MASC Business Meeting 2003

Saturday, June 21, 2003, 12:30-2:00 pm
Capital View Room, 2nd Floor, Memorial Union
Madison, Wisconsin

Minutes

Members present: Thomas Altmann, Monica Carabelli, Jens Freitag, Mary Lou Guerinot, Chris Helliwell, Pierre Hilson, Maarten Koornneef, Sean May, Lutz Nover, Veronica Ongaro, Mike Sussman, Chris Town, Bernd Weisshaar; Rebecca Joy, Coordinator

Observers present: Parag Chitnis, US NSF; Machi Dilworth, US NSF; Catherine Kistner, German DFG; Rob Last, US NSF

I. Welcome and introductions

- Mike Sussman, Chair of MASC, welcomed all members and observers to the meeting and thanked them for attending.

II. Annual report discussion:

- Should it be prepared before the Conference and distributed at Conference, as is currently done, or should it be discussed and drafted at the Conference and published and distributed after?
  - It was agreed that the Conference presents the best opportunity to distribute the report to the community; format and content for the next year's report should be discussed at each year's meeting.
- This year's document – it was agreed that the format is satisfactory.
- Next year's content:
  - Better update on functions of genes – quantification for how many genes the function is known for.
  - This requires
    1. Catagorization
    2. definition of "unknown" – this is a job for the Bioinformatics Subcommittee to look into;
  - But should the MASC at large be involved in setting a "minimal information" standard for what constitutes a "functional characterization?"
  - The quantification will have more meaning we present numbers for how many genes have been annotated or functionally characterized to different levels
    - Gold Standard = A gene has been fully functionally characterized when we know:
      1. For genes that encode a protein:
         - Protein activity (catalytic or otherwise)
         - Tertiary structure
         - Expression pattern of protein at cell and tissue level
         - Subcellular localization
         - Phenotype of genetic knockout/ other loss-of-function alleles
         - Protein interaction data
         - Post-translational modification data

2. For genes that do not code for a protein
    - Activity of RNA/ gene product
    - Expression pattern at cell and tissue level
    - Structure of RNA/ gene product
    - Subcellular location for RNA/ gene product
    - Phenotype of genetic knockout/ other loss-of-function alleles
    - Interaction data
- For report, it would be nice to have numbers for how many genes we have data for for each of these catagories
- The opposite of the Gold Standard – when we "don't know anything"
    - Sequence has no homology to any sequence that we know the function of
    - ORF has no expression
    - no cDNA has been isolated, just predicted
- It will be important to make clear that the Gold Standard is a VERY HIGH standard. We would like to have the Gold Standard for all genes. It is feasible, we are getting there.
- A rephrasing of the ultimate goal for success may be that in seven years, at least one of these pieces of information known for every gene in the genome.
- Can we have a quantification of the proportion that we will have the gold standard for in 7 years?
    - This will be feasible next year, when the first rounds of analysis have been done and the numbers of genes in each functional characterization category are known.
- After next year (first round of numbers), a yearly quantification "in thermometer style" should be included in the annual report
- We should be using the GO ontology, trait ontologies for functional categorizations
- This type of quantification will be important to encourage the community to tackle the unknown genes, drive the funding for these investigations, and focus the thinking of the community.
- Unknowns can be elaborated by what their expression profiles are – this should drive interest as well

III. 2004 Arabidopsis Conference planning - Thomas Altmann

- Arabidopsis XV will be held in Berlin, Sun., July 11- Wed., July 14, 2004
- Program board has been set up including Arabidopsis scientists from all over the world
- Four local organizers – Thomas Altmann, Jens Freitag, Lothar Grube (Head of Administration at MPI-MP, Golm), and Lutz Nover
- The Max Plack Institute of Molecular Plant Physiology (MPI-MP) in Golm, outside of Berlin, is the official meeting organizer – made possible by the participation of Lothar Grube
- Estrel Convention Center in Berlin has been reserved, which will allow the meeting to be run like it is in Madison – Lunch and Dinner on site at the conference
- □230 per participant for the venue and the catering
- Additional support will be applied for from the DFG for about □15,000
- German Botanical Society is giving □5,000
- Other support will be applied for

- Rebecca will compile a list of the companies who gave and the amount given for this meeting
- Structure has been determined; and emphasis will be placed on young scientists, in the tradition of the Arabidopsis conference
- The Program Board is also concerned with providing an overview/ entry point into Arabidopsis Science
    - Two plenary sessions with overview speakers, who will also present their own data, about 45 minutes apiece, on two different topics
    - Followed by two parallel, break-out sessions of poster talks on the two topics
    - So each attendee will hear talks on 12 topics, and will have the opportunity to hear follow-up sessions on half of those topics
    - Also to be included are two extensive poster sessions and workshop times have been allocated
- Future Conferences:
    - XVIth Conference on Arabidopsis Research will be back in Madison, June 14-19, 2005

IV. Subcommittees - Evaluation and new directions

A. Evaluation of current structure:

- Multiparallel Analytical Tools and Functional Proteomics, Metabolomics, and Phenotype Analysis subcommittees will be joined to create one subcommittee, called the Multiparallel Analytical Tools subcommittee.
- Reverse Genetic Stocks subcommittee will be expanded to include forward genetic stocks as well. Natural variation and markers included as well.
    - Proposed new members for the subcommittee:
        - Magnus Nordborg
        - Randy Scholl
        - Thomas Altmann
        - Maarten Koornneef
        - cc Sean May on all correspondence

B. Concerns and issues brought to the fore by each subcommittee:

- Bioinformatics:
    - Needs for the community:
        - All experimental data needs to go into publicly accessible databases
        - Project PIs need to be incented to get data into Dbs
    - There are 2 parts to getting data into databases
      1. formats and standards for data – these exist, by and large; but the producers of the data need to use them (Information on where to get these formats should be consolidated)
      2. also the issues of actually getting the data into the databases
        - All the data doesn't have to go into one database; the databases can be interlinked
        - Issues for getting data in include:
            - Quality control
            - Papers vs. unpublished data and where does it go?

