MINUTES OF THE MASC BUSINESS MEETING HELD ON TUESDAY JULY 13th 2004

- Welcome by Thomas Altmann
- Introduction of participants:

MASC members: Paola Vittorioso, Keith Lindsey, Jianru Zuo, Ian Small, Ottoline Leyser, Masatomo Kobayashi Motoaki Seki and Takanari Ichikawa for Kazuo Shinozaki, Philip Benfey, Thomas Altmann, Sean May, Lutz Nover (new member)
MASC subcommittee representatives: Mary Lou Guerinot, Bernd Weisshaar, Pierre Hilson, Chris Town, Heiko Schoof for Klaus Mayer, Eva Huala for TAIR.
MASC observers: Machi Dilworth, Rob Last, Parag Chitnis, Catherine Kistner, Jens Freitag
MASC executive secretary: Isabell Witt

- Reports from subcommittees, recommendations and goals

c-DNA and clone-based functional proteomics:

- 12.000 ORF clones are available via stock centers.
- The next goal is to generate clones from low level expressed genes to finally achieve a full orfeome.
  The majority of c-DNA clones are either in the pUNI or in the pGATEWAY format. Since it is not possible to convert between the two systems by simple recombination Ian Small will list the advantages and disadvantages of both systems and how conversion could be achieved (in most cases this will require PCR amplification and recloning and resequencing). He will also suggest a preferred standard format for future clones to make them as versatile as possible and as widely compatible as possible.
- Principally it is desirable to have all ORF clones with and w/o stop in the two systems or a preferred standard format.
- AFGN c-DNA clones should also be available in either one of the formats or at least the templates should be made available.

Multiparallel Analytical Tools and Phenotype Analyses

- As was already pointed out in the report, microarray data analysis still is too cumbersome for many researchers. Often it is not clear how one should look at the data. TAIR will provide RMA-normalized microarray data to enable the community to access, use and analyze the huge Affydatasets from AtGenExpress and other sources that will soon be available at TAIR. Tools such as MapMan will be provided and it was agreed that more links to other analyzing or visualizing programs will be given at TAIR and that they will be accompanied by critical reviews on what their potentials and limits are. Results from

array data should be linked to GO data or in the future to all kinds of data formats like e.g. metabolite, proteome or literature. One future goal is to have an interactive interface that makes the user aware of connecting data and knowledge about the genes of interest.

Comments
NASC has already done many of the desired objectives - it has the tools, very good access for the users to the AtGenExpress data and other data out there in a large number of complementary databases with third party tools such as MapMan and Genexplorer; NASC has transcriptomics locally linked to gene models, germplasm and amplicons etc.

The Genevestigator Programme generates data on Affymetrix data generated in the Gruissem lab or contributed by NASArrays (NASC), ArrayExpress (EBI), GEO (NCBI), AtGenExpress and diverse other sources.

To make the AtGenExpress data a source that is used by many Arabidopsis researchers it is planned to carry out workshops in Germany and the US.
TAIR employees who are actively working on these data or sites will initiate these workshops in close collaboration with the bioinformatics subcommittee. It was suggested that three days would be sufficient for hands on workshops for PhD students and Post Docs to inform about tools, train them to use the tools and inform about future plans.
Comment [redacted]*:*
TAIR will be funded to give one 3 day workshop at the Carnegie in each of years 2-5 of our new grant (2006, 2007, 2008, and 2009) for 20 participants. In addition we will give 1-2 hr workshops at the major plant meetings, including Arabidopsis, ASPB and PAG. It's possible we could expand some of the meeting workshops to be a bit longer (half a day?) if people were interested but we don't currently have the money to send curators around the country (or world) giving 3 day workshops. We are committed to doing all we can to help people use the new data but we can't promise something we don't have the budget for.
Suggestion Isabell
The workshop in Germany should be initiated by NASC also in close collaboration with the bioinformatics subcommittee.

- Isabell will prepare a leaflet with web addresses of all microarray databases/datasets (she can possibly find).

- In order to understand what the Arabidopsis researchers need most, it is useful to poll lots of users. TAIR routinely makes surveys. Isabell will be provided with texts of recent surveys by TAIR to avoid redundancy. Surveys from other data bases are more than welcome as well.
- Since in an increasing number of projects (AGRIKOLA, AtGenExpress, GABI, mutant collections, Promoterfusions and so forth) plant pictures are taken and their visible phenotype is described, it would be very useful to use controlled vocabulary (GO, MIAME) for this. As an outlook plant pictures should be linked to the corresponding GO. NASC has a picture database with standardized phenotype descriptions. INRIA is working on a vocabulary free picture analysis tool using the NASC data that would be complementary to text descriptions but will not replace them. Isabell will contact Ian Small, Sean May, Ottoline Leyser, Leonore Reiser or Eva Huala, Randy Scholl, David Meinke and Maarten Koornneef (suggestions for more people?) to get an overview and describe the state of the art here.

