Must be typed

（For JSPS Fellow）

Form B-5

Date（日付）
26/12/2014 （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）: Steven Bowden （ID No. P 12811）

- Participating school（学校名）: Aichi Prefectural Jishukan high school

- Date （実施日時）: 25/08/2014 （Date/Month/Year:日/月/年）

- Lecture title（講演題目）: （in English） Tools to understand how bacterial genes interact and my experiences in science.

（in Japanese）

- Lecture summary（講演概要）: Please summary your lecture 200-500 words.

I am a scientist from the UK researching microbiology at Nara Institute of Science and Technology in the laboratory of Professor Hirotada Mori. I am researching how genes interact in the well-studied bacteria, *Escherichia coli*.

Bacteria are microscopic organisms found everywhere on planet Earth. They are incredibly diverse and have important impacts on human beings in areas such as health and disease, agriculture, the food industry and biotechnology.

E. coli lives within the large intestine of humans and other warm-blooded animals. Most *E. coli* strains exist harmlessly in animals but some can cause diseases such as gastroenteritis and urinary tract infections. The harmless laboratory strain of *E. coli* called K12 has been very useful to scientists because we can make lots of changes to its DNA and use it as a tool to understand how bacteria work. However, despite nearly 130 years since *E. coli* was first discovered, we still do not know how hundreds of its genes are functioning!

To address this problem, Professor Hirotada Mori's laboratory knocked out all of the 4000 genes in *E. coli* strain K12 that are not essential for growth under laboratory conditions. This library of mutants is called the Keio Collection and is used by many international labs to understand how genes influence biological functions in bacterial cells. Many genes in bacteria interact with each other and to study this, we are constructing *E. coli* mutants knocked out in two genes to assess how this affects the cells growth. This is necessary because often the same biological process can have more than one pathway. In these situations it can require multiple mutations to see what the genes are doing. By employing genetic principles such as epistasis, we can determine which genes are involved in the same physiological pathways and learn how genes come together to control what a bacterial cell does. I will introduce the strategies we are using to achieve these aims that employ robotics and next generation DNA sequencing technologies.

I will also describe what attracted me to become a scientist and what it is like to be a life scientist

researcher.

- Language used（使用言語）: English

- Lecture format（講演形式）:

◆Lecture time（講演時間） 70 min（分）, Q&A time（質疑応答時間） 45 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））

Powerpoint presentation with projector

◆Interpretation（ex.: assistance by accompanied person, provided Japanese explanation by yourself）（通訳（例：同行者によるサポート、講師本人による日本語説明））

I was accompanied by Japanese interpreter

◆Name and title of accompanied person（同行者 職・氏名）

Prof. Hirotada Mori

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

- Impressions and opinions from accompanied person（同行者の方から、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。）: