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Taking advantage of the travel support, I attended the ICCFGG 2024, hosted by the University of Helsinki at Little Finlandia in downtown Helsinki from June 9th to 12th. The ICCFGG was held biennially, alternating between the US and Europe, offering a platform for scientists and clinicians who study inherited diseases, behavioral and morphological traits, evolutionary biology and genomics in dogs and cats. Due to the refurbishment of Finlandia Hall, the conference took place at Little Finlandia, an event and café space adjacent to the Hall, which rendered a relaxing atmosphere. Approximately 250 attendees primarily from Europe and the US participated in the conference, with more than half of the presenters being female. Among the four researchers from Japan, I was the only PhD student. At the conference, I presented my poster on the epidemiological study using medical records data of cats, received valuable feedback and information on my current and future studies, and networked with fellow researchers in this field. This experience expanded my perspective and opened up new opportunities for my future career.



Left: The conference site Little Finlandia in black in front of the grand Finlandia Hall in white, which acts as the temporal site for hosting events.
Right: Attendees were sitting casually in the event site. The posters were in café space next

Approximately 80% of the oral presentations focused on canine studies, demonstrating great width and depth compared to feline studies. Most studies utilized genome-wide analysis based on either case-control or pedigree designs. Two main aspects were particularly beneficial to my

current research. Firstly, I gained valuable insights into establishing a disease model for GWAS. I was amazed that the sample size could reach up to 3000 dogs. However, it was also noted that the power of GWAS does not increase linearly with sample size. One talk that captured my interest in GWAS design was by Prof. Elinor Karlsson from the Broad Institute, who outlined three ways to enhance the power of GWAS: 1) add more samples; 2) use simple traits; 3) focus on highly heritable traits. Points 2 and 3 exactly matched our strategy. Another intriguing presentation was from the Wisdom Panel, a pet healthcare and insurance company which applied within-app questionnaire to gather data from cat owners. If possible, I am keen to apply and expand this idea in a broader scale, incorporating data not only from behavioral and morphological traits but also disease information such as biomarkers and physiological scores. When combined with genotyping, this could facilitate a deeper association study of breed-phenotype-genotype.

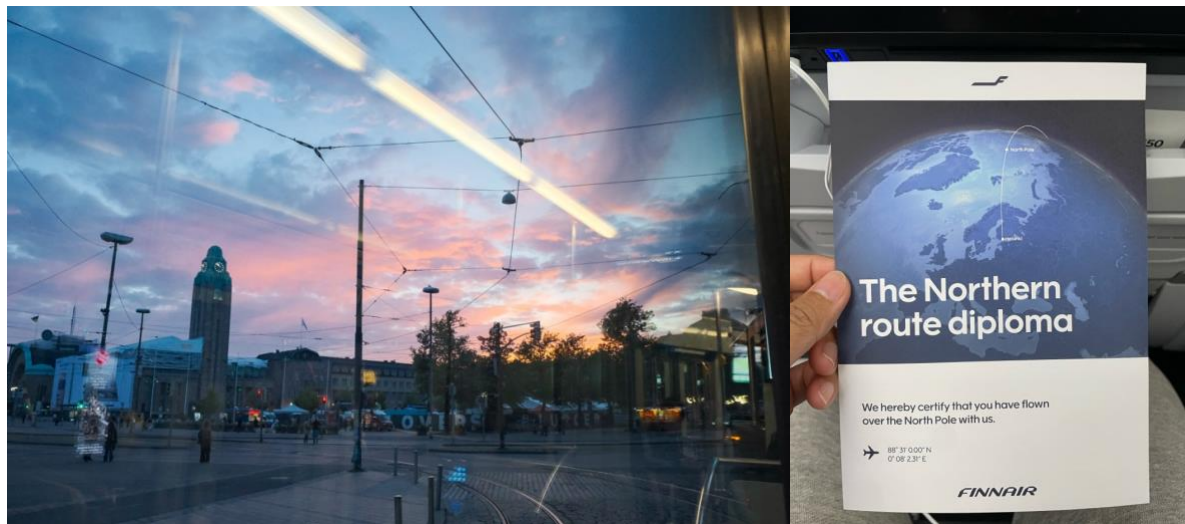
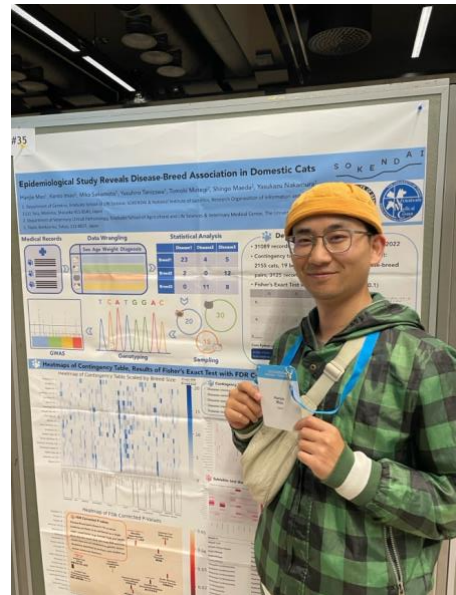


