Plan Overview

A Data Management Plan created using HKUL DMPTool

Title: Synergistic Translatome Remodeling by Quizartinib and Omacetaxine mepesuccinate in FLT3-ITD AML

Creator: King Wai Kelvin Wong

Affiliation: The University of Hong Kong

Principal Investigator: Professor Jason Wing Hon Wong, Professor Anskar Yu Hung Leung

Data Manager: Professor Jason Wing Hon Wong, Professor Anskar Yu Hung Leung

Project Administrator: Professor Jason Wing Hon Wong, Professor Anskar Yu Hung Leung

Template: HKU Template

Project abstract:

Acute Myeloid Leukemia (AML) with FMS-like tyrosine kinase 3 internal tandem duplication (FLT3-ITD) mutations is known for its poor prognosis and high relapse rates. Targeting FLT3 kinase is a critical therapeutic approach, and both Quizartinib (QUIZ) and Omacetaxine mepesuccinate (OM) have shown promising anti-leukemic effects in FLT3-ITD AML. However, the molecular mechanisms and specific targets of OM are not well understood. This research project aims to investigate the synergistic impact of QUIZ and OM (QUIZOM) in FLT3-ITD AML cell lines MOLM-13 and MV4-11 using advanced chemical proteomics techniques at the protein translation (i.e. the translatome) level. This study will represent first of its kind to compare the translatome changes at ultra-deep coverage to reveal the unique susceptibility of FLT3-ITD cells to protein synthesis inhibitions.

Start date: 01-01-2023

End date: 05-01-2025

Last modified: 08-27-2024

Synergistic Translatome Remodeling by Quizartinib and Omacetaxine mepesuccinate in FLT3-ITD AML

Data Collection

What data will you collect or create?

Mass spectrometry (LC-MS/MS) raw data, text data and numbers will be collected. The total data file will be more than 10GB size. When the proteomics results are published, the data will also be uploaded according to manuscript requirements to the PRIDE proteomics data depository at https://www.ebi.ac.uk/pride/

How will the data be collected or created?

Researchers will gather data through experimental procedures and observations. Files and folders will be organized and named based on their respective categories. Each file will include a version number and the date of the most recent revision. A standardized format will be implemented for all content. To guarantee statistical significance, experiments will be conducted using biological replicates. Researchers will receive training in data collection, and all entered data will undergo verification to minimize errors and ensure accuracy.

Documentation and Metadata

What documentation and metadata will accompany the data?

A comprehensive readme document will be created to provide an overview of the methodology and analytical techniques used, enabling secondary users to comprehend and repurpose the data. Upon publication of the proteomics findings, the data will be submitted to the PRIDE proteomics data repository (https://www.ebi.ac.uk/pride/) in accordance with the manuscript guidelines, ensuring accessibility for all interested parties.

Ethics and Legal Compliance

How will you manage any ethical issues?

No human participants or live animal models (e.g. mouse or rat) will be involoved in my PhD project. Only human cells will be studied.

How will you manage copyright and Intellectual Property Rights (IP/IPR) issues?

The student will retain copyright of the written thesis, while ownership of the data will be shared among the laboratory, principal investigator, and the student. The University grants permission to utilize the thesis for non-commercial purposes.

Storage and Backup

How will the data be stored and backed up during the research? i. e. until stored in the final location (e.g. on your password protected laptop)?

Data will be securely stored on a password-protected laptop, external hard drive, and laboratory backup server. Monthly backups will be performed on the lab server, ensuring a minimum of three copies are maintained. Furthermore, upon publication of the proteomics findings, the data will be submitted to the PRIDE proteomics data repository (https://www.ebi.ac.uk/pride/) in accordance with manuscript guidelines, providing access to all interested parties.

How will you manage access and security?

Laptop, external hard drive and server will be protected by password. Risk of leakage of data is also low. Only relevant people will have the access right, unless there is approval from the Supervisors.

Selection and Preservation

Which data are of long-term value and should be retained, shared, and/or preserved?

Data will be preserved for a minimum of three years following the project's conclusion. Upon request, the data will be utilized to confirm research findings. Additionally, the data may serve as a basis for any subsequent studies. Three years after publication, the data may be deleted.

What is the long-term preservation plan for the dataset?

Prior to deletion, the dataset will be securely stored on a password-protected laptop, external hard drives, and the laboratory server.

Data Sharing

How will you share the data?

When the proteomics results are published, the data will also be uploaded according to manuscript requirements to the PRIDE proteomics data depository at https://www.ebi.ac.uk/pride/ so that all secondary users can access the data.

Are any restrictions on data sharing? If yes, Why?

No data sharing will be available unless the proteomics data are published.

Responsibilities and Resources

Who will be responsible for data management?

The principal investigators and all researchers involved in this project will hold the responsibility for executing the Data Management Plan (DMP).

What resources will you require to deliver your plan?

Hardware and software are needed to deliver my DMP. The prospective data that will be generated by this project will be uploaded to the PRIDE proteomics data depository at https://www.ebi.ac.uk/pride/ , which is maintained by a global consortium jointed by laboratories and universities worldwide and is free of charge.