  Comment [redacted]

  Takashi Kuromori and Minami Matsui of RIKEN, RIKEN GSC has started a phonome project to analyze visible phenotypes of 5,000 Ds unigene KO lines and RAFL cDNA oxerexpressors

Reverse and Forward Genetic Stocks

- Is RNAi a good system? What about stability and specificity issues? Many data generated in the AGRIKOLA project will give better insight into this. RNAi was rated as complementary tool.
- 50% (Bernd, Joe is that number correct?) of the genes are covered by T-DNA insertion mutants in Salk. In order to reach saturation 50.000 more insertion lines need to be produced, which is very expensive. The suggestion here is to fill gaps with lines from the TILLING project and transposon derived insertion mutants.
- The subcommittee needs to define new goals and what kind of working group(s) would be useful.

  Comments [redacted]*:*

  Concerning the reverse genetic stocks section - I would agree that until the doubts over stability and specificity are resolved, RNAi will not replace insertion mutants (when they are available) for classical genetic studies. But a) insertion mutants are not available for many genes (at least 25%) and b) insertion mutants will never be available for some genes (e.g. gametic lethals) and are unusable for many others (homozygous lethals). Complementary approaches are essential and RNAi is probably

the easiest and maybe the best alternative method at the current time.
Inducible or tissue-specific RNAi can also be used for more sophisticated studies that are difficult or impossible by other means. AGRIKOLA should inform us about the limits of the approach...
TILLING is another alternative for reverse genetics and which would be more acceptable than RNAi to classical geneticists (although personally I think it requires much more work than RNAi...). It is worth stating that at present there is (as far as I know) no large-scale systematic TILLING project for Arabidopsis anywhere in the world (the American efforts, whilst laudable, are not systematic) and maybe we should push for one. That's probably a discussion that the reverse genetics subcommittee should have.

Addition [redacted]
(RIKEN GSC has collected 18,000 DS tagging lines. Among them more than 5,000 lines are unigene knock-out mutants. These lines are now used for phonome analysis)

Bioinformatics

- The major issue here was to organize a serious discussion about the future of seamless database usage. Momentarily two approaches are developed and need to be evaluated: 1. the warehouse model, where as many as possible databases and programs are under one roof (TAIR, SALK, PlantDB, NASC) or 2. The federation model where the experts stay with their database and the seamless access is made possible via e.g. BioMoby and .xml data formats (PLANET). Chris Town was already active in organizing the corresponding expert workshop that will take place in the near future.
- There is a high demand for mouse over functions that link different types and formats of data e.g. Affy gene lists to visible mutant phenotypes to metabolite, proteome, promoter, pathway…….data. MAPster

- Discussion on community demands/priorities/concerns regarding bioinformatics and coordination of multinational bioinformatics activities. See above.
- **Future MASC activities:**

  -Role of MASC managing office/executive secretary
  Besides the tasks mentioned above, there is a need to improve the communication with the EU. ERANET and EPSO would be good platforms to begin with.
  -Need to list genomics scale materials and data available with and without MTAs and their prices (transparency)

Isabell will establish lists on availability of clones and stocks (MTA or other limitations and costs) for

- ORFeome
- c-DNA
- update of reverse genetics list

and place them on the MASC web page at TAIR
- Isabell will send the MASC report to funding agencies in the world.

- **Activity of subcommittees; membership; rotation of chair persons? Additional meetings organised by MASC managing office?**
  It was decided to keep the subcommittees structure and to build expert working groups for new topics. Natural diversity (Olivier Voinnet), Proteomics (Harvey Millar and Hans-Peter Braun)
- **New MASC members; rotation of MASC members**
  New MASC member: Martin Fellner is the representative of EEAA (Eastern European Arabidopsis Activity), Lutz Nover (Germany)
  Within some subcommittees rotations are planned; please don't forget to inform Isabell about this.
- **MASC annual report (structure, print/online; thermometers further procedure of their development)**
  The suggestion to only have an online version in the future was denied, because also politicians, funding agencies and public related institutions will receive the report.
  The thermometers will be continued with the help of TAIR, Chris Town and Hank Wu from TIGR and Joe Ecker from SALK. The questionnaire that was sent to AFGN and 2010 researchers by Isabell will be sent out again to them and in addition to the community (TAIR could provide its E-mail distribution list of the 13.000 users). TAIR will receive a document with all abstracts from this year's ICAR to filter for new gene function annotations. With these tools it should be possible to get quite a good overview of how many genes have been functionally characterized to what extent.
- Arabidopsis meeting 2006; organizer/location?
  2005, the meeting will be in Madison
  2006, Mary Lou Guerinot will ask ASPB meeting organizers whether there are possibilities for the ICAR at the US West coast
  2007, Ian Small will explore possible venues in France
- New MASC chairperson/vice chairperson
  The new Chair is Philip Benfey (USA)
  The new Co-chair is Ian Small (France)

Best wishes

Isabell