



Cold Spring Harbor Laboratory

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Dr. Aaron Mackey
Statistical and Computational Genomics
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Dear Aaron.

I was pleased to hear of your and Mark's plans for MAKER-NGS. Today's genomics community sorely needs a fully next-generation enabled genome annotation pipeline. Based on your successes to date with MAKER, I am confident of your ability to deliver on this important and innovative project.

As you are aware, Mark and I are already collaborating to use MAKER to systematically QC the Maize Version 3 annotation dataset which we at Gramene have prepared in coordination with MaizeGDB. We are also working together to integrate MAKER into the Amazon EC2 Cloud prototype as part of the iPlant cyber infrastructure project.

As Mark and I are now preparing to attempt a trial annotation of several plant genomes using MAKER, I read of your plans for MAKER-NGS with great enthusiasm. Plant genomes have a large repeat-rich genome and many pseudo genes; existing gene-finders perform poorly. Thus your plans (aim 1) for enabling MAKER-NGS for probabilistic pseudo gene identification using re-sequencing data are especially timely; as are your plans for more comprehensive use of NGS-data for annotation-pipeline configuration and gene-finder training. This Aim (aim 3) holds much promise to improve the annotation of the agriculturally important plant genomes. And of course better annotation of alternative splicing (Aim 2) is a basic area for improvement for all annotation projects.

As we proceed with our current plans to annotate plant genomes with MAKER, I already look forward to updating and improving the resulting annotations using MAKER-NGS

I look forward to our collaboration.

Sincerely,

Doreen Ware