PREFACE

Proteomic insights into parasite biology

MICHAEL L. GINGER[1], PAUL G. MCKEAN[1], RICHARD BURCHMORE[3] *and* KAREN M. GRANT[2]

[1] *Faculty of Health and Medicine, Division of Biomedical and Life Sciences, Lancaster University, LA1 4YK, UK*
[2] *Faculty of Health and Medicine, Lancaster Medical School, Lancaster University, LA1 4YA, UK*
[3] *Institute of Infection, Immunity, and Inflammation, College of Medical, Veterinary and Life Sciences, University of Glasgow, G12 8QQ, UK*

Advances in mass spectrometry have allowed different laboratories to apply proteomic approaches towards the study of diverse biological questions. Whilst the output from tandem mass spectrometry is peptide sequence, and this can facilitate protein identifications in the absence of comprehensive genome sequence information in any organism (discussed in Burgess and Burchmore (2012) and Brophy (2012) within this Special Issue), the more conventional, contemporary approach is to match peptide mass spectra against a virtual proteome derived from the *in silico* trypsinisation of a sequenced genome or transcriptome. In the case of parasites, there is now complete or comprehensive nuclear genome coverage for many parasites of medical, veterinary or agricultural importance (*e.g.* Sanger: http://www.sanger.ac.uk/resources/downloads/helminths/ http://www.sanger.ac.uk/resources/downloads/protozoa/ http://eupathdb.org/eupathdb/). The advent of cost-effective next-generation sequencing means that the already significant volume of sequence data in the public domain is likely to continue to increase rapidly for the foreseeable future making more parasites tractable to this type of investigation.

Traditionally, many parasites have been difficult organisms to study experimentally, and some continue to prove refractory to facile genetic analysis. Genome sequencing, followed by community-led annotation has therefore provided, and indeed continues to provide, a powerful 'first-pass' approach for predicting biological characteristics that are important for virulence. Moreover, the increasingly small amounts of material required to perform expression profiling (at either the transcriptome or proteome level) has made the study of the dynamic expression of protein-coding genes more feasible, especially for the experimentally demanding context of difficult-to-study parasites within the context of their natural life cycles (*e.g.* Wass *et al.* 2012).

The importance of expression profiling becomes clear if one remembers that for many organism-specific genes, 'function' is not a parameter that can be predicted with confidence from sequence analyses alone. Indeed, the problem can be accentuated in parasites due to the presence of novel multigene families and other parasite-specific genes where the gene-products function in diverse aspects of the host-parasite, vector-parasite or parasite-environment interface. For parasites that can be more readily cultured *in vitro* or maintained in laboratory animals, the biochemical fractionation of biomass, followed by proteomic analysis, allows the molecular characterization of organelles or other structures, such as the exoskeleton in parasitic worms. Whilst subsequent localisation experiments are required in order to confirm the candidature of novel proteins and their function, the application of proteomics is generally key for facilitating in-depth characterizations of structures and organelles that are essential in virulence, but which are often absent from more widely studied model organisms, such as yeast or *Caenorhabditis elegans*. Thus, the British Society for Parasitology (http://www.bsp.uk.net/) held a meeting in September 2011 at Lancaster University, UK entitled '*Proteomic Insights into Parasite Biology*'. The compilation of reviews in this Special Issue of *Parasitology* describes the presentations from invited speakers.

In the opening two articles, a major focus is the technical consideration of different proteomic tools, their general application to the study of parasite biology, and the integration of proteomics data within systems-led biological studies (Burgess and Burchmore, 2012; Wastling *et al.* 2012). Holistic views of dynamic proteomes during the transmission of malarial parasites through mosquitoes and the promastigote-amastigote differentiation of *Leishmania* are discussed in the reviews by Wass *et al.* (2012) and Tsigankov *et al.* (2012), respectively. In the reviews by Field *et al.* (2012) and Portman and Gull (2012) the emphasis shifts to the proteomes of organelles with discussions of the nuclear envelope, endocytic network and cytoskeleton in African trypanosomes. Proteome-led views of the

Parasitology (2012), **139**, 1101–1102.
doi:10.1017/S0031182012000947

interface between parasite and host during schistosome infections, and the value of identified proteins in diagnostics and vaccine development are subjects addressed in the articles by Mutapi (2012) and Wilson (2012). In contrast, Brophy *et al*. (2012) provide a forward-looking view of how proteomics might usefully contribute to mechanistic understanding of drug metabolism and resistance in parasitic helminths; here the application of proteomics is likely to be timely, given an increasing global threat of anthelminthic resistance to food security. Our final review deals not with proteomics, but with the complimentary analytical discipline of 'glycomics' (van Diepen *et al*. 2012). Here, the parasite focus is again schistosomes, where complex arrays of immunogenic cell surface-associated glycoproteins and glycolipids have likely roles in antibody-mediated immunity and thus, offer potential for vaccine development programmes. We thank all of the contributing authors to this Special Issue for their frank and informative discussions, which we trust will be of wide general interest to the readership of *Parasitology*. The symposium organisers also wish to acknowledge Cambridge University Press for their continued and generous financial support.

REFERENCES

Brophy, P. M., MacKintosh, N. and Morphew, R. M. (2012). Anthelmintic metabolism in parasitic helminths: proteomic insights. *Parasitology* **139**, 1205–1217.

Burgess, K. and Burchmore, R. (2012). Strategies to dissect parasite proteomes. *Parasitology* **139**, 1119–1130.

Field, M. C., Adung'a, V., Obado, S., Chait, B. T. and Rout, M. P. (2012). Proteomics on the rims: insights into the biology of the nuclear envelope and flagellar pocket of trypanosomes. *Parasitology* **139**, 1158–1167.

Mutapi, F. (2012). Helminth parasite proteomics: from experimental models to human infections. *Parasitology* **139**, 1195–1204.

Portman, N. and Gull, K. (2012). Proteomics and the *Trypanosoma brucei* cytoskeleton: advances and opportunities. *Parasitology* **139**, 1168–1177.

Tsigankov, P., Gherardini, P. F., Helmer-Citterich, M., and Zilberstein, D. (2012). What has proteomics taught us about *Leishmania* development? *Parasitology* **139**, 1146–1157.

Van Diepen, A., van der Velden, N. S. J., Smit, C. H., Meevissen, M. H. J. and Hokke, C. H. (2012). Parasite glycans and antibody-mediated immune responses in *Schistosoma* infection. *Parasitology* **139**, 1219–1230.

Wass, M. N., Stanway, R., Blagborough, A. M., Lal, K., Prieto, J. H., Raine, D., Sternberg, M. J. E., Talman, A. M., Tomley, F., Yates, J., III and Sinden, R. E. (2012). Proteomic analysis of *Plasmodium* in the mosquito: progress and pitfalls. *Parasitology* **139**, 1131–1145.

Wastling, J., Krishna, R., Armstrong, S. and Xia, D. (2012). Parasites, proteomes and systems: has Descartes' clock run out of time? *Parasitology* **139**, 1103–1118.

Wilson, R. A. (2012). Proteomics at the schistosome-mammalian host interface: any prospects for diagnostics or vaccines? *Parasitology* **139**, 1178–1194.