JAMES RENNIE BEQUEST

REPORT ON EXPEDITION/PROJECT/CONFERENCE

Expedition/Project/Conference Title: First Annual BioMalPar Conference on the Biology and Pathology of the Malaria Parasite ....

Travel Dates: 2 – 4th March 2005 ....

Location: EMBL, Heidelberg, Germany ....

Group Member(s): Joanna Sharman..

Aims: To learn about the latest advances and discoveries in the field of malaria parasite research, to gain information and ideas that may influence the direction of my own project, and to make contacts and talk to people about my work and how it fits in to the field ....

OUTCOME (not less than 300 words):-

Brief description of my PhD project

The aim of my project is to develop ways of integrating and visualising structural, functional and comparative genomic and transcriptomic datasets from the malaria parasite in a 'workbench' type of environment. The workbench should aid researchers in exploration and analysis by combining information from different kinds of datasets. Users will be able to utilise the workbench to find out information about specific genes or groups of genes of interest.

Brief description of the conference

The conference I attended was the first annual conference of the new BioMalPar (Biology and Pathology of the Malaria Parasite) Network of Excellence. The BioMalPar Network currently brings together groups belonging to 17 European institutes and universities with 3 African partners in Mali, Sudan and Uganda to form a large research community with expertise in malaria, which aims to encourage research through personnel exchanges, shared resources and joint research activities. More information about the Network can be found on their homepage: http://www.biomalpar.org/.

The Network's research activities focus on these four areas of parasite biology:

- Development and Gene Regulation
- Functional Cell Biology and Metabolism
- Molecular and Cellular Biology of the Pathogenesis of Malaria
- Immune Response and Defence Mechanisms in the Host and the Vector.

The structure of the conference was based around these four themes, with participating researchers and guest speakers from outside the Network presenting their work under the banner of the relevant theme. Over the three days of the conference there were almost 50 talks, lasting from 10 to 30 minutes each, and two poster sessions, where a similar number of posters were displayed.

Outcome of my attendance at the conference

Among the many interesting presentations, the ones that particularly stood out for me were given by Hagai Ginsburg of the Hebrew University of Jerusalem about data mining of the transcriptome of *Plasmodium falciparum*, David Roos on behalf of the *Plasmodium* Genome Consortium about the *Plasmodium* genome database, Matthew Berriman of the Sanger Institute about comparative *Plasmodium* genomics, Andrea Crisanti of Imperial College London about proteome analysis of the immune response against malaria, John Barnwell of the Center for Disease Control and Prevention, Atlanta, about the RBL family of proteins and their role in merozoite invasion, and finally, Henk Stunnenberg of the Nijmegen Center for Molecular Life Sciences, Netherlands, who talked about transcriptome regulators.

During the poster sessions I was particularly pleased to read the poster of Andrew Berry from the Sanger Institute and chat with him about his results and about my work. Dr Berry was very helpful and pointed me towards some useful software for comparative genomics and genome browsing that I will be able to use in my project. Dr Berry is part of Matthew Berriman's group at the Sanger Institute, who are involved in sequencing of *Plasmodium* species and their functional and comparative genomics. I was also pleased to have a brief chat with Dr Berriman about my project and I think that they may prove to be useful contacts in the future.

I was also glad to read the poster of and speak to Celine Carret, also from the Sanger Institute but a member of the Pathogen Microarrays team. She has been doing some interesting work on comparison of genomes using microarray technology and I look forward to reading an up-coming publication comparing different strains of *Plasmodium falciparum*. I am hopeful that the data her group collected will be useful to include in the workbench tool I am developing.

Another interesting poster I saw was by Gunther Zehetner from the Max-Planck Institute for Molecular Genetics in Berlin, creator of the MalariaBase database for new annotations of *Anopheles* mosquito and *Plasmodium* genes. Part of the functionality of this database is similar to the design remit for my workbench, in that it allows the user to search for genes of interest and it combines data from many resources, including genome browsers, transcriptomic data, functional data such as Gene Ontologies and metabolic data. However, its main functionality is as a searchable front-end to the database which returns results that link to other databases and websites. Unlike my workbench, MalariaBase's main purpose is to return specified types of data for specific genes and it is not a tool for exploration and integration of different large scale datasets like mine. However, MalariaBase may prove useful to me for downloading some of the latest sets of functional data for *Plasmodium*.

While I was at the conference I had the chance to talk to some young researchers in the field of malaria parasite and vector research. Having described to them the ideas behind and the proposed functionality of my workbench, I received positive feedback about the potential usefulness of such a tool to the malaria community, which is greatly reassuring.

In conclusion, all the above mentioned talks, posters and conversations, and others not mentioned specifically here, gave me a lot of new ideas about possible data and functions to include in my workbench and about the direction I would like my project to take. They also highlighted some potential problems I might encounter and gave me encouragement about the ideas I have had so far.

Furthermore, I will give a presentation on 12th May to the Structural Biology Group and Biocomputing Research Unit members on Swann level 3 at our floor meeting, where I will discuss my experiences at the conference and highlights of the research presented there.