

2/10/00  
*Antonis Rokas*  
*I.C.A.P.B.*

## **Report for James Rennie Bequest**

On June 2000 James Rennie Bequest granted me the amount of £300 for covering my travelling expenses for participation in the "Workshop on Molecular Evolution" at the Marine Biological Laboratory, Woods Hole, Massachusetts, U.S.A. My trip included participation in the "Extended Topics Session" of the workshop. My flight ticket cost £411 so the amount given significantly contributed towards covering my travelling expenses to the U.S. The choice of participating in this workshop was correct. Most topics covered are areas of research I actively pursue in my Ph.D. here in Edinburgh.

More specifically, the first week of the workshop was devoted to the theory of molecular evolution with particular emphasis on (molecular) phylogenetics. William Pearson (University of Virginia) covered the issue of DNA and protein sequence alignment and demonstrated his program FASTA, which is designed for efficient retrieval of DNA (or protein sequences) from databanks. Joe Felsenstein (University of Washington) and Paul Lewis (University of Connecticut) spoke about how to use maximum likelihood for reconstructing phylogenies, with Paul Lewis also covering the interesting area of genetic algorithms and Markov Chain Monte Carlo simulations. More on the last topic was delivered by John Huelsenbeck, who spoke extensively about the application of Bayesian statistics to phylogenetic problems. Having recently commented on one of his recent papers (Rokas, A. and McVean, G. 2000. A Bayesian guide to tree felling, *TREE* 15: 396), it was very profitable talking with him about the Bayesian method as well as about the phylogenetic position of Strepsipteran insects, a topic that both of us have published studies on (Huelsenbeck, J.P. 1998 *Syst. Biol.* 47:519-537; Rokas, A. et al. *Insect Mol. Biol.* 8:527-530).

Apart from the "theoretical molecular evolution" talks and practicals, there were a series of lectures from people who are working on experimental molecular evolution. I thoroughly enjoyed Anne Yoder's (University of Chicago) talk about the

phylogeny and phylogeography of mammals in Madagascar with special emphasis in lemurs. Scott Edwards (University of Washington) also gave a superb lecture covering topics that are central in my Ph.D. such as comparative phylogeography (alas in birds). There were also two talks in evolutionary genomics. Claire Fraser (The Institute of Genomic Research) gave a brilliant overview of the field of genomics and the rate of progress as well as about their attempt to construct an organism with a "minimal" genome. Jonathan Eisen (The Institute of Genomic Research) spoke about how you can use phylogenetics as a tool for genomic analysis and characterisation of open reading frames. He is also responsible for the complete sequencing of the bacterium *Wolbachia*, which I am also studying in Edinburgh (see my previous application for funding from James Rennie Bequest) and I had an interesting conversation with him concerning phylogenetics of *Wolbachia* strains. The genomics talks were particularly interesting, especially for the entirely different scale of data collection and handling.

The two most important contacts I made were with Nipam Patel (University of Chicago) and with Dave Swofford (Smithsonian Institution). Patel gave a very interesting talk on evolution of regulatory elements, an area that I am very attracted to and thinking of doing my post-doc in. He showed interest in my work and ideas and invited me in Chicago (offering to pay a substantial amount of my travel expenses) for a more formal discussion and visit, as well as for a potential collaboration before the end of my Ph.D.). I am already planning to visit his lab during early next year. Swofford did a splendid presentation of his phylogenetic analysis software PAUP. Although I was a user of PAUP before I went to this workshop, I had the opportunity to learn a lot more on how to use the program and ask specific questions about certain of its features. Additionally we talked a lot concerning the debate between the use of statistical (i.e. maximum likelihood and Bayesian) versus parsimony methods for phylogenetics.

The third week of the course was devoted to analysis of my own data sets under the guidance of the Teaching assistants and the Course director Mike Cummings. They offered us a lot of computers and I was able to run some very intensive analyses in a reasonable amount of time. Additionally I had the chance to implement a few tips that the faculty told me in my analyses. During the week I managed to almost complete the analysis of the second first-author paper produced from my Ph.D. thesis which I am now preparing for submission (Rokas *et al.* A

maximum likelihood analysis of eight phylogenetic markers using gallwasps (Hymenoptera; Cynipidae); implications for insect phylogenetic studies, to be submitted in *Molecular Phylogenetics and Evolution*).

The informal style of the workshop and the relatively small number of participants gave me the opportunity to discuss phylogenetic “hot topics” extensively. Additionally I had the opportunity to get reprints from a few *in press* or *in preparation* manuscripts from faculty/students who work on areas within my interest. Two particularly useful ones were: a. one from Peter-Klaus Koepfli (UCLA) who has done the same type of analysis as I have done for gallwasps (see above) but in a group of rodents (in preparation), and b. one from Scott Edwards and Peter Beerli (University of Washington), who discuss the difference between gene divergence and population divergence for comparative phylogeography studies (to appear as a Perspective in *Evolution*). My presence was appreciated from the Workshop organiser and the faculty. I have already received an offer from the workshop director (Mike Cummings) to participate in next year’s course as a teaching assistant.

I would like to express my gratitude for your support in my participation in this workshop. It was a great scientific and social experience!

With Kind Regards,

Antonios Rokas

