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With over 300 microbial genomes now completely sequenced and more than a 1000 more in progress (Genomes Online Database: http:// www.genomesonline.org/), it was not surprising to see three reviews dealing with genome scale approaches in this volume.

'Genome trees and the nature of genome evolution' by Snel *et al.* describes the different approaches being taken to apply information of whole genomes in phylogeny. The traditional methods have used single gene phylogeny based on either the 16S rRNA or other highly conserved genes, but these only represent a small fraction of the genome. Although different parts of the genome may have different evolutionary histories, the genome trees allow one to use all the information content of genomes and then combine them into a phylogenetic tree.

The subject is treated systematically and is ideal for the initiate. A must read for all biologists even remotely interested in this emerging area. The five methods ('Five methods and Counting' as the authors put it to indicate we are still in an early phase of this subject) include (a) simple alignment-free genome trees that are 'quick and dirty' using overall word frequency (such as of a 5-amino acid stretch) or a similar statistic that are in complete contrast to the alignment-based trees that are routinely used, (b) gene trees based on shared gene content, wherein the importance of normalizing for genome sizes in such analysis was discussed, (c) gene order-based trees and how they can be used for greater resolution of more closely related organisms, (d) the 'blastology' methods based on average sequence context and, finally (e) genome trees based on individual gene trees which are 'combined' into super trees ('phylogenomics') and appear to show the greatest promise.

In their exposition into each of these methods the authors clearly explain the principles, the advantages and the limitations in a manner easily understandable by the non-specialist. One of the surprising insights being revealed by these genome trees is that despite the relatively large amount of horizontal gene transfer (HGT) that is observed in organisms, it is actually a less important factor in genome dynamics than vertical inheritance. This is in contrast to what was imagined when the important contribution of HGT to genome content was first realized with the emergence of the genome sequences. An interesting issue that is dealt with is how to utilize metagenomic sequence data for phylogeny (there are 28 metagenome or environmental genome sequences already available).

'Yeast evolution and comparative genomics' by Liti and Louis discusses the impact of sequencing of the different yeast genomes (7 in the *Saccharomyces* genus as well as several other model organisms like the pathogens *Candida albicans* and *Candida glabrata*, *Schizosaccharomyces pombe*, *Kluvyeromyces lactis* and a few others) in understanding how yeasts have evolved.

The review focuses on how the comparative analysis of these genomes has allowed one to obtain deeper insights into the 'whole genome duplication' of *Saccharomyces cerevisiae* genome followed by the molecular processes of evolution (rearrangement, translocation, gene loss, etc.). Although it is of special interest to yeast biologists, *Saccharomyces* continues to remain at the forefront of genome analysis and comparative genomics, and will remain a model for understanding the molecular processes involved in the evolution of all other organisms.

The review also briefly describes other important aspects that have emerged from comparative genomics of yeasts that include insights into non-coding regions, as well as evolution of yeasts to different life styles.

The third review 'Genome-wide responses to DNA damaging agents' by Samson and co-workers deals with genome-scale methodologies and should be an enjoyable read to all who are interested either in 'transcriptional profiling' or in the broad area of 'stress response'. It describes how microarray-based transcriptional profiling is being used in different systems. It has revealed many new genes even in the well studied *E. coli* SOS pathway, although most of the new genes seem to be involved in a secondary response to the stress. In mammalian cells, under stress conditions, a surprisingly limited transcriptional response has been seen (only 3 genes were induced >1.5 fold as compared to around 900 genes in yeast). Furthermore among mammalian cells the response differs drastically with cell types as seen with fibroblasts and Hela cells.

The meat of the review is on yeast where many environmental stresses have been examined for profiling purposes and is the system in which the authors themselves work upon. An interesting point that has emerged from these profiling studies is the lack of correlation seen between 'transcriptional responsiveness' and 'phenotypic responsiveness'. In other words, just because a gene is induced under a stress response does not mean its function is essential for survival under that stress. The review also summarizes efforts in networking genes through a variety of computational and experimental approaches to arrive at a more 'systems biology' perspective of the stress response. Some interesting approaches include integrating localization data into toxicity modulating gene data sets, as well as the possible impact of high density microfluidic chips to examine multiple samples in a single experiment.

For those interested in gene regulation there are two articles, both incidentally on post-transcriptional gene regulation. The first article 'Translation regulation of GCN4 and the general amino acid control of yeast' by Alan Hinnebusch describes the present level of our understanding of the GCN4 protein that has been the model system for translational control, and seems to be addressed to the more advanced reader. The second article 'The regulation of bacterial gene expression by riboswitches' by Winkler and Breaker revealed how 4% of genes in *Bacillus subtilis* are regulated by genetic control elements involving RNA, working either in *cis* or in *trans*. An increasing number of these elements are being discovered now by bioinformatics methods looking for conserved regions in non-coding DNA. These 'riboswitches' have either proteins, RNA or metabolites as their effector molecules, and was a useful knock on the head for someone like me who is struggling to emerge from the idea that most regulation is at the transcriptional level.

ANAND KUMAR BACHHAWAT

Institute of Microbial Technology,
Sector 39-A,
Chandigarh 160 036, India
e-mail: anand@imtech.res.in