（様式２）

令和 4 年度研究助成（海外渡航費）研究成果報告書

令和 4 年 11 月 15 日

公益財団法人遺伝学普及会 代表理事 殿

貴財団より助成のありました研究の成果を下記のとおり報告します。

海外渡航者氏名 Sharlyn Mae Buendia Chua

出席学会等名称 American Society of Human Genetics 2022 Annual Meeting

開 催 場 所 Los Angeles Convention Center

開 催 期 間 令和 4 年 10 月 25 日 ～ 令和 4 年 10 月 29 日

渡 航 期 間 令和 4 年 10 月 24 日 ～ 令和 4 年 10 月 31 日

研 究 成 果 の 概 要

Through the funding of 遺伝学普及会 研究助成, I was able to attend the American Society of Human Genetics 2022 Annual Meeting in Los Angeles. The conference was attended by many clinicians and researchers from all over the world with over 7,000 registrants. It was jam-packed with many different topics on human genetics, and it was a platform to showcase what is new in the genomics community.

I was fortunate that the meeting was face-to-face and that I could watch numerous plenary talks, discuss ideas and questions with other scientists, and present my very own poster. In my poster, I showed how a ciliary transcription factor could affect the regulation of ciliary genes and the prognosis of patients with glioma. There were certain talks and discussion which I find interesting in the way they approached their research. I learned their methods and I intend to try them on my study too.

This conference also gave me a chance to attend meetings with clinical geneticists. In research, we are often focused on one idea and how we can discover something from it. But, attending the said meeting gave me an overview of how the collection of knowledge in research impacts patients in real life. I also became aware of the logistics, security, political, and societal issues that hinders patient access to healthcare. This meeting bridges researchers, physicians, and officials on how to deal with these issues and improve medical management.

All this experience and learning is made possible with the 遺伝学普及会 研究助成 hence, I would like to give my appreciation.

Title

RFX transcription factors regulate genes involved with primary cilium in glioma

Abstract

The brain and spinal tumors derived from the neuron-supporting glial cells called glioma are classified as astrocytoma, oligodendroglioma, and the highest-grade glioblastoma. Glioblastoma cell lines and patient tumors have abnormal primary cilium or lack it entirely. The primary cilium is crucial for glioma proliferation and drug sensitivity as it houses the sensors for extracellular signals and regulates signaling pathways. We hypothesize a gene is causing the defect to the primary cilium, and identifying this gene may have the potential to restore ciliary function. To investigate, we used publicly available ATAC-sequencing, RNA-sequencing, and clinical data of glioma.

We found a ciliary transcription factor Regulatory factor X (RFX) Xbox motif enriched in the active chromatin regions of patients. We also found that *RFX1, RFX2,* and *RFX3* are differentially expressed in patients compared to normal brain samples. The abundance of the Xbox motif indicates that the irregularity of *RFX1-3* expression may affect numerous regulated genes, which our gene ontology analysis showed are essential for ciliogenesis. Furthermore, we show that *RFX1* expression can be a prognostic marker for low-grade glioma patients and can be used to determine high- and low-risk groups. This study provides target genes for manipulating primary cilium formation or length and opens the potential of ciliotherapy as a therapeutic strategy in glioma.