

The report of SMBE 2016 conference

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The Society for Molecular Biology and Evolution (SMBE) Conference 2016 was held at the Gold Coast Convention & Exhibition Centre, Queensland Australia, from 3 - 7 July 2016. The SMBE is one of the largest society related to evolutionary biology in the world, and leading researchers from many countries attended the meeting. Overall, I enjoyed discussions with researchers attended the meeting and many exciting presentations by them.

In my project, I have been analyzing a heterogeneous mouse population and selective breeding mediated genetic mapping for tameness. I have been investigated the evolutionary consequence in the mouse genome via the selective breeding. The mouse stock I used is Wild-derived heterogeneous stock which has been made by crossing eight wild strains originated from various place in the world. Since the stock has a diversity in tameness, I performed selective breeding for active tameness, one type of tameness (another tameness is passive tameness). As a result of selective breeding, I successfully made a mouse population in which mice exhibit high level of tameness. As a next step, I conducted genomic analysis to detect selected locus where selective sweep (the reduction or elimination of variation among the nucleotides in neighboring DNA of a mutation) could be observed. I utilized a simulation to detect the sweep via the estimation maximum allele frequency by using a simulation with non-selection model. After the analyses, I found two candidate selected loci from MSM strain, one of the founder strain of *Mus musculus musculus* subspecies, which is significantly increased in allele frequency compared to the estimated maximum allele frequency. Additionally, by using the association analysis between phenotype and the number of MSM haplotype, I confirmed the region with significant association within the selected loci. Furthermore, using the mouse genomics informatics database (MGI), I searched the candidate genes within the detected SNP and performed the comparative genomic analyses between mouse and dog, which is one of the major domesticated animal and shows tameness. In the meeting, I presented these results in a poster presentation. Given that I have found only two genetic loci related to active tameness even though association of multiple loci is assumed, I expected to get idea to find more genetic loci for this phenotype.

Attending the conference was useful experience to me because it stimulated my idea via the presentation and discussions with the leading researchers and helped to

deepen my understanding in evolutionary and behavioral genetics. Especially three topics were worth reporting in this report. First, a detection method of selective sweep, the Singleton Density Score (SDS), was presented by Jonathan Pritchard from Stanford University in USA. It is a powerful measure to infer very recent changes in allele frequencies from contemporary genome sequences. I will use this statistics for my project to detect additional candidate loci associated with active tameness. I hope the statistics will catch the other candidate regions associated with active tameness.

Second, there was the exciting presentation by a researcher who have researched fox domestication experiment. The experiment is including phenotyping for tameness in red fox and selective breeding for tameness and aggression using the score of phenotyping. The research have been mainly performed by Lyudmila N Trut from the Russian Academy of Sciences in Russia, although currently Anna V Kukekova from University of Illinois in USA is the chief researcher of the project. They used a method, similar to our method, detection of selective sweep on the fox genome via the selective breeding for tameness. However the researchers used no analysis combined information of pedigree and founder genome although our research used the information. They detect some regions associated with tameness, but they did not show the details of the method and the results. In near future they will publish the results, so I willing to wait the paper.

Third, the discussion with other researchers made my researchers soul higher. Some researchers presented clear research question, research answer, and the results. In addition they have published in so called "top journals", such as Nature and Science. In the future I want to become like them.