

## JAMES RENNIE BEQUEST

### REPORT ON EXPEDITION/PROJECT/CONFERENCE

**Expedition/Project/Conference Title: 10th Congress of the European Society for Evolutionary Biology (ESEB)**

**Travel Dates: 15 - 20 August 2005** .....

**Location: Krakow, Poland** .....

**Group Member(s): Katalin Csillery** .....

**Aims:** (i) learn about recent applications of pedigree and marker-based relatedness estimates in natural populations and (ii) get feedback on my work, (iii) learn about the new advances in Approximate Bayesian Computation .....

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#### **OUTCOME (not less than 300 words):-**

The Congress of the European Society for Evolutionary Biology (ESEB) is the largest meeting in evolutionary biology in Europe organized every other year to bring together scientists from all over Europe and overseas as well. In 2005 the conference was organized by the Institute of Environmental Sciences at the Jagiellonian University, Krakow, Poland. The conference was organized very efficiently even though the organizers had to face the challenge of transporting over thousand people, an unusually large number of participants. I particularly welcomed one aspect of the organization. That is, the talks were organized in symposia by one or two leading scientists of a subject area, whose job was to select speakers for invited talks and also bring the whole program together, as opposed to conferences, where the organizers decide on the sessions after registration. As a result some symposia may have seemed too specific for the first sight, but in practice, symposia, at least the ones that I attended, were integrated and well structured.

The conference has proved to be very useful to me for many reasons. Perhaps most importantly, I had a chance to present my MSc thesis (MSc/Diploma in Quantitative Genetics and Genome Analysis) in the form of a poster. I received some very useful comments that will certainly help me to write up my thesis as manuscript. My poster summarized results on evaluating the performance of marker-based relatedness estimators by directly comparing them with the traditional method, which is calculating relatedness from pedigrees. I used data sets of four natural populations, where both type of information, marker data and pedigree, were available. The author of one of the relatedness estimation methods (Jinliang Wang, Institute of Zoology, UK) has made comments about the statistics I used for the improvement of my work. Also, my work would be more general if based on a wider range of data sets and, fortunately, I met potential collaborators who might be able to provide me additional data set.

The symposium "Evolutionary dynamics of phenotypic traits in wild populations" offered a wide range of talks amongst many illustrated the widespread use of pedigrees and marker-based relatedness estimators, which is a great interest of mine. The symposium brought together researchers who are quantifying selection pressures, heritable variation and the evolutionary dynamics of life history, morphological or behavioural traits in natural environments. Perhaps one of the most exciting advances is quantitative trait locus mapping in natural populations, which was illustrated by Jon Slate's talk (University of Sheffield, UK).

Another symposium was organised to focus on the problem of estimating demographic and other ecological parameters from genetic data. Likelihood-based methods are often restricted to relatively simple models. New progress based on computationally intensive simulations may allow one to estimate parameters and use models of almost arbitrary complexity. The method is called Approximate Bayesian Computation and is one of my current research interests. The symposium provided good balanced mixture of theoretical and applied talks. I particularly enjoyed the talks by David Balding (Imperial College, UK) and Arnaud Estoup (INRA, France), and also the discussions following them as they highlighted some of the potential pitfalls of the method.