JAMES RENNIE BEQUEST

REPORT ON EXPEDITION/PROJECT/CONFERENCE

Expedition/Project/Conference Title: SMBE 2008 .....

Travel Dates: 5-8 June 2008 .....

Location: Barcelona .....

Group Member(s): Lucy Weinert .....

Aims:

- To become familiar with new advances in the field of molecular evolution
- To present my poster, Phylogeny, life history evolution and recombination in intracellular Rickettsia bacteria

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OUTCOME (not less than 300 words):-

The Society for Molecular Biology and Evolution (SMBE) is an annual conference that typically attracts ~700 delegates from the field of genetics, evolution, ecology and molecular biology. SMBE 2008 was held in the beautiful city of Barcelona and this year, the symposia had a particular emphasis on genome analysis. Since the development of new sequencing technologies, genome sequencing has become much cheaper and so there is now a need to develop and apply novel techniques to genome analysis that will cope with the vast amounts of sequence data.

An interesting area of research is the detection of population structure on microorganisms that are identified by sequencing all reads from a sampled community. Metagenomics is a burgeoning field of research, attempting to assess the diversity of uncultivable microbial life. The number of microbial cells in the environment relative to the number of sequencing reads means that each read comes from a different individual with almost complete certainty, enabling estimation of some key population genetics parameters. Philip Johnson presented a poster, which showed that he has developed techniques that have enabled accurate estimations of the mutation and recombination rate to be calculated from individuals that have good sequence coverage. The upshot of this is, in the future we should be able to identify the effects of natural selection on these unique organisms, which will give us the insight in to the important factors that have shaped their adaptation to particular environments.

On the subject of metagenomics, Gabriel Marais gave an interesting presentation on *Pelagibacter*, of which I have a particular interest as it is a distantly related bacterium of the endosymbiont that I conducted my PhD research on (*Rickettsia*). *Pelagibacter* make up approximately 25% of rDNA extracted from metagenomics of seawater, making it a bacterium with some of the largest population sizes on earth. Despite being so numerous, hardly anything is known about the natural history of this organism, but sequencing its genome has shown that is the smallest free-living bacterium ever discovered. Many distantly related relatives of *Pelagibacter* also have considerably small genomes (including *Rickettsia*) but this is because they are endosymbionts and are assumed to be undergoing reductive evolution that accompanies a change to living within a host. However, since *Pelagibacter* are free-living, the reasons for its small genome size cannot be the same. One hypothesis is that the *Pelagibacter* genome is streamlined to cope with living in a nutrient-poor environment. Marais presented an alternative hypothesis; that *Pelagibacter* could be a “hypermutator”. The acceleration of mutation rate could help the bacterium to respond to rapid environmental change and would also help to explain the reduced genome. Testing of these hypotheses may lead to some exciting conclusions in the future.

The opportunity to attend SMBE 2008 also allowed me to present my PhD research on *Rickettsia*. *Rickettsia* are most noted for causing arthropod-vectored human diseases but my work has expanded on what is known about the genus *Rickettsia* as a whole. I have uncovered at least 20 new species of *Rickettsia* from arthropod DNA and used a multi locus strain typing (MLST) approach to show how *Rickettsia* spread and how they are maintained in arthropod populations. In addition I have uncovered a strain that shows that the arthropod vectored vertebrate pathogens and purely arthropod strains recombine. This has important implications for the evolution of disease as beneficial genes can sweep through different genetic backgrounds and bacterial species, which has in some cases, been shown to increase bacterial pathogenicity. I was pleased with the audience that my poster attracted and encouraged that people in the field of reductive evolution were also interested. Although my poster didn't target this audience, it has implications for this research, as horizontal gene transfer in *Rickettsia* suggests that it may be more efficient than previously thought in purging deleterious mutations. The reduced ability to do this in endosymbionts is thought to be one of the key reasons that the mutation rate is higher than in free-living bacteria.

In conclusion, SMBE 2008 was a very productive meeting and conveyed lots of exciting avenues for further research. I would therefore like to thank the James Rennie Bequest to whom I am completely indebted for travel expenses.