

Molecular approaches to malaria: MAM 2004 and beyond

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This special issue of *Trends in Parasitology* comprises a collection of timely reviews arising from the 2nd Molecular Approaches to Malaria meeting held 1–5 February 2004 in Lorne, Australia, four years after the successful inaugural meeting. As the name suggests, Molecular Approaches to Malaria focused on the latest molecular developments in malaria research, and their biological and clinical implications. By no means is this special issue intended to represent a comprehensive recapitulation of all of the presentations at the meeting. Rather, the articles address, in more general terms, recent advances on broader themes that were prominent at Molecular Approaches to Malaria meeting 2004.

In recent years, we have witnessed a dramatic increase in our understanding of malaria parasites at the molecular level. The underlying reason for this burst in knowledge on this important lethal human pathogen has been the availability of the complete sequence of the 23 Mbp *Plasmodium falciparum* genome. This is a particularly spectacular achievement for many reasons, not the least of which being the technical hurdle posed by the extreme AT-richness of the genetic sequence of this organism. The publicly available information, together with emerging sequence data from other *Plasmodium* spp., notably *Plasmodium vivax* and the rodent malaria parasite *Plasmodium yoelii*, has proven significant in itself, but its real power has been in the range of associated studies that have flowed from these resources. In particular, a vastly improved understanding of global gene and protein expression patterns has provided considerable insight into many areas of *Plasmodium* biology, of the molecules and mechanisms underlying pathogenesis, and of the set of metabolic processes that operate in *Plasmodium*. Some of these processes (e.g. those specific to the plant-like apicoplast organelle) represent attractive targets for novel therapeutic strategies. Furthermore, advancements in the understanding of the biology of mosquitoes, the techniques for transgenic manipulation of mosquitoes and the completion of the *Anopheles gambiae* genome sequence, the major malaria vector in Africa, together with the complete sequence of the human genome, have opened up opportunities for studies of host–parasite relationships and comparative genomics.

It was most apparent that the *Plasmodium* genome sequencing effort has profoundly affected the research

field. Although the complete *P. falciparum* genome sequence was published in 2002 in a series of landmark papers in *Nature* (2002, Vol. 149), several reviews in this *Trends in Parasitology* special issue outline how the genome sequencing effort is, in fact, ongoing on many fronts. Improvements continue to be made to the sequence itself (e.g. in gap closure and re-annotation), in the accessibility of the genome and linked expression profiling data, for example, via PlasmoDB (<http://www.plasmodb.org>), in addition to new gene assignments by comparison of *P. falciparum* open-reading frames with those present in the genome sequences of other *Plasmodium* spp. This special issue includes reviews that highlight numerous opportunities to study gene function and to understand complex biological processes that are now abundant as a result of this sequencing effort, and of the development of associated technologies such as microarray, proteomics and transfection of a range of *Plasmodium* spp.

Despite these incredible advances in molecular understanding, all in the field are acutely aware that malaria remains one of the world's most devastating infectious diseases and the urgency to translate new discoveries into real health solutions. With this in mind, the breadth of topics presented at the meeting included several issues directly relevant to clinical malaria, such as new insight into defining severe disease, as well as understanding and dissecting the molecular basis of the pathogenic mechanisms that underpin this highly complex process. In particular, C.L. Mackintosh *et al.*, and K.W. Deitsch and L. Hviid address the issues of clinical features and pathogenesis, and virulence determinants, respectively. J.E. Tongren *et al.* focus on the important and still poorly understood mechanisms of antimalarial immunity, and the possibilities for an effective vaccine against *P. falciparum*.

The attendees of the meeting would, we think, agree that there is much that still needs to be done to realize the multitude of opportunities provided in this post-genomic era.

Collectively, our relatively small group of malaria researchers will need to function more effectively and, most importantly, cooperatively. We believe that meetings such as MAM 2004 perform a significant role in this regard. As B.M. Cooke and R.L. Coppel point out in this issue, let's transform the present skies to an even brighter shade of blue by the next MAM meeting in 2008.

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