- MGED, MIAMI idea to establish a format, get the journals on board to "force" people to use the standardized format
- Data standards
    - should be summarized in next year's report (what they are, where information can be found)
    - spreading the word – getting standards on the web – page at TAIR
- A further note: MIPS-TIGR-TAIR are meeting here in Madison to coordinate AtG coding for genes.

- cDNAs
    - resources getting put together; it is time to do more, but people involved in the projects need to be willing
    - ORFs exist; what to do with them? who will do it? what format should the clones be put clones in?
    - Pierre has talked to Joe Ecker, who has agreed to exchange information, but the exchange has not taken place
    - In Europe, six labs (some funded) are getting together to create a library. Each lab will do a similar number of clones, in Gateway. They will make clones available to each other, and hopefully the rest of the community. They will be in an open format = no stop codon.
    - Perhaps there should be a workshop in Berlin?
    - cDNAs as a resource
        - KOs are good paradigm now, but it took tens years to get to where we are now with the KOs
        - IP conditions are standing in the way
        - "MTA" and "IP" are separate; liability or disclaimer MTAs are not a problem; but IP restrictions are
        - IP problems have been worked out in the past, i.e., with CATMA
        - It would be useful of MASC to suggest to groups that these issues be worked out so that the resources can be made available

MOTION: Functional Genomics resources availability

It was moved by Sean May and seconded by Chris Town that the MASC put forth this motion:

> "Research in plant biology is an international effort that spans national borders. Given this, the Multinational Arabidopsis Steering Committee strongly recommends that member countries in which Arabidopsis resources are being produced encourage that these resources be made available to all researchers without pass-through IP restrictions."

- cDNAs, continued
    - Generation of a list of cDNA resources is extremely difficult.
    - Each clone needs to be itemized as to whether it is partial, full, in progress, planned for, etc. and as to which lab is working on it

- Pierre Hilson proposes a web resource (ORFeous) in which a sequence can be uploaded and information on the stage of production the clone is in (and in whose lab) returned to the user.
    - Questions include how to coordinate all the information into one list
    - Pierre suggests that if all the groups are willing to give the information, the web resource can be handled in his lab until January or February of next year.
    - After this time point, where will it go, who will maintain the database? – Pierre and Chris Town will continue discussion
    - This would also be within the purview of PLANet
    - Information about the IP status of each clone should also be on the list
- Pierre and colleagues have established MIAO – the Minimum Information About an ORF for the cDNAs in the databank. One standard is the extent to which the clone has been sequenced
- In conclusion, for cDNAs we need to:
    - establish vigorous coordination for now
    - more forward into functional analysis of clones
    - work together on the functional aspects

- Multiparallel Analytical Tools
    - Made up of former subcommittees "Multiparallel Analytical Tools" and "Functional Proteomics, Metabolomics, and Phenotype Analysis"
    - Currently main thrust of subcommittee is tracking of the various efforts
    - For microarray projects, there has been a lot of data produced, which currently is not very available for data mining
        - GARNet data is a good example – all freely available on the web
        - TAIR is also working to establish a microarray data repository to not only store but to ensure that the data is described appropriately as it is submission so that it will be useful for those who would like to data mine
        - Some further effort in this area underway at Mary Lou Guerinot's webs site; that URL should be put onto TAIR

V Other discussions

A. Coordination of the MASC with Steering Committees for other model organisms

- Suggestions:
    - Emails to other communities
    - Invite chairs of other SCs to the Arabidopsis Meeting
    - A session for other communities in Berlin?
- Exchanges such as these may be good for the exchange of technology, but may be of limited usefulness otherwise.
- May be of secondary importance right now
- Reaching out is good, invitations to the meeting to other communities are good

B. IP issues –

- Problem is that none of us is an IP expert
- Perhaps an IP expert could be brought in to Berlin

- Standardization of MTA isn't generally a good solution, because most folks interested in using an MTA will not accept it
- There seems to be some lack of understanding about how powerful IP restrictions can be
- We need to ask the groups that are putting out the IPs – "We, as the international community, need these resources. How can we do this?"
- We need to examine the IP issues in each place; produce a white paper
    - For the US: Mike Sussman and Rebecca Joy will write
    - For Europe: Thomas Altmann and Jens Freitag will write
    - For Japan: get someone to write

VI. MASC business

A. Coordinator position

- Rebecca will be resigning the position at the end of the current grant (end of December 2003)
- How does the committee feel about continuing the position or not?
    - Position is important
    - It should be stationed in the US for Conference Coordination
- Where are potential sources of funding?
    - NSF: needs a minimum of three months lead time to get grant going
    - DFG: given the close relationship between NSF and DFG, there may be something that can be worked out
    - European Science Foundation – most likely not, they don't have any money to grant
    - ERANet? Political grant, and not restricted to Arabidopsis; so not a good possibility, either

B. New chair and co-chair

- At last year's business meeting it was determined that
    - 1. The Chair of MASC should be from the country where the next Conference will be held, and
    - 2. That the co-Chair position will be the fly-up position for Chair
- Thomas Altmann, current co-Chair will be Chair for 2003-2004
- New co-Chair needs to be from the US, as the Conference will be back in Madison in 2005.
- Mike Sussman is stepping down from MASC; Mary Lou Guerinot can not take on the co-Chair position as she will be the president of ASPB next year.
- A new MASC member will be chosen from NAASC and that member will be co-Chair.

VII. The meeting was adjourned.

rej
7/1/03