

MGEC-NSF meeting

On Sept. 8, 2010 four members of the MGEC (Brutnell, Buckler, Lawrence, and Walbot) met with Jane Silverthorne and Diane Jofuku Okamuro to discuss the concerns of and opportunities for the maize genetics community. Issues listed below emerged from a “committee of the whole” meeting during the March 2010 annual maize genetics meeting. A summary of the points raised with NSF (bulleted), discussions, and action items are given below.

1. Need for maize genome annotation, genome assembly, new genome builds, and current progress on annotation

- Current genome assemblies – B73 RefGen_v2 has been available at MaizeGDB since May 2010 and the associated annotation file is due soon.
- Plans for future genome assemblies and annotations are unknown, however, sequencing is ongoing. Thus, continued assembly and annotation of the maize genome sequence as well as display of data (including SNP's and expression data, especially RNA-seq) are of the highest priority.
- Community annotation of maize genome was discussed at the 2010 Annual Maize Genetics Conference and some efforts are now underway in collaboration with iPlant to facilitate this process.

Discussion:

We discussed the need for coordination among annotators and the importance of maintaining a high quality sequence for the community. DNA subway (an iPlant tool) may be implemented for this project, but would need to be modified for this task.

Jane suggested that there are programs at NSF that might support these activities. One such program is Advances in Biological Informatics (ABI) (http://www.nsf.gov/funding/pgm_summ.jsp?pims_id=5444&org=DBI&from=home). For bringing together a multinational team for annotation, the Research Coordination Network (RCN) program may provide another option. She encouraged the community to learn more about the RCN program. An excellent example of a PGRP-supported RCN is the RCN: Epigenomics of Plants International Consortium (EPIC) (see: <http://www.nsf.gov/awardsearch/showAward.do?AwardNumber=0925071>). She also strongly suggested that, as always, best practice is to contact the cognizant Program Director for guidance before submitting a proposal.

The RFA for Plant Genome also has language that specifically addresses the need for annotation:

“Four kinds of activity will be supported in FY 2011: (1) Genome-Enabled Plant Research (GEPR) awards to tackle major unanswered questions in plant biology on a genome-wide scale; (2) Transferring Research from Model Systems (TRMS) awards to apply basic biological findings made using model systems to studying the basic biology of plants of economic importance; (3) Tools and Resources for Plant Genome Research (TRPGR) awards to support development of novel technologies and analysis tools to enable discovery in plant genomics; and (4) **Improving Plant Genome Annotation (IPGA) to improve existing tools or develop new tools for improved annotation of the genomes of plants of economic importance.**

Action items:

Develop a “Maize Genome Annotation Consortium” to perform structural and functional annotation of the maize genome and interface with MaizeGDB. Personnel at TAIR or other community databases should be brought in as advisors and participants.

Carolyn Lawrence has taken the lead on this issue.

2. The role of iPlant/informatics in shaping maize genomics research

- A number of excellent informatics tools exist for *A. thaliana* (e.g., eFP browser, ATTED), but are not currently available to researchers for work with the maize genome
- New sequencing technologies are likely to be more widely and rapidly adopted for maize, tomato, and legume research communities than for *A. thaliana* or rice as no common transcriptome profiling platform exists for maize.

Discussion:

To encourage the development of informatics tools, we suggested a focus area for the Plant Genome Research Program (PGRP) (e.g., the recent Heterosis Challenge focus area) on the theme of “crop plant informatics tools”.

Jane mentioned that a US-EC taskforce has been established to generate dialogue between the EU and US on bioinformatic tool development. See http://ec.europa.eu/research/biotechnology/ec-us/index_en.html

The maize community sees a great opportunity to coordinate informatics tools for maize that transcend national boundaries. Although discussions are underway with EC colleagues, nothing immediate is planned for joint funding opportunities. However, Jane mentioned that EU Framework 7 proposals are

due the same time as Plant Genome proposals thus coordination between the groups is possible.

