Cold Spring Harbor Laboratory

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SUBJECT: Letter of collaboration for your NSF-PGRP proposal entitled *"GERP: Functional Structural Diversity Among Maize Haplotypes"*

TO: Carolyn Lawrence

USDA-ARS Research Geneticist
1034 Crop Genome Informatics Laboratory
Iowa State University
Ames, IA 50011

Dear Carolyn,

I am writing on behalf of the MaizeSequence.org and Gramene projects to express my enthusiasm to commit to working with MaizeGDB on your proposal with Pat Schnable to evaluate the functional and structural diversity of maize haplotypes. I understand that you plan to integrate sequence and phenotypic datasets from the NAM RILs (both Panzea-derived and to be generated as a component of your project) into MaizeGDB as a deliverable. You also plan to genetically and cytogenetically map the locations of structural variation, including knobs. This will allow structural variation to be placed within the context of the B73 genome assembly, both at MaizeSequence.org and MaizeGDB.

As you are aware the diversity data in Gramene is entirely derived from Panzea. I understand that Ed Buckler has outlined the Panzea data release schedule to you and that you plan to contribute the NAM RIL data you will generate back to Panzea, which will allow it to become a part of Gramene through the inclusion of the GDPDM modules as part of the sequence and phenotypic variation component in Specific Aim 3 of Gramene . The addition of sequence and phenotype data from the NAM RILs into the Maize GDPDM module hosted at Gramene and MaizeGDB constitutes a dataset that can be used to further interconnect the MaizeGDB and MaizeSequence.org/Gramene websites via shared information. In addition to the GDPDM modules, we will also work with you to develop Ensembl core variation databases that will be used to visualize the data in the context of an Ensembl Genome Browser which is currently used at Gramene, MaizeSequence.org and Ensembl Genomes.

I understand that you have included sufficient bioinformatic support within your proposal to generate the necessary file formats for easy integration of (1) the diversity data into Panzea and (2) the locations of structural variation into MaizeSequence.org, which we plan to fold into Gramene at the conclusion of the Maize Genome Sequencing Project.

I appreciate the careful thought your group is giving for how best to allow researchers to visualize and analyze genotype data for deeply sequenced maize inbred lines (B73 and Mo17) as well as the sequence-indexed phenotypic data forthcoming from research groups analyzing the NAM RILs including your own group in this proposal. As a member of the MaizeGDB Working Group, I know that the MaizeGDB Team is currently considering how best to visualize the deluge of sequence-based SNP and other diversity data soon to be made available within the context of the B73 reference genome.

I wish you the best of luck with the proposal.

Doreen Ware USDA-ARS
Gramene Principal Investigator
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