

Overseas Practice on (Field Epidemiology • Collaborative

Research) report form (For Student)

2015/10/22 (Year/Month/Day)

Name	Oroszlany Balazs
Laboratory	Toxicology
Year (Grade)	D4
Place of practice	Arizona State University (ASU), Tempe, Arizona, USA
Period of practice	2015/10/03~2015/10/21
Purpose	To learn the basics of bioinformatics through reptilian (Squamata) RNA-Seq data analysis pipelines

Summary of activities (about 800 words, provide photos, tables and figures that clearly show the activities during the period)

While genomics became the base of nearly every field of biomedical research, the number of available reptilian genomes (even with recent year's progresses) is still only one digit. This lack of information makes harder to work with reptilian species, and empathizes the importance of Next Generation Sequencing (NGS) techniques. Due to the rapidly evolving and changing bioinformatics tools and pipelines, the easiest way to learn the state-of-the-art of the NGS field is to gain hands-on experience in a laboratory where NGS and data analysis is a central element.

Professor Kenro Kusumi's laboratory at the Arizona State University is one of these leading groups, especially in the field of reptile genetics. While their main focus of interest is the *Anole* lizard family, with regard of development and regeneration, their work also includes tortoises, with the first annotated tortoise genome, the desert tortoise (*Gopherus agassizii*) is prepared for publication, and amphibians – the whole genetic data of the African clawed frog (*Xenopus laevis*) will be invaluable for all researches working with *Xenopus* as a laboratory animal.

Also, while there are larger laboratories working with similar themes, Professor Kusumi's small but very effective team ensures that all members have a good overlook of the whole research method.

These were the two main reasons why I've approached Professor Kusumi for a short visit to get a glimpse how to work with NGS data.



The postgraduate room and the laboratory

My weekdays were focusing on the computer works – with the help of Mariana Grizante, John Cornelius, Juan Rodriguez, Cindy Xu and Minami Tokuyama. I've covered the *in silico* part of generating and handling NGS data.

I've started with an introduction to the command line, and by learning the basics of operating a Unix-based OS. This involved installing the necessary bioinformatics tools on a virtual machine, acquiring the basics of data management, and the very first steps of shell scripting.

After the basics, I've followed Dr. Elizabeth Hutchins's (a former postdoc) workshop tutorial, and with the help of the Anolis data (and, more importantly, Juan Rodriguez), I've learned how to conduct differential gene and transcript expression analysis of RNA-seq experiments with TopHat and Cufflinks. While the data we used were from normal samples, the same method would reveal the up- and downregulations of the genes that are involved in the metabolic reactions in an exposure study.

Parallel to this tutorial, with Mariana Grizante, we were learning about using BLAST locally, a very useful method to work with local data not yet uploaded in the global databases.

My schedule allowed me to visit the Molecular & Cellular Biology Graduate Retreat, an event similar to our SASSOH meeting, and a luncheon seminar by the Center for Evolution and Medicine, a newly established research group with human-health centered interdisciplinary approaches not dissimilar to the One Health initiative.

I also had the opportunity to attend classes, and to discuss and present my research not only with the Kusumi group, but also with Professor Melissa Wilson Sayres and Professor Dale Denardo.



Poster session of the Molecular & Cellular Biology Graduate Retreat (left) and seminar by the Center for Evolution (right).

Screenshot is from the Center's Twitter feed – all institutes of the university have a strong social media presence.

During the weekends I was introduced to the nature and wildlife of Arizona. I've visited the Boyce Thompson Arboretum, participated on a one-day trip to the Grand Canyon, and joined Professor Brian Sullivan and his wife with their desert tortoise and horned lizard study where they use radiolocation to follow the movement of these two desert reptile species.

Professor Kenro Kusumi was a generous host, and all of the lab members were extremely helpful, letting me turn this short visit into a valuable learning experience.

This two weeks also allowed me to glance into the everyday life of a leading American research institute. If I have to concentrate my impression in just two words, I have learned what *relaxed professionalism* means.

Regarding everyday life my biggest concern before leaving to the US was accommodation and transportation – fortunately Tempe, as a university city, was not as automobile-centered as I feared, and I could find a room within 15 minutes' walk from the Campus. Also, the multicultural neighborhood around and inside the university let me try new tastes every day.



Wildlife of Arizona. Upper row: the reptiles. Western diamond-backed rattlesnake, desert tortoise and horned lizard. The later two animals are carrying Professor Sullivan's radio transmitters. Lower row: Greater roadrunner and elk.

Coming back to Hokkaido University, I immediately started looking for opportunities to use what I have learned at ASU. I realized that while in the near future I won't be able to use NGS on my target species (due to ingredient cost), the publicly available sequence data from various reptile species allows me to look into the variety and evolution of xenobiotic metabolism enzymes in this class of animals.

During my short visit, I was not only filled with the warmth of the Arizonan Sun, but with inspiration and enthusiasm to choose new paths to my research.

I would like to thank all the professors and students at the Arizona State University and the Leading Program to allow me this opportunity.

(Field Epidemiology • Collaborative Research) Evaluation by supervisor

Institution • Official title • Name	印
Describe overall evaluation on the applicant's activity in overseas practice.	

- ※1 Send the electronic file to the Leading School section, International Affairs Office, also submit the original print out with seal of supervisor to the Leading School section, International Affairs Office.
- ※2 The Steering Committee of the Leading Program will first confirm the content of this report and the report will be forwarded to the Educational Affairs Committee for credits evaluation.

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Ext: 9545 e-mail: leading@vetmed.hokudai.ac.jp