We also discussed the vast amount of sequencing data that is coming out of China – largely at BGI -- and how little is being done to coordinate sequencing projects with Chinese colleagues. The MGEC has one member from China, and the community is interested in worldwide coordination. NSF-OISE has a Beijing office (see: http://www.nsf.gov/news/news_summ.jsp?cntn_id=107006); the former director of that office William Chang is now based in Washington DC and new director Alexander DeAngelis has recently started. Thus, it would be prudent to start dialog with this office.

In the long term sequencing is a commodity but informatics and QC are needed.

Jane also pointed to the value of leveraging existing tools for *A. thaliana* and other species in bringing maize informatic tools up to par quickly.

Action items:

Contact the NSF Head of the NSF Overseas Office in Beijing to discuss coordinating maize sequencing project between US/BGI. We should begin a dialogue with colleagues at BGI where there is a strong interest in maize research. Buckler has been involved in some of these discussions already and perhaps Jinsheng Lai (a member of the MGEC) could help facilitate these interactions with other members of the MGEC and BGI to discuss common needs in informatics and visualization.

As discussed above, the development of an RCN in maize bioinformatics may be a very effective way of coordinating these activities between US, European and Asian bioinformatics communities. Lawrence, Buckler, Brutnell and other volunteers from the MGEC could spearhead this initiative.

3. Value of strong basic and applied science funding streams through Plant Genome and single investigator grants

- Much left to discover in taxon-specific gene functions and in regulation of acclimation (arguably more important than adaptation for short term crop sustainability).
- Fewer than 25% of genes have biological support for function – thus need to support functional genomics and exploratory research.
- The shift in AFRI target areas has made it very difficult for many single

investigator genomics-enabled projects to be funded. While large-scale field operations cannot be done this way, a single lab can sequence and analyze a genome or add another important trait to a larger study already funded.

Discussion:

Jane was quick to point out that NSF does not support applied research. The Basic Research to Enable Agricultural Development (BREAD; see: http://www.nsf.gov/funding/pgm_summ.jsp?pims_id=503285&org=BIO) does support projects with a focus on smallholder agriculture in developing countries, but the focus is on basic research at an early concept stage rather than downstream applications.

Diane emphasized that single investigator grants are supported by the PGRP and that the program welcomes these applications. She also noted that single investigator grants are funded at rates that are very similar to multi-investigator grants; however, only a handful of single investigator grant proposals are received each cycle. The program was recently reviewed by a Committee of Visitors (COV) team (see: <http://www.nsf.gov/od/oia/activities/cov/covs.jsp>), and their report will be online by November.

Jane also mentioned that many projects to address taxon-specific questions should go through core programs for review with a possible co-review from the PGRP, if appropriate.

Action items:

This report will be circulated to the MGEC and posted on MaizeGDB to inform the community that we should be more aggressive in applying for single investigator grants.

4. Postdoctoral/graduate student fellowships

- Need infusion of new skills to sustain research in new directions and recruiting postdocs into plant science is a very efficient mechanism that was used for molecular biology and now for mathematics and physical sciences (see: <http://www.nsf.gov/pubs/2010/nsf10587/nsf10587.htm>)

Jane mentioned that the NPGI has identified Plant Breeding as an area in greatest need for training new students and that plans are in the works via the NPGI to address this issue.

5. The maize stock center: community needs and mechanisms for funding

- Acknowledge that long-term support of Stock Center is an ARS responsibility. Nevertheless, the lack of funding is threatening to impact of several NSF-funded projects through limiting the distribution of materials
- Marty Sachs anticipates receiving 3,000 to 5,000 additional stocks/yr. mostly from NSF-funded projects
- As part of National Plant Germplasm System, Marty cannot charge for seed distribution.

Discussion:

It would greatly help NSF if funds for distribution and propagation of stocks were explicitly stated/requested. This could be either by Marty directly, or Marty could request that the groups developing the stocks do the initial increases using NSF funds before depositing stocks with the Stock Center.

Action items:

Bill Tracy has offered to draft a letter that will be sent to USDA representatives stating the maize community's strong support for the Stock Center from the MGEC.