



NEWSLETTER

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Terry Miller (Primary Industries and Regional Development, Western Australia) collecting freshwater fishes in the Cairns region for parasite discovery from endemic and exotic origins with fellow ASP member Rob Adlard (Queensland Museum). Photo credit Rob Adlard and Terry Miller

Shazia Ruybal Pesántez of the Bio21 Institute at the University of Melbourne reports on a fruitful trip to the USA and Ecuador.

Thanks to the generous support of the Australian Society for Parasitology through the JD Smyth Postgraduate Travel Award, I was able to travel to the American Society of Tropical Medicine & Hygiene (ASTMH) Annual Meeting in Baltimore, USA and following this, to partake in a researcher exchange in the laboratory of Dr. Fabian Saenz in Quito, Ecuador.

The ASTMH Annual Meeting was held in Baltimore from the 5th to 9th of November, 2017. It is the largest gathering of scientists, public health, industry and government professionals working on global health and infectious diseases with over 4,400 participants from over 100 countries. I was selected to present in the ASTMH Young Investigator Award (YIA) Presentations alongside an international pool of promising young scientists as well as in the regular ASTMH Poster Sessions. I presented my abstract entitled "Var code: a new molecular epidemiology tool for monitoring *Plasmodium falciparum* in a high transmission setting of Ghana, West Africa", consisting of the major results of my PhD thesis, including laboratory and analytical methods recently published in Scientific Reports in September 2017 and unpublished results currently being written up. The selection process for the YIA was based on my abstract and the potential impact of my PhD findings to the malaria field and is highly competitive. Overall, I received considerable exposure to leading malaria researchers and experts in the field and importantly, I received positive feedback on my work as well as had the opportunity to discuss possible postdoctoral opportunities upon my graduation. I have now incorporated several important suggestions from the feedback I received, including new ways to discuss our results in light of cutting-

edge research and novel results from other studies that were presented at this meeting, to improve my manuscript that is close to submission.

Following the ASTMH conference, I traveled to Quito, Ecuador from 13th November 2017 - 14th February 2018 to partake in a researcher exchange in the laboratory of Dr. Fabián Sáenz at the Center for Research on Health in Latin America (CISeAL) at the Pontifical Catholic University. The aim of this exchange was to apply the "var code" to examine *Plasmodium falciparum* malaria parasite populations in Latin America for the first time, specifically in Ecuador where countrywide malaria elimination is being attempted. The "var code", a novel and cost-effective molecular epidemiology tool under development as a direct result of my PhD work, can be applied to genetically fingerprint parasite isolates using var genes, the genes encoding the major variant surface antigen involved in immune evasion, as biomarkers for surveillance. The work from this collaborative research project represents a novel examination of malaria parasite populations in Ecuador using molecular and genetic tools that are not traditionally used for malaria surveillance in Latin America.

When I first arrived I focused on capacity building at CISeAL involving the specific training of the Sáenz laboratory members (MSc and PhD students) on the laboratory protocols and the population genomic analytical framework we have developed in Prof. Day's Research Group at Bio21 Institute/ University of Melbourne (Bio21/UoM) to process parasite isolates collected in the field, focusing on our specific protocols to avoid cross-contamination of field isolates and ensure repeatability and consistency for subsequent epidemiologic analyses. I also presented a series of short lab talks on various topics related to *P. falciparum* var genes, epidemiological var studies, and the applications of the var code, since this is not their area of expertise. This worked out well since there were unforeseen delays in receiving the reagents we needed to complete the laboratory work.

Following this, I genotyped the var genes of Ecuadorian *P. falciparum* isolates that Dr. Sáenz and his research group collected during a malaria outbreak in the coast of Ecuador from 2013-2015. Intriguingly, Ecuador had declared that they were in a malaria pre-elimination phase when *P. falciparum* malaria cases reached a striking low after



2012. Yet in 2013 there was a national malaria outbreak and there has been a considerable spike in *P. falciparum* cases since then. We have the unique opportunity to examine parasite isolates collected during this outbreak.

