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（For JSPS Fellow）

Form B-5

Date（日付）
07/11/2016（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）: Chia-Feng Tsai （ID No. P15343 ）

- Participating school（学校名）: KAMAISHI HIGH SCHOOL

- Date （実施日時）: 14/10/2016 （Date/Month/Year:日/月/年）

- Lecture title（講演題目）:（in English） 1st part:The detective in science-Mass Spectrometry 2nd part: From Chemistry to Phosphoproteomics
（in Japanese）

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

The pathway specificity of the phosphorylation-mediated signaling cascade is orchestrated by interaction between protein kinases and a variety of its downstream molecules. Despite the analytical approaches for phosphoproteomics has matured within the last decade, enrichment and detection towards comprehensive phosphoproteomic profiling with limited sample amount remain further improvement. Besides, it is still difficult for conventional phosphoproteomic approaches to distinguish whether the fold-change of phosphopeptides is induced at the phosphorylation level or is caused by the change at the expression level of proteins. Furthermore, two-fold changes in absolute values of phosphorylation stoichiometry such as 0.5% to 1% or 50% to 100% may represent fundamentally different cellular functions. Here, we firstly developed a StageTip based phosphoproteomic assay which minimizing the steps of sample transfer and increasing the detection sensitivity. We has further developed a highly sensitive kinase motif targeting proteomic assay for specific kinase substrate purification. Up to 6490 motif targeting tyrosine sites and 4026 S/T sites can be detected via kinase reaction. Through sequence motif analysis for identified motif targeting phosphopeptides, the specificity of kinase recognition was higher in S/T kinase than tyrosine kinase. Finally, we can measure the phosphorylation stoichiometry of 7392 phosphorylation sites by integrating dephosphorylation and isotope tagging with kinase motif targeting proteomic assay. Comparing gefitinib-resistant and sensitive lung cancer cells, we reveal that post-translational phosphorylation changes are significantly more dramatic than those at the protein and messenger RNA levels, and find potential drug targets within the kinase–substrate network associated with acquired drug resistance.

- Language used（使用言語）: English

- Lecture format（講演形式）:

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◆Lecture time（講演時間） 90 min（分）, Q&A time（質疑応答時間） 20 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 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））

No accompanied person

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

◆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。）: