The report of SWFS 2017 conference

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The Society for Wildlife Forensic Science (SWFS) 2017 meeting has held at the Edinburgh University's John McIntyre Conference Centre, Edinburgh, Scotland during 5-9th June. The SWFS is a society related to forensic science and conservation biology for wild and captive animals. I am interested in the application using my findings for tameness in mice to the conservation biology of wild animals. In the conference, 220 researchers and politicians from over 30 countries attend the meeting. I have discussed with many researches who work at the field of conservation biology and it was a chance to consider how I can apply our findings of tameness in mice to the conservation biology. Overall, I enjoyed discussions with researchers attended the meeting and many exciting presentations by them.

In my project, I have been analyzing a genetically heterogeneous mouse population and selective breeding mediated genetic mapping for tameness. I have been analyzed the selective pressure in mouse genome via the selective breeding for tameness. 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, including *Mus musculus musculus*, *M. m. domesticus*, *M. m. castaneus* subspecies. 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 an association analysis between phenotype and the number of MSM haplotype, I confirmed the region with significant association within the selected loci. Furthermore, using the messenger RNA sequencing, RNA-seq, I try to narrowing down of the candidate genes related to active tameness.

I presented these results in a poster presentation in the meeting. The poster title was “Two genetic loci associated with tame behaviour in mice and its effect on dogs”. In

the presentation, especially I focused on the application to the wildlife conservation using my research project. Attending the conference was useful experience to me because it stimulated my idea via the presentation and discussions with researchers who majored in conservation biology and helped to deepen my understanding for behavioral genetics contributing the conservation biology.

Not relating to conservation biology, but I note that the most exciting discussion was about the Greater cane rat (also called grasscutters), which is a large sized rodents in Ghana, Africa. I discussed with a researcher who research about the novel domestication for grasscutters in Ghana. Meat resources are poorly avairable in Ghana, but recently novel domestication of the grasscutters have been performed for production as a meat. I have considered that my research project potentially applly to the grasscutters project. This is because the candidate gene or genetic region associated with tameness found in my research might be allowed us to select a tame animal in the captive grasscutters population. In the future I will applied my project to the grasscutter domestication.