

様式 A-1
(FY2025)

2025年10月17日

サイエンス・ダイアログ 実施報告書

1. 学校名: 川口市立高等学校
2. 講師氏名: Dr. Elie Marcel TEYSSONNIERE
3. 講義補助者氏名:
4. 実施日時: 2025年10月17日 (金) 13:00~14:30
5. 参加生徒: 理数科2年次生36人、普通科中高一貫コース2年次生6人 (合計 42人)
備考: 普通科中高一貫コース生は希望者、理数科は海外研修事前学習の一環として実施
6. 講義題目: Exploring gene expression regulation in a large population
7. 講義概要: 個体間での遺伝子発現制御の差異は、個体間の生理学的差異の重要な要因であることが知られている。遺伝子発現の不完全な制御は、がんや糖尿病など、多くのヒト疾患の特徴もある。したがって、この制御がどのように機能するかを明確に理解することは極めて重要である。こうした背景から、プロジェクトは、個体間での遺伝子発現制御の差異を探求し、同じ種の個体間の差異の根底にある細胞および遺伝学的メカニズムをより深く解明することを目指している。この目的を達成するために、単細胞真菌である酵母を1,000個体を超える大規模な集団を用いて研究を行っている。
8. 講義形式:
 対面 オンライン (どちらか選択ください。)
 - 1) 講義時間 60分 質疑応答時間 30分
 - 2) 講義方法 (例: プロジェクター使用による講義、実験・実習の有無など)
プロジェクター使用による講義
 - 3) 事前学習
 有 無 (どちらか選択ください。)
使用教材:
9. その他特筆すべき事項:

Form B-2
(FY2025)
Must be typed

Date (日付)
20/10/2025 (Date/Month/Year: 日/月/年)

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

- Fellow's name (講師氏名): TEYSSONNIERE ELIE (ID No.P24378)

- Name and title of the lecture assistant (講義補助者の職・氏名)

- Participating school (学校名): Kawaguchi municipal high school

- Date (実施日時): 17/10/2025

- Lecture title (講義題目): **Exploring gene expression regulation in a large population**

- Lecture format (講義形式):

◆ Onsite • Online (Please choose one.) (対面・オンライン)((どちらか選択ください。))

◆ Lecture time (講義時間) 60min (分), Q&A time (質疑応答時間) 20 min (分)

◆ Lecture style(ex.: used projector, conducted experiments)

(講義方法 (例:プロジェクター使用による講義、実験・実習の有無など))

Projector

- Lecture summary (講義概要): Please summarize your lecture within 200-500 words.

Like all complex organisms, including plants and other animals, humans are made up of individual cells that, despite their specialization in specific organs, have a very similar basic organization and workflow. Each cell contains a nucleus that houses **DNA**. This DNA is a molecule that contains a code with all the information necessary for the cell to function properly and fulfil its role within an organ or tissue. The function of the cell itself is achieved by molecules called **proteins**. These proteins serve to build the cell itself, maintain its basic functions (e.g. energy production and waste elimination) and enable the cell to perform its specific function. For example, the contraction of muscle is driven by the combined action of actin and myosin, which are both proteins. Structurally, each protein is made up of individual building blocks called amino acids, and their precise assembly into a protein is encoded in the DNA. This DNA sequence containing the protein sequence is called a **gene**. Due to the central role of proteins in cell function, their cellular abundance is tightly regulated. This process is achieved through a mechanism called **gene expression**, whereby genes (DNA sequences) are first transcribed (in a process called **transcription**) into an intermediate molecule called **RNA**, which then serves as a basis for protein synthesis in a process called **translation**.

Variations in the regulation of gene expression across individuals are known to be key factors in the physiological differences between them. Faulty regulation of gene expression is also a

hallmark of many human diseases, such as cancer and diabetes. Therefore, it is crucial to clearly understand how this regulation works. In this context, my project aims to explore variation in gene expression regulation across individuals in order to better characterize the cellular and genetic mechanisms underlying differences between individuals from the same species. To achieve this, I am working with yeast, a unicellular fungus, using a large population of over 1,000 individuals. My results demonstrate that gene expression relies on highly complex regulatory mechanisms.

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

- Impressions and comments from the lecture assistant (講義補助者の方から、本プログラムに対する意見・感想等がありましたら、お願いいたします。):

Exploring gene expression regulation in large populations

Élie TEYSSONNIÈRE



JSPS science dialogue
Kawaguchi Municipal High School
October 2025

