Completion Report for BSAS Scholarships

Name and affiliation:

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Award Name and value of the award:

BSAS Scholarship – Alan Robertson

Was any additional funding secured to support the activity?

Yes, £112 for transport, supported by the applicant's current BBSRC grant

Start/end date of the award: May 15th -17th, 2013

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

(approximately 300 words)

The objective was to attend the 2013 Sanger Institute Applied Bioinformatics & Public Health Microbiology Conference in order to further the applicant's knowledge of bioinformatics and genome sequencing and their potential use in animal health. This conference focused on communicating the many applications of whole genome sequencing of pathogens of humans and animals in public health. Whole genome sequencing is novel and allows the study of bacterial populations in a way that was never before imaginable.

One of the applications for whole genome sequencing is to study the microbiome; this is the collective genomes of the microbes that live inside and upon the body. Whole genome sequencing allows the rapid study of bacteria and to be able to compare different bacteria or bacterial populations within a specific niche. This technique can be used to study the role of the host microbiota in the resistance to infection in animals.

The applicant is currently working on a project investigating the chicken gut microbiota and its role in the susceptibility of chickens to colonisation by *Campylobacter.* The hypothesis is that the chicken gut microbial communities may be involved in the susceptibility of chicken to colonisation by *Campylobacter*.

The conference allowed the applicant to learn how it is possible now more than ever to examine poultry microbial ecosystems and see the potential for the exploration of chicken gut microbiota as a tool to enhance animal health. Use of whole genome sequencing to study chicken microbiota will permit the study of this interaction on a mass scale and be able to investigate whether factors such as breed, rearing systems, diet or welfare have an impact on the microbiota and its interaction with *Campylobacter.*

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):

Technology in the field of genomics has greatly advanced in the last few years and this conference allowed me to get up to speed with the latest developments in next generation sequencing and to explore the many potential uses of this recent and increasingly popular sequencing method.

I learned about the different platforms available for the study of gut microbiota. The gut microbiota is very important in animal health as it can affect an animal's interaction with pathogens and their susceptibility to infection. This subsequently has an impact on animal health, productivity and welfare.

I also learned from the course about a technology platform called TraDis (Transposon Directed Insertion site Sequencing) which can be applied to study animal pathogens. This sort of technique allows parallel sequencing of bacterial genomes and is combined with traditional transposon mutagenesis in order to identify putative gene functions in a high-throughput manner. This was very valuable information for me as I am planning to apply for funds to use TraDis to study pathogens in the food production chain in order to see if the biology of the pathogen present in the animals at the farm is the same as that of those in their meat products in the market.

I have become more familiar with high-throughput genotyping platforms and bioinformatics, and also with the principles of interpreting next-generation sequencing data. After the course I feel more confident that I understand the information generated in our experiments and that I will be able to interpret faster and to a greater extent than with my previous experience. This will assist me greatly in interpreting the bacteria community data and its role in colonisation by *Campylobacter*.

I also learned about the application of new technologies to study disease outbreaks. The majority of the presentations focused on bacterial outbreaks that affected humans, but these can easily be applied to disease outbreaks in animals too.

The conference was an excellent opportunity to interact with staff from the Sanger Institute, which is a world leader in genomic research and I have had the opportunity to meet and interact with other researchers working on *Campylobacter* in chickens. They were using next generation sequencing to look at whether bacteria present in chicken at the farm, at the retailer or in the human patient with campylobacteriosis were actually the same or whether there was a "selection" for specific genotypes with time. This was very interesting to me as I would like to do a similar study in the ready to eat meat food chain. There is also the possibility that we may be able to collaborate in the future, benefitting both our research groups and institutions.

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

From a food safety point of view, the interaction of chickens with *Campylobacter* is one of the most important bacterial interactions in the poultry industry as consumption of chicken meat contaminated with *Campylobacter* is currently one of the main causes of gastroenteritis in humans in the UK. Reducing *Campylobacter* colonisation is important for the chicken host and for humans. Reduced infection will improve consumer confidence in eating chicken which in turn will boost sales and therefore benefit the British poultry industry. There are also potential benefits for the NHS and UK industry in terms of lower disease burden and fewer days off work.

These new genomic technologies allow the study of large microbial communities directly in their natural environment and this is very important when studying the chicken microbiota. These studies can yield important information about the populations of microbes associated with the animal and their role in disease and this is what we want to determine in our current research project on *Campylobacter* in chickens. This can be transferable to other animal species where the microbiota also play an important role in the animal's health and resistance to infection. So far this technology has been used to determine species composition in the gut microbiota but this technology can generate even more information such as gene expression and the role of the bacteria in the gut health and function. With greater knowledge of the bacteria-host interaction, it will be possible to reduce the need for pharmaceutical products in livestock production, thereby reducing costs for the producer and avoiding the development of bacterial resistance to those products.

Although the conference focused on the use of this technology in bacterial genomes, this technology is also being applied to animal genomes. With next generation sequencing technologies it is now feasible to implement genomic prediction based on complete genome sequences of higher organisms. Next generation sequencing will be very relevant for animal genetics as association mapping across genomes will provide a new insight into topics such as species' adaption. Whole genome sequencing could be used for fingerprinting, net merit or marker-assisted breeding, which will be very useful in animal production. Marker-assisted breeding in particular is becoming more and more relevant due to the increasing environmental pressures of feed supply and cost, and emissions associated with animal production. Breeding towards more efficient genotypes is essential for the food animal industry to remain sustainable. Whole-genome sequencing information can assist in identifying or selecting progeny with traits of interest and it is speculated that farm animals breeding programs using this technique are likely to be adopted in the next couple of decades.

The knowledge I gained from attending this conference will be disseminated to the animal science community as I further incorporate next-generation sequencing into my current and future projects, and present the methodology and findings at international meetings. Attendance at these meetings will also give the opportunity for me to interact with other scientists and give them the benefit of my new-found knowledge.

Other supporting information: