

Cold Spring Harbor Laboratory

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Matt Vaughn Research Assistant Professor Cold Spring Harbor Laboratory 1 Bungtown Road Williams #5 Cold Spring Harbor, NY 11724 USA

I write to confirm the willingness of the Gramene team to collaborate with you and your colleague Nathan Springer at University of Minnesota on your NSF proposal, entitled "Epigenetic Variation in Maize".

Based on our discussions you plan to study the prevalence, heritability and potential consequences of epigenetic variation in maize. Specifically you will catalogue epigenetic variation in four different tissues of B73 and in seedling tissue from 26 different inbred lines that are the parents of the NAM population. The project will generate expression data and H3K9me3, DNA methylation, and H3K27me3 ChIP data for four B73 tissues, derived from 2.1 million probe genomic tiling microarrays as well as comparative expression data for B73 versus the 26 NAM parental lines. This will provide the potential to identify examples of epigenetic variation that contribute to phenotypic variation within a species and contribute to the enhancement of genome annotation for the maize community.

Currently Maize is hosted independently as part of the maize sequencing project and is anticipate to be integrated as part of the Ensembl resources at Gramene in 2010. We would be happy to integrate the data described as part of the Ensembl Functional Genomics module for Maize. It will be the responsibility of the software developer on your project to work with Gramene staff to integrate the resources coming from your project with existing resources in Gramene and have budgeted sufficient resources to accomplish this task. Gramene currently functions on a 6 month cycle and we will require the data be available for integration 4 months before the anticipated release data. Based on the timelines stated in the proposal the first data release is expected in 2011. If the project is funded we will work with you to define timelines for deliverables of the project. In the first year while the data is being generated, we can use the available time becoming familiar with the infrastructure, standard operating procedures in anticipation of the large data sets.

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We are happy that you are willing to work with Gramene and look forward to a productive collaboration. Please beware the Gramene project is currently funded until the end of 2011 and at this time can only guarantee access to the data until that time.

I wish you the best of luck with your submission.

Sincerely,

Doreen Ware

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