

Form B-2  
(FY2020)  
Must be typed

Date (日付)  
12/11/2020 (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): Joonseong Lee (ID No. P19112 )

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

No accompanying person

- Participating school (学校名): Hirano senior high school attached at Osaka kyoiku university

- Date (実施日時): 02/11/2020 (Date/Month/Year: 日/月/年)

- Lecture title (講義題目):

Regulation of gene expression in pluripotent stem cells

- Lecture format (講義形式):

◆Lecture time (講義時間) 40 min (分), Q&A time (質疑応答時間) 10 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))

I used a projector for a lecture. (a power point file)

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

This lecture aims to introduce:

- 1) the process of the development
- 2) an application of induced pluripotent stem cells in biomedical research
- 3) the process and regulation mechanism of gene expression (post-transcriptional modification, especially).
- 4) The basic principles of qRT-PCR (to determine expression levels of mRNAs) and NGS (next generation sequencing) which are broadly used in molecular biology.

During development, cells differentiate to all the different types of cells in the body. Few decade ago, development had been generally considered an irreversible process. However, in 2006, Dr. Yamanaka showed that somatic (differentiated) cells can be reprogrammed to pluripotent states by introducing by defined transcription factors (Oct3/4, Sox2, Klf4, and c-Myc) and generated induced pluripotent stem cells (iPS cells). Since iPS cells are originated from somatic cells, and their derivation does not require destruction of embryos, it can avoid ethical problems. iPS cells have diverse scientific applications. For example, iPS cells can be used to examine the effect of coronavirus (COVID-19) on organs; to identify novel targets that promote survival / kills cancer cells; to make tissues.

Gene expression is the process the synthesis of a functional gene product, proteins. mRNA is transcribed by RNA polymerase and mRNA is translated by protein. Thus, mRNA levels, which are a direct reflection of gene expression. Single-stranded RNA molecules fold into complicated secondary structures that enable its pivotal roles in biology, ranging from regulation of gene

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expression to enzymatic functions. Therefore, identification of changing of RNA secondary structure, one of the post-transcriptional mechanisms tuning gene expression, can provide profound insights into a system regulating gene expression. However, phylogenetic analysis for RNA structure probing requires extensive sequence information. The combination between in vivo RNA structure probing, next-generation sequencing (NGS), and bioinformatics tools enable the analysis of pools of many different RNAs at once.

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

- 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。):