-authored volume comprises 24 chapters by workers who are (at least for the areas I know) authoritative and active in the field they review. The quality of the articles is correspondingly high, in terms of both content and clarity, and the book should serve as a useful reference. I shall merely pick out some of what I found interesting high points.

There are nice summaries by Bradley and co-authors on the phylogeny and domestication of cattle. Both are active topics and the former is particularly controversial with the recent claims of high relatedness of the ruminants to cetaceans (whales etc.). Although cattle are rarely useful as a model species, they are of course the model for the study of milk proteins, and have been important in blood group and immunogenetic developments. For other important topics which are well covered, such as the physical and molecular linkage maps, by Fries and colleagues, there is no question yet of cattle being an important model and the critical need is to identify synteny to the human and mouse maps. As cattle genetics progress, however, and more becomes known about the genetics of lactation and of ruminant gut development and physiology and of how the relevant genes evolved, so will our knowledge of general biology rise. On the more applied side, both Goddard and Wiggans (dairy cattle) and Kinghorn and Simm (beef cattle) do a good job of putting a quart into a pint pot of describing both production genetics and improvement, and Simon takes a rational view of conservation.

The presentation is clear, but I do have one niggle, presumably due to copy editing. It is odd to write of animals producing '10000/ of milk year⁻¹' and of a rate of eating in which the average number of gulps s⁻¹ (is) 1.46. Although the volume is aimed mainly at the dairy cattle geneticist, the general geneticists will find it a useful source.

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Microsatellites: Evolution and Applications. Edited D. B. Goldstein and C. Schlötterer, Oxford University Press, 1999. 368 pages.

The importance of microsatellite-based studies in the field of biology has grown enormously in recent years and this growth phase, as yet, shows no signs of abating. The exceptional variability of microsatellite sequences has allowed microsatellites to be utilised in diverse applications such as genetic mapping, forensic science, conservation and evolutionary ecology. This book describes the biology and uses of repetitive DNA sequences with the emphasis on microsatellites, although minisatellites are also mentioned.

The first half of this book, consisting of nine chapters, concentrates on the evolution of microsatellite markers. Evidence for the most appropriate mutational mechanism is gathered from population and pedigree analysis and from *in vitro* and *in vivo* studies. Work reported in several chapters reveals the mutation patterns to be tremendously diverse, with microsatellite repeat motif and size influencing the mutational process. Topics raised in other chapters include possible functions of microsatellites and how selection may be acting upon microsatellite markers. Several authors also discuss possibilities such as an upper limit to microsatellite size, a mutational bias in favour of gains in length and heterozygote instability.

The second portion of the book (11 chapters) deals with the practical applications of microsatellite data.

Some of the subsequent chapters reflect “classic” uses of microsatellite data, including forensic applications and genetic mapping. Applications of microsatellite markers to human populations are described, with examples of how they were used to elucidate the evolution of human population on global and local scales. Other chapters discuss conservation genetics, and the application of microsatellites in the identification of hybridization events and social organisation. The application of microsatellite markers to investigate fitness consequences in natural populations of red deer and harbour seals is discussed in another chapter. Selection may cause a particular mutation to become fixed, one chapter investigates the possibility of using neutral microsatellite markers to identify such selection events.

Microsatellites: Evolution and Applications comprehensively reviews the evolution of microsatellite markers. The book also depicts microsatellites as universal tools suitable for a diverse set of applications. This book will be of immediate interest to research scientists and graduate students working with microsatellites. However, the broad ranges of topics covered make this book worth reading for anyone wishing to obtain a summary of microsatellite approaches to research.

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