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Dated: February 21, 2012

Subject: letter of collaboration with Gramene for the 2012 DOE grant (DE-FOA-0000598)

Dear Oswald,

I am writing this letter of collaboration as PI for the Gramene grant to support your 2012 DOE proposal "**Functional genomics approaches for improvement of sweet and lignocellulosic sorghums for bioenergy**". We are very interested in integrating your datasets into Gramene. Based on our discussions, you will have three types of sorghum data available for integration:

- (1) Raw and normalized gene expression data from RNA-seq and microarrays (2013-2015)
- (2) Results from data analysis, genes and gene networks associated with specific bioenergy traits (2014-2015)
- (3) Phenotypic data from field, as well as compositional analysis (2013-2014)

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 sorghum 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 GEO. 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 sorghum. If so, 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. 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.

The data from the gene networks and phenotypes data will be useful for supporting functional annotation of the gene models. For this work, we will work with your group on formats for submission.

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 produce 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.

To support training on standards and formats, we request that a project member on your team 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*, as well as resources for gene networks that may relate to your research.

Please be aware that we can only commit serving the data for the length of the current Gramene grant that will be ending in September of 2012. Gramene is currently under consideration for funding for 2012- 2016, if this funding is awarded we will be happy to collaborate with your group. We look forward to working with your group and wish you the best of luck on your proposal.

Sincerely,

A handwritten signature in black ink, appearing to read 'Pankaj'.

Pankaj Jaiswal