Left: Barnacle goose family swimming freely on the beautiful lake next to Little Finlandia. I was amazed that they were not afraid of human at all.
Right: The symbol architecture Helsinki Cathedral was under refurbishment.

The other area of my interest is the function and role of regulatory regions in feline evolution and pathogenesis. Most studies routinely filter candidate genes by focusing solely on coding sequences (CDS), often ignoring non-coding regions. Only one case study on canine compulsive disorder discussed a potential mutation in the gene flanking region which might affect gene expression. Additionally, in the gene regulation session, the state-of-the-art canine and feline studies were not very satisfying, primarily due to incomplete annotation of regulatory elements (REs), which limited efforts to study the function of REs. I had the opportunity to discuss this with Prof. Carsten Daub and Prof. Guillaume Bourque, who emphasized that technology remains to be advanced not only for identifying and locating REs but also for revealing the connections between REs and genes under their regulation. Despite

the challenges, this session was insightful and greatly augmented my interest in studying regulatory regions.

During the poster session, I presented my poster to a diverse audience, including veterinarians, PhD students, professors and cat breeders. A clinician from Cornell University provided instructive advice on potential future collaborations to expand the data size of medical records. For my study on Bengal cats, I discussed data availability with Prof. Christopher Kaelin from Stanford University and received guidance on processing the lcWGS data. An interesting comment came from Anthony, a renowned Bengal cat breeder and a member of TICA (The International Cat Association). He expressed interest in bringing a Bengal cat from Japan to the US for breeding, since according to my result Bengal cats in Japan are less prone to kidney problems. He also offered to gift me a Bengal cat if I attend the next ICCFGG, which will be hosted by Cornell University in Ithaca, NY two years later. Additionally, I made friends with several PhD students and discussed future opportunities with various professors.



Left: Dusk near the Helsinki station at around 11PM.
Right: The Northern route diploma received from the flight attendant.

Lastly, thanks to the elongated daytime in summer at high latitudes, sunset in Helsinki was quite late, allowing me to explore the city after the conference at “night”. The flight between Tokyo and Helsinki over the Arctic Sea and across the Birling Strait. I was pleasantly surprised to receive a certificate for flying over the North Pole.

From many aspects, my experience in Helsinki was unique and memorable. I am glad of the opportunity to attend ICCFGG 2024, where I presented my work, receive valuable feedback and information, and most importantly, connected with researchers in canine and feline studies. I would like to express my sincere gratitude to Genetic Programs in National Institute of Genetics and Association for Propagation of the Knowledge of Genetics for the generous travel supports, which made this fruitful and unforgettable visit to Finland possible.