Book Review

Trypanosomes, After the Genome (ed. Barry, D., McCulloch, R., Mottram, J. and Acosta-Serrano, A.), pp. 423. Horizon Bioscience, Wymondham, Norfolk, UK. ISBN 13:978-1-904933-27-4. £140
doi:10.1017/S0031182007003496
First published online 31 August 2007

Over the last decade the Trypanosomatidae have benefited from not one but 7 genome sequencing projects of varying depth and quality. New technologies already mean it is possible to obtain the primary sequence of trypanosomatid genomes for a reagent cost of less than $20 000. This cost will continue to fall rapidly, so we are likely to see even more trypanosomatid genome sequences being published. The phenotypic diversity of the Trypansomatidae offers a remarkable opportunity to identify pathways that might be responsible for that variety. Now that genome sequencing is becoming routine the real effort is to extract meaning from them. *Trypanosomes, After the Genome* provides 11 groups the opportunity to set the insights that the genome sequences have provided in the context of existing knowledge in their areas of research.

Since reviewers are supposed to find some faults with a book, I will confine my criticism to the title that mixes plural parasites with a singular genome. My impression is that this is a reflection of the editors' aspiration to present a text on comparative genomics of the 3 annotated trypanosomatid sequences being confounded by chapters that describe what the *Trypanosoma brucei* genome has to say about *T. brucei* biology. Frequently the *T. cruzi* and *Leishmania major* genomes are only referred to where they have relevant differences or similarities to *T. brucei*. Comparative eukaryotic genomics is a science that is still catching up with the data; the trypanosomatid genomes will provide a rich landscape to explore as the techniques mature.

The first chapter '*The Genome of Trypanosoma brucei*' is the user manual for the genome sequence. It describes the strategies used for sequencing, finishing and annotating the *T. brucei* genome together with a global summary of protein content and statistics on gene density in comparison with *Plasmodium falciparum* and *Theileria annulata*. This may seem dull stuff to the bench biologist but an understanding of how the data were created and annotated is critical to its interpretation. The mixture of strategies used by the two genome institutes has important implications for the interpretation of the data. The Institute for Genome Research used shotgun sequencing of BAC clones of chromosomes 2–8, whilst The Wellcome Trust Sanger Institute (WTSI) used whole chromosome shotgun sequencing for chromosomes 1,9–11. In consequence the BAC-based sequence contains a mosaic of both strands but with representation from only one strand at any one position; chromosomes 1,9–11 also contain a mosaic of both strands but with representation from both. Consequently the published chromosomes generated by both methods are artificial constructs but differ in what they may exclude or include; this may be important for the interpretation of some gene models particular in the subtelomeric regions that can vary substantially in length between strands, such that some regions are essentially haploid.

'*Reverse and Forward Genetics*' reviews the tools available for the discovery of the function of genes in *T. brucei* with particular emphasis on RNAi and screens for phenotypic variants. RNAi was discovered in *T. brucei* at almost the same time it was identified in *C. elegans*. It has become a powerful tool for manipulating the *T. brucei* genome, adding to its attractions as a model organism. Unfortunately RNAi only appears to be effective in *T. brucei* and not in *T. cruzi* or *L. major*, which lack a homologue for TbAGO1.

'*Genetic Exchange*' focuses on *T. brucei* for which genetic exchange can be studied in the laboratory. The development of a genetic map makes it possible to use the powerful tools of classical genetics to discover gene function. Nevertheless it is still laborious to create and phenotype genetic crosses in *T. brucei*, so unfortunately this important approach is likely to remain restricted to specialist laboratories.

'*Chromosome Structure and Dynamics*' covers the arrangements of genes in arrays and the organization of polycistrons and telomeres.

'*Replication, Recombination and Repair*' describes the contrasting evidence from the *T. brucei*, *T. cruzi* and *L. major*. I was surprised to learn that despite the evidence that genetic exchange is very limited in the latter two parasites all three have more genes involved in meiosis than the fruitfly.

'*Transcription in Trypanosomes*' reviews the transcription mechanism and the very limited number of identified transcription factors in trypanosomes in contrast to the abundant RNA binding proteins that are presumably involved in post-transcriptional regulation.

'*Post Transcriptional Control in African Trypanosomes*' describes motifs associated with RNA stability, export from the nucleus and translational control.

'*Cell Structure, Cell Division and Cell Cycle*' provides a detailed description of what was already known of the *T. brucei* cell and its cell cycle augmented by new insights from the genome sequence.

'*Intracellular Transport Systems*' describes mechanisms for endocytosis and the construction and recycling of the distinctive cell surface coats of these parasites.

'*Surface Architecture of Trypanosomatids*'; the surface coats of the trypanosomatids have been the subject of detailed study for many years due to their intensely antigenic nature. This chapter stands out for its detailed comparative analysis of the different surface coats used by the Tritryps for both defence and offence in their distinct host and vector environments. It is suggested that the extreme antigenic variation of *T. brucei* is a consequence of having a protein surface coat in contrast to the glycocalyx of *Leishmania* and *T. cruzi*. Both strategies can have high costs; *T. brucei* devotes 10% of its genome to VSG molecules while *T. cruzi* devotes 20% to mucins and transialidases for decorating them. The LPG and GIPL coat of *Leishmania* in contrast has not been subject to large-scale gene expansion.

'*Trypanosome Metabolism*' provides a systematic survey of the gene content of the major metabolic pathways in *T. cruzi* and *T. brucei* and the implications for their respective metabolic capacities. The evidence for acquisition of genes and pathways from plant and bacterial sources by horizontal gene transfer is also discussed.

This volume is not just a manual for the genome sequences but a detailed review of much of the fundamental biology of *T. brucei* with some references to *T. cruzi* and *L. major*. It will be an important resource for all workers on *T. brucei*, not just the molecular biologists, and provides a taste of what is to come from the other trypanosmatid genome sequences.

HARRY NOYES
School of Biological Sciences
University of Liverpool
Liverpool
UK

https://doi.org/10.1017/S0031182007003496 Published online by Cambridge University Press