

Title of Research:

^{17_S05-01} Development of Novel Analytical System of Biological Responses to Chemicals by Deep Phenotyping Method

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Summary of Research:

Today, organisms are always exposed to chemicals in every situation to some extent. Wide variety of chemicals exist around us and the chemicals affect organisms not one by one but simultaneously like a complex. The fact prompts us to care "multiple exposure". To achieve the appropriate and correct prediction of multiple exposure of chemicals, it is necessary to comprehend the effects of chemicals even if those are hidden and difficult to be detected. In this study, we tackle with the theme by omic approaches with innovative techniques in both data acquisition and data analysis method.

This study consists of two pillars: (1) a novel acquisition method of proteome profile data by 2-dimensional electrophoresis (2DE) and (2) a new analysis method of profile data. In the 5th term, we carried out fine-tuning of these two.

As for 2DE, we have investigated intra-day deviation of profile data because it is indispensable for the construction of database. HeLa cells treated with or without bortezomib were lysed and the specimens were subjected to 2DE. The difference between days were smaller than that between treatments (bortezomib and DMSO as a control). We have written the detailed protocol of our 2DE method to minimize the dependency of the data on investigators.

As for data analysis, we have summarized the results so far and it was accepted by *Scientific Reports*. By this method, it is expected that profile data of samples subjected to multiple exposures can be separated in unsupervised manner, and it can be estimated what kind of action is combined. In this term, we searched for data subjected to combined exposure from Gene expression omnibus (GEO; https://www.ncbi.nlm.nih.gov/gds), and analyzed the data analysis with OLSA. Six combined exposure data were found (ID: GSE10466, GSE16816, GSE16816, GSE24065, GSE35230, GSE59882). Of these, combined exposure data of GSE16816, GSE24065, and GSE59882 were expressed in a linear combination of vectors obtained by OLSA.

Timeline:

March 1, 2018 - February 28, 2019

Topics:

2018 LRI annual meeting, "Development of Novel Analytical System of Biological Responses to Chemicals by Deep Phenotyping Method"

Publications:

Akademi) 第2回日韓若手薬剤学研究者ワークショップ, Seul, 2018/7/9-11; GPEN2018,



Development and assessment of new risk assessment methods Singapore, 2018/9/25-29; 33rd JSSX, Ishikawa, 2018/10/1-5; CBI 2018, Tokyo, 2018/10/9-10/11; 第 40 回生体膜と薬物の相互作用シンポジウム, 2018/10/18-19, Miyagi; THE 13th SUGIYAMA LABORATORY (RIKEN) OPEN SYMPOSIUM, 2019/2/22, Yokohama Journal) Mizuno T, *Sci Rep*, 2019