

BOOK REVIEWS

Annual Review of Genomics and Human Genetics. Co-Edited by Aravinda Chakravarti and Eric Green. Annual Reviews, 4139, El Camino Way, P.O. Box 10139, Palo Alto, California 94303-0139, USA. 2007. vol. 8. 375 pp. Price not mentioned.

This volume of the *Annual Review of Genomics and Human Genetics*, edited by Chakravarti and Green, comprises of 16 articles. The editors have done a commendable job of identifying themes for inclusion in this volume and inviting researchers of high renown to contribute articles.

The volume starts with an article by Luca Cavalli-Storza on human evolution and its relevance to genetic epidemiology. Cavalli-Storza provides a succinct overview of genomic inferences on human evolution. He also provides a commentary on the continuity of genetic variation over geographical space, but underscores the fact that behind this continuity is a discontinuity, arising from barriers among social groups, that needs to be studied in greater detail. He also clearly, albeit briefly, explains that the demographic history of humankind has resulted in clustering of cases of specific genetic diseases that originated from a single or a few mutations, which is why the study of evolution of human populations is relevant to genetic epidemiology. The occurrence of diseases causing mutations on specific chromosomes, i.e. haplotypic backgrounds, has been a major attraction for the conduct of genomic association studies, especially for common diseases. Efficient design of such studies is important for guarding against false-positive inferences and for cost-minimization. Elston *et al.* (article 15) have discussed multistage sampling designs for this purpose, and have additionally stated that the (currently discontinued) strategy of conducting a linkage study before a genome-wide association study may still be useful. Genome-wide association studies require a large number of phenotypically well-characterized samples, which are difficult to collect within a short period of time, making bio-banking essential. Long-term banking of biospecimens raises a host of ethical issues, especially because hundreds of thousands of genomic markers are assayed on every sample that can potentially conflict with the ethical guideline of confidentiality of donors of

samples. Henry Greely in the last article of this volume, clearly brings these ethical issues to the fore and presents some possible solutions to the problems.

The theme of dissecting molecular architectures of complex diseases and traits has also been dealt with in article 7, where the emphasis is on quantitative traits in domestic animals. In this article, Michel Georges has provided a nice review of methodologies – study designs, statistical and genomic and advances – for mapping quantitative trait loci, and has rightly emphasized that most of these loci have been mapped using simple statistical methods, which was possible using specific mating designs (not possible in humans!).

With the availability of sequence data from large genomic regions, computational approaches to genome annotation have become important and useful. Two articles in this volume relate to this theme. Blanchette (article 9), has reviewed key algorithms for multiple sequence alignments and has argued for the need to develop faster algorithms. The problem of annotating novel RNA genes in non-coding regions, an important issue in proteomics and evolutionary research, has been addressed by Sam Griffiths-Jones (article 13). This field of activity is presently immature at a genome-wide scale, but with the startling discovery of microRNAs in non-coding RNA, it is certain to attract more attention.

The importance of microRNAs in vertebrate physiology and human disease has been reviewed by Chang and Mendell (article 10). The physiologic functions of only a small number of microRNAs have been definitively established and the roles of microRNAs have been delineated for only a small number of human disease states. However, the potential role of microRNAs in human physiology and disease is important. The authors have also discussed the influence of variation in the genome on microRNA-mediated regulation of human genes.

The structure of the human genome and processes operating to shape this structure in relation to diseases are the themes of three articles. McKinnon and Caldecott (article 3) discuss DNA strand break repair and human disease; Bernard Conrad and Antonarakis (article 2) discuss phenotypic diversity and human disease mediated by gene duplication, and Jurka *et al.* (article 11) discuss the structure and evolution of repetitive se-

quences in complex genomes. There are some common outcomes of DNA repair defects such as radio sensitivity, immunodeficiency, lymphomas and other cancers, but the spectrum of effects is broad. Similarly, small-scale genomic duplications produce diverse phenotypic variation, including in disease states. Repetitive DNA sequences derived from transferable elements may be the driving force in the evolution of epigenetic regulation.

Four articles provide state-of-the-art knowledge on human genetic diseases. Paracchini *et al.* (article 4) describe genetic studies on dyslexia and associations with four candidate genes, on which detailed functional studies are awaited. The genetic basis of Fragile X syndrome is discussed by Penagarikano *et al.* (article 6), although here again functional studies and molecular details of regulation are required for a clearer understanding of the role of the *FMRI* gene. Article 12 is on congenital disorders of glycosylation by Jaeken and Matthijs. Defects in the synthesis of glycans and their attachment to other compounds result in a wide range of human diseases for which there are no systematic methods of genetic screening. These methods are required to be developed urgently. Genetic factors underlying host predisposition to micro bacterial diseases and their progression – BCG and tuberculosis infections – are reviewed by Fortin *et al.* (article 8) A surprising finding of these studies is that patients with lesions in the IL-12-IFN- γ loop seem to be resistant to most infectious diseases. Studies on host susceptibility factors in infectious diseases are gaining importance, and therefore this review is timely.

Higgs *et al.* have reviewed (article 14) conceptual and technological developments to analyse transcriptional and epigenetic programmes at the whole-genome level. These developments are crucial to providing a deeper understanding of the regulation of the human genome and its impact on human genetic disease.

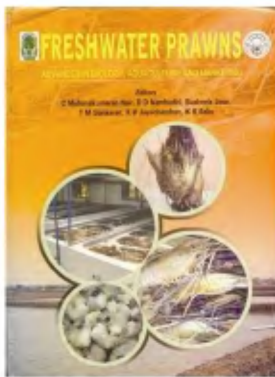
Finally, there is an application-oriented article by Martin and Caplen (article 5), who have reviewed various applications of RNA interference that include creation of model systems, identification of novel molecular targets, genome-wide dissection of gene function and clinical therapeutics.

Overall, this collection of articles is timely and provides state-of-the-art re-

views. Most articles end with succinct summaries and perspectives for the future. I would have liked to see a better organization of the articles by theme. The lack of any foreword or editorial statement was surprising, in spite of the excellent job that the editors have done in collecting the articles included in this volume.

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Freshwater Prawns: Advances in Biology, Aquaculture and Marketing. C. Mohanakumar *et al.* (eds). Allied Publishers Pvt Ltd, A-104, Mayapuri, Phase II, New Delhi 110 064. 2007. 779 pp. Price not mentioned.

This book is the proceedings of an International Conference on Freshwater Prawns held at Kochi, India during August 2003. The conference was attended by over 500 delegates from 14 countries. Among the 126 papers presented by a galaxy of international experts, 86 peer-reviewed manuscripts are organized into 15 chapters in this book. Fifteen papers are the status reports of 10 countries, 11 are on hatchery technology, 10 on farming, 9 each on biodiversity, genetics and biotechnology, nutrition, 7 on sustainability and environment, 4 each on capture fisheries, and economics and Marketing, and 3 on Diseases and Man-

agement. The book also has a couple of chapters on the plenary session, in which a series of recommendations are listed; an author index is also appended.

Better lessons of intensive coastal aquaculture penaeids prompted the organizers to adopt a more careful approach, while popularizing farming of freshwater prawns. India is the native country of the giant prawn, *Macrobrachium rosenbergii* that has become the second most important cultured crustacean. Prawn farming requires a comprehensive aquaculture support service that involves training, research, extension, infrastructure facilities, marketing and distribution systems, so that it may provide rural employment and additional income, and improve aquatic environment and public health. Hence both the conference and the publication of its proceedings (this book) are timely and amply justified.

Summarizing the global status of freshwater prawn farming and recent research with a view towards the future, new indicates that despite having a larger culturable area, India stands as the third highest producer of the prawn (24,230 mt), following China (128,338 mt) and Vietnam (28,000 mt). As the major problem is our inability to realize the installed capacity of our hatcheries, we have much to learn from others. For instance, pH is an important factor in a hatchery; at the salinity of 12 g/l, the highest hatching success is 92% at pH 7, but less than 13% at pH 6.5 or 7.5. We are yet to diversify our culture systems; for example, Vietnam practices open recirculating, and modified static green water models, and has shown that the latter is more widely used due to the ease of operations, limited use of water and *Artemia*, higher survival and profit. Thailand has shown different methods of replacing *Artemia nauplii* in the hatchery, either completely or partially. The Government of Bangladesh is formulating a strategy for the shrimp sector on the basis of the National Fisheries Policy.

Sankolli and Shenoy have raised an important question whether India should go for a single species-based prawn culture? Soni *et al.* provide a comparative account on the larval biology of three large Indian freshwater prawns, which may prove important to develop new hatchery technology for large-scale seed production for their culture in different agro-climatic zones of a large country like ours. However, Sankolli and Shenoy

continue to state that they have successfully crossed *M. rosenbergii* and *M. malcomsoni*, and generated a 167% fast-growing fertile hybrid. However, it is not clear as to why they have not popularized the same. A pioneering contribution is provided by Sarin who describes optimum procedures for cold anaesthetization of *M. rosenbergii* larvae at 15°C for packing, live storage and revitalization. He has also shown that clean moistened and chilled at 2–3°C, coarse saw dust as a medium of live storage and transportation of brooders. Vartak and Singh have found that a dose of 125–150 mg clove oil/l is optimum for induction and recovery of juvenile *M. rosenbergii*. It is in this area of research that India requires contributions urgently.

In farms, a complex population structure composed of three major morphotypes is known to occur the small male (sm), medium-sized, orange-clawed male (om) and giant-sized, blue-clawed male (bm). From long-term, well-planned investigations, Karplus has shown that in the absence of bm, the sm grew to a large size and hence they may be reservoir males. Among the tested factors, competition for food, inefficient conversion of food and chemical factors, the chemical factors proved to be the real cause for the emergence of the three morphotypes. The following few chapters describe the usefulness or disadvantages of high vs low-density culture, size or sex-graded culture and culture systems. Many studies undertaken in Bangladesh suggest that rice cum giant prawn culture increased the profit by 3–4 times.

Despite the fact that the giant prawn is cultured in 43 countries in all the five continents, we know almost little about genetics of the prawn. Removal of androgenic gland (AG) from mature females results in complete sex reversal. Injection of farnesylacetone (FL), a compound secreted by the AG inhibits vitellogenesis. However, injection of FL into females is a skilled and costly technique, which cannot be widely practised. Attempts have been made to produce all male progenies using androgenic steroids like testosterone, methyltestosterone and norethindrone, but these hormones neither masculinized nor accelerated growth. Research must be undertaken on chemical ablation or silencing of genes responsible for specific-sex differentiation stages, which could lead to sex reversal. Alternatively, a parental stock to produce all