



Cold Spring Harbor Laboratory

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USDA ARS

Adjunct Associate Professor

Dear Siobhan,

I am writing this letter of collaboration as PI for the Gramene grant to support your 2012 DOE proposal "**Integrative analysis of plasticity in cell fate determination in plants**". We are very interested in integrating your datasets into Gramene. Based on our discussions, you will have four types of data available for integration in rice, Medicago and tomato:

- (1) Gene expression data from RNA-seq from root and shoot meristems of all three species, as well as from tissues exposed to drought stress and waterlogging.
- (2) ChIP-seq data (H3K27me3 and H3K4me3) from root and shoot meristems of all three species, as well as from tissues exposed to heat stress, drought stress and waterlogging.
- (3) Sequencing data from translome assays from root and shoot meristems of all three species, as well as from tissues exposed to heat stress, drought stress and waterlogging.
- (4) Sequence protection data from ribosome assays from root and shoot meristems of all three species

To support integration of your data within Gramene, we will be requesting that you provide primary and associated metadata using standard descriptors and in a format requested by the Gramene project. The use of these descriptors will support data integration and interoperability with other data resources. For the expression profile data sets, we will be able to provide views of the experiments on the Ensembl Genome browser hosted at Gramene via Distributed Annotation Server (DAS). In addition, we are requesting that all project participants format and submit the data to an appropriate reference repository such as NCBI-SRA. In this next round of funding, Gramene will be collaborating with the EBI ATLAS project to prototype integration of Arabidopsis, rice and maize expression data. The scope of the EBI ATLAS collaboration may be extended to include other species but at this time the collaboration would focus on the integration of the rice data sets. To support future integration activities, we will request that your project submit the expression data to the EBI ATLAS project to support meta-analysis, which will be available as additional gene-based views in the browser for the tomato and medicago species. To that end, we will host web-based meetings at least quarterly to support training of collaborators in the use of standard descriptors and formats needed to support data integration and interoperability.

We will request that participants from your team contribute to regular user meetings to support the integration of these data sets. We will request that your group be responsible for a collaborator's page on Gramene that will include information on the project and example links to available data within Gramene. We would also request that your group produces a video tutorial that demonstrates how to navigate to the data within Gramene. You will be responsible for providing twice-yearly updates to the collaborators page to coincide with Gramene updates, including the development of the content and the video tutorial. We also request that you contribute to the Gramene news blog at the time of integration and when a publication of the data set is published. Your data will be publically released in Gramene to coincide with your publication.

To support training on standards and formats, we request that a project member on your team

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attend a collaborators meeting at least 6 months prior to the anticipated submission of the data. The Gramene project can also provide you with resources for comparative analysis to support cross-species comparisons of function and phenotype for maize, rice and *Arabidopsis*. Please be aware that we can only commit serving the data for the length of the current Gramene grant that will be ending in May of 2017. We look forward to working with your group.

Sincerely,

Doreen Ware

A handwritten signature in cursive script that reads "Doreen Ware".

Signed: _____

Organization: Cold Spring Harbor Lab, USDA ARS

Date: July 16, 2012