Completion Report for BSAS Scholarships

Name and affiliation: Duncan Marriott, UWE Bristol

Award Name and value of the award: Alan Robertson, £345

Was any additional funding secured to support the activity?
(If yes, please state the value and source of funding): Approximately £120 for travel. Paid from PhD funding.

Start/end date of the award: 14th – 16th May 2012

Summary of the award (Briefly describe the objectives and how was it undertaken):
(approximately 300 words)

The objective was to attend the 'Open Door Workshop' held at the Sanger Institute, Cambridge, UK. This was to further the applicant's knowledge of online and freely available bioinformatic tools and databases. This knowledge would save the applicant spending project funding on expensive commercial software and also improve the quantity and quality of the results generated from their research project. The knowledge gained would be distributed to other scientists both within the applicant's home institution and in the larger scientific community, at national and international meetings and conferences. The course was intensive and therefore a large amount of material was covered in a short space of time. However, it was presented in a way that made it easy to follow, backed up with a detailed course manual and friendly instructors that were readily available throughout the course. As the course was residential, it gave the opportunity to socialise with other researchers on the course. This was particularly interesting as most of them worked in human rather than animal research although we found plenty of common ground in our work and discussed different approaches to particular research questions. Since attending the course I have been to meetings in Edinburgh, Bratislava and Beijing where I have discussed what I have learned from the course with other British and international animal scientists. I have also presented results generated using the knowledge gained from the course. In addition, the course was a great opportunity to visit the world-famous Sanger Institute and fortunately the course included a tour around the site. It was inspirational to see the vast scale of DNA sequencing that was going on and to see first-hand the sequencing methods that made it possible to generate the large online databases that the course covered.

Benefits of the Award:

This is the main part of the report and the two sections below should be approximately 1000 words in total. You may focus on benefits to yourself, to the animal science community, or both – depending on the nature of the activity undertaken.

Benefit of the award to you (e.g. new knowledge or skills, new contacts and collaborations):

As mentioned above, the course covered a large amount of material that was largely new to me. It was taught at exactly the right level for me so that I didn't get lost in the wealth of information but still managed to cover a huge amount in a relatively short space of time. The majority of the course covered online nucleic acid and protein databases. Before the course I had some understanding of these databases, specifically for looking at coding regions of genes. This knowledge was greatly enhanced during the course regarding both the types of database available (and how they overlap) and the huge amount of information they can display. Bioinformatics databases are relatively difficult to understand if you have never used them before and although there is online help available, it's still hard work to learn what all the information displayed actually means. The course made learning much easier by providing computer-based tasks to work through step-by-step. The course tutors were extremely knowledgeable as they actually work at Sanger annotating the database entries. During a conversation with one of the tutors, I learned that the pig genome (on which my PhD is based) was being annotated by them. They even offered to prioritise any genes I was interested in. The importance of- and interest in the major histocompatability complex (MHC) was highlighted and has given me ideas for future research in pigs, possibly as a collaboration with the Sanger Institute.

One important skill that I picked up during the course was how to compare your own DNA sequence with those in the various online databases. This is extremely useful for seeing how your animals differ genetically to those studied previously, possibly in different countries and different breeds. The course taught how this can be done purely through open access websites, with no need for software programs. I have already put this knowledge to extensive use in detecting single nucleotide polymorphisms (SNPs) within the population of pigs I have been studying for my PhD.

It was also demonstrated how genomes can be compared between species to estimate how closely related different breeds and species are, and even which part of the world they originated. This type of application is a fascinating example of how genetic data can be analysed in great detail without the need to use the laboratory (beyond the initial sequencing of genetic material). The results of such a study on the pig genome have recently been published, giving new information on exactly how a modern commercial pig breed relates to its wild boar ancestors (Nature 491 pp391-398). One of the papers authors was a tutor on the course, further demonstrating the high level of knowledge that they had.

Benefit of the award to the animal science community, academic and industrial:

The course attendees were almost exclusively researchers in human disease. As part of the course we all had to give a short presentation about our work and I described my project on discovering genetic markers related to intramuscular fat deposition in pigs and how the results could be used to develop a genetic test for marker-assisted breeding. Several people came up to me afterwards interested in my project and were surprised that research in animal breeding was as cutting edge as that for human disease. Therefore I feel my attendance has promoted the animal sciences within the greater scientific community and could lead to greater collaboration in the future between the fields.

The course notes are well written in an easy to follow manner. They are freely accessible on the Sanger Institute website so whenever I meet a researcher working with sequencing I point them in the direction of these notes so they can teach themselves the skills I have learned. If and when I have the opportunity, I show people in person what I have learned as the easiest way to understand how these web-based resources is to have them open in front of you during the explanation. As mentioned previously, since attending the course I have been to a number of meetings (and continue to do so) where I have both presented results generated using the knowledge from the course and also spoken with other animal scientists and shared this knowledge.

Regarding the benefit to industry, greater knowledge of the skills taught from the course amongst the animal scientist community will improve the depth and breadth of genetic research possible, as well as improving the efficiency and therefore cost of this research. This gives better value for money for industrial investment in external genetic research. Industry will also benefit from government-funded research as the results of this research (i.e. novel genetic markers) are commonly published and presented openly. This allows industry free access to these discoveries which they can then use to improve phenotypes of food animals. Greater emphasis is now being given to marker-assisted breeding as a method of tackling not just the challenge of ensuring consistent quality but also improving feed efficiency, breeding efficiency and reducing emissions.

Other supporting information:

Course materials are accessible here:
http://www.sanger.ac.uk/resources/talksandtraining/opendoor/uruguay.html under 'course materials'. The course materials in this link are the same as the course I attended.