

(For JSPS Fellow)

Form B-2
(FY2018)

Date (日付)
01/02/2019 (Date/Month/Year: 日/月/年)

Activity Report -Science Dialogue Program-
(サイエンス・ダイアログ事業 実施報告書)

- Fellow's name (講師氏名): Chun-Yu LIN (ID No. P17353)
- Participating school (学校名): Aichi Prefectural Kariya High School
- Date (実施日時): 25/01/2019 (Date/Month/Year: 日/月/年)
- Lecture title (講演題目): Bioinformatics, Systems Biology, and Network Biology in Cancer Research
- Name and title of your accompanying person (講義補助者 職・氏名)
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- Lecture format (講演形式):
- ◆Lecture time (講演時間) 110 min (分), Q&A time (質疑応答時間) 30 min (分)
 - ◆Lecture style (ex.: used projector, conducted experiments)
(講演方法 (例: プロジェクター使用による講演、実験・実習の有無など))
used the projector and conducted a board game, "The evolution of cancer: how good cells go bad" (20-25 min), designed by the Department of Oncology, University of Oxford, UK, for illustrating a plausible story of the evolution of a tumor.
- Lecture summary (講演概要): Please summary your lecture 200-500 words.

In this lecture, I briefly introduce myself and my own country, Taiwan. Next, I also shared my motives for becoming a scientist and "The Illustrated Guide to a Ph.D. - explain what a Ph.D. is to new and aspiring graduate students" proposed by Matt Might, a professor in Computer Science at the University of Utah.

Cancer is the second leading cause of death globally. In this lecture, I tried to let students understand "How good cells go bad" via explaining the profound in simple terms and a board game, "The evolution of cancer: how good cells go bad," designed by the Department of Oncology, University of Oxford.

Cancer is a consequence of abnormalities in various cellular processes in a complicated network. As an increasing number of genomic and proteomic data become available, there is a growing need to integrate these data with the biological network for understanding the cancer mechanisms. For example, alterations in some membrane proteins (MPs) and their related pathways have been established as cancer hallmarks and extensively targeted in clinical applications. However, the analysis of MP-interacting proteins and downstream pathways across human malignancies remains challenging. In

the second half of the lecture, I introduced the technologies of microarray and next genome sequencing as well as the strategies from protein-protein interactions to biological networks for establishing the cancer membrane protein-regulated networks. Finally, I used a case to explain how to use the networks to discover the potential biomarker(s) for precision medicine.

- Overall advice or comments to future participants in the program (今後の講師へのアドバイス):

The charts and situational cases are useful and understandable for students. The easy and alternative English vocabularies and sentences are also helpful for students to catch on the lecture contents.

- Other noteworthy information (その他特筆すべき事項):

It is worthy to encourage students to ask and discuss in the lecture.

- Impressions and comments from the accompanying person (講義補助者の方から、本事業に対する意見・感想等がありましたら、お願いいたします。)

For this lecture, I didn't ask for the accompanying person. But I really appreciate all the help given by 齋藤 純先生 and 加藤 ゆき先生 at Aichi Prefectural Kariya High School. They provide great help (e.g., lecture device preparation in advance, lecture content discussion, and translation on Q&A) before and in the lecture.