Plan Overview

A Data Management Plan created using DMPTool

Title: Profiling Chromatin Dynamics in Response to Pathogen Attack in Zea mays

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Copyright information:

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Data will be files collected from mass spectrometry (MS) analysis as well as derived forms of the data from analysis software There will be prototypical molecular analysis-based data comprised of PCR analysis gels, western immuno-blotting, and co-immunoprecipitation image files. Images detailing a quantitative pathogen-disease infection assay will be used for phenotyping screens of candidate maize mutant plants.

MS data will be available in raw and processed formats. Raw data will be used to create processed data with a human readable and statistically analyzed output type. The majority of the molecular biology analysis-based data will be qualitative images to detect presence/absence of proteins/DNA molecules. Experimental measure type data will be our camera images showing quantitative disease infection of our pathogen on the maize host.

MS raw data will be from a ThermoFisher Q-Exactive Plus mass spectrometer. Raw files will be processed using MaxQuant software developed by the MaxQuant institute. . Molecular biology data will be visualized on a BioRad ChemiDoc XRS gel/membrane system.   Phenotyping screen images will be taken using a digital camera. Versioning control implemented in folders containing the files. Naming methods include the researcher, data of analysis, and methods of analysis.

Mass Spectrometry raw data will be available in .raw format as this is the output form the XCalibur software we are running on the machinery. Necessary for downstream analysis.

The processed MS data will be stored in folders composed of txt files and pdf files. The txt files are the majority of the output and make a great platform to allow for data parsing via a variety of user-friendly graphical user interface software(s) as well as command-lines tools decided upon by the researcher doing the analysis. The txt files are low size and transmissable between researchers. The pdf files are also universally viewable with their content being primarily summary files of the run (the metadata).

Molecular biology-based results will be primarily image files in .tiff format to allow for high resolution image analysis via software. The images will also be saved as .scn files which is readable by the BioRad documentation machine. This file format allows for image analysis, touch-ups, and manipulation.

Camera images will also be saved in a .tiff format. Photo analysis software will be used on the images.

Metadata outlining the data will be in the form of "read me" files distrubted in the same storage directory folders as the data.

Primary ownership and responsibility for data managment will be shared by the principle investigator and the lead researcher generating the data. Time allocations will not be enforced, neither will the project managment of technical aspects. Minimal training required.

The lead researcher will also be responsibe for monitoring of the data managment plan. Adherence to the data managment plan will be checked by the PI. Decision making for long-term ownership of the data will be administered by the PI.

All data published in peer-reviewed scientific jounals will be made readily available to all interested and preserved long-term.

Data will be made available via open-access repository following acceptance of the peer-reviewed publication by the publishing scientific journal. We plan to use available Iowa State University systems. Tranformation of the high-resolution images may be necessary prior to data sharing. The "read me" metadata files will be submitted and

deposited along with the data on the repository. No further manipulation/transformation of these file(s) is necessary prior to depositing them.

The process for gaining access to non-publically accessible data will be straighforward and involve email communication to the PI in order to gain access to the data. We expect no embargo periods for political/commercial/patent or publisher reasons.

There will be no need for permission restrictions to be placed on the data. Ethical and privacy issues will also be of no concern.

The principle advisor, main researcher, and Iowa State University will be the entities which will retain the property rights to the data. Data access will be allocated at the discretion of the university as the experimental procedures are performed using Iowa State University-owned equipment and materials.

Foreseeable uses of the data may be for further expermentation performed in the lab under leadership of the principle investigator. The users may include current and/or former graduate students, post-doctoral researchers, and other lab personnel involved in the project.

Physical storage of the material will be in a controlled access facility accessible to the PI and other researchers in the lab. They will be placed in a secure storage device that is flood, fire, and damage proof. There will be extra physical copies of all physical materials stored in a physical repository at the Iowa State University library. Short term storage will be in laboratory notebooks. Digital storage will be on Iowa State University server systems that are secure and under supervision by the university itself for long term storage. Short term storage will be on cloud services including but not limited to DropBox as well as CyBox (an Iowa State University monitored "box" storage system).