Towards the end of my exchange, I was invited to give a seminar to CISEAL and all institute members including laboratory heads, principal investigators, undergraduate and postgraduate students. My talk entitled “¿Por qué es difícil controlar la malaria?/ Why is it difficult to control malaria?” was well received. One attendee, a former official from the Ministry of Public Health in Ecuador who was very interested in the applications of the var code and overall scientific findings from my PhD work for malaria surveillance in Ecuador. This talk was live streamed to other institute members and the CISEAL collaborating institution, Ohio University, USA.

Now, we are currently in the process of sending the samples genotyped in Ecuador for illumina high-throughput sequencing that will be completed here in Melbourne since my return.

This exchange has facilitated the establishment of an ongoing collaboration between the research



groups at CISEAL and Bio21/UoM. Discussions that took place during my exchange have led to new lines of inquiry into this project and relevant questions that need to be answered, which were a direct result of combining their expertise in malaria epidemiology in Latin America and our expertise in genetic epidemiology and population genetics of malaria. We are currently exploring ways in which we can disseminate the results from this work to the malaria community as well as the broader infectious diseases (ID) community. We are also encouraging new avenues for collaborations between the broader ID community in Ecuador/Latin America through CISEAL and Australian researchers interested in conducting ID research in Latin America by circulating information about the 5th International Meeting of Research in Infectious Diseases and Tropical Medicine, to be held at CISEAL in late 2018.

During my exchange, I was also able to successfully network with the broader ID community at other top universities and institutions in Ecuador and disseminate my PhD work through several presentations. I was invited to speak at the highly-regarded University of San Francisco of Quito. Additionally, I was invited to give a talk on malaria at the Ecuadorian Red Cross National Blood Center and lead a training workshop for the laboratory technicians on PCR techniques for their donor blood screening protocols. The blood center is interested in examining the risk of transfusion-transmitted malaria in Ecuador since it hasn't been investigated before. Following these discussions, we are exploring the possibility of applying for a grant through Roche that will fund a pilot study in Ecuador to assess the prevalence of malaria parasites in blood donor samples. Furthermore, I was invited to work as a malaria field epidemiology consultant for the Tropical Medicine Disease Outbreak Team from the Central University of Ecuador, as they were responding to a serious malaria outbreak in the Ecuadorian coast and collecting samples for subsequent genetic and laboratory analyses. Unfortunately, due

to bomb threats, I was unable to attend, however, we have continued to explore ways to collaborate and for me to provide my genetic epidemiology expertise upon my return to Melbourne.

Overall this exchange was extremely productive and successful. I acquired important skills in communicating my scientific findings to different audiences (and communicating them in Spanish), developing and leading training workshops, as well as establishing important contacts and possible opportunities for future collaborations. The success of the exchange at CISEAL would not be possible without Dr. Fabián Sáenz and his lab members who opened their doors and welcomed this collaboration. Particularly, Ms. Claudia Vera-Arias was extremely helpful in providing all the necessary equipment, reagents and worked alongside me during the genotyping of the samples. In addition, Dr. Saenz and his wealth of knowledge of malaria epidemiology and elimination efforts in Ecuador, has been invaluable for discussions on how to write up the findings from this work to be useful for publication and dissemination to malaria researchers in Latin America, the broader international malaria community as well as the Ministry of Public Health of Ecuador for use in their future malaria elimination strategies. The insights and results we will obtain from this work will be important to better understand malaria transmission patterns in the region, and provide new ways to monitor the source of new malaria cases in Ecuador and to distinguish whether they are due to local or imported transmission. This will be vital information for malaria elimination campaigns in Ecuador. Importantly, through this work we will also validate a cost-effective molecular epidemiology tool that can be incorporated into existing surveillance systems in the Latin American region.

Next page: more pictures from Shazia's exchange to the USA and Ecuador.

