

## **Draft MASC Meeting Agenda**

MASC meeting on Saturday 12:30 to 2:00 pm during lunch

- 1) **Welcome by Philip Benfey**, chair of MASC (3 min)
- 2) **Introduction of meeting participants/MASC members** (5 min)
- 3) **Planning of Arabidopsis Conference in 2007** (10 min)  
Beijing?
- 4) **Ongoing MASC activities** (30 min)
  - MASC Bioinformatics Workshops (10 min)
    - Summary
    - Working group for data format synchronization
  - Reorganization of MASC subcommittees (10 min)
    - Proteomics, reference proteome (chair Wolfram Weckwerth?)
    - Metabolomics, reference metabolome (?)
    - Natural variation and comparative genomics (chair Tom Mitchell-Olds)
    - Genetic Resources (chair Bernd Weisshaar?) replacing the forward and reverse genetics resources subcommittee
    - Organization of the phenome?
      - Should it be part of the genetics resources subcommittee?
      - Should we have a specific working group for this?
  - The MASC report (10 min) :
    - Format and updating chapters.
    - New contacts for some countries needed.
    - Stock center representation?
    - Thermometers - measurement of results in an automated way.
    - Responsiveness and chapter preparation.

## 5) **Future activities** (25 min)

Half way point of 2010 Program:

- Short-term goals
- Mid-term goals
- Long-term goals

Overview with the goals from the planning document in comparison to where we are (5 min., Isabell)

Discussion (10 min)

Future funding recommendations (10 min):

- Recommendations for basic science
- Resources for translational biology

6) **Miscellaneous points** (10 min)

- Improving communication with other plant communities.
- Availability of KO lines produced in the community.

**END OF MEETING**

## Appendix

Miscellaneous suggestions by community members (mostly addressed in the agenda):

*But coming back to the use of the data: as this develops this could become an excellent source to aid gene annotators to identify who is obtained and can provide d relevant data to help them in their mammoth task. Is it planned to use it this way and if so how is the implementation planned. One of the major tasks in my view in Arabidopsis research at the moment is to develop ways to increase the speed and efficiency with which 'wet bench results' are translated into improved gene annotation and assignments. This is not only important for Arabidopsis research but also is a and probably the key element in the usefulness or non-usefulness of Arabidopsis as a reference system for crop plants. Is this being discussed in MASC??*

*One recommendation from my side would be that there is a financial pool is generated from which microarray studies or massspec work could be payed from without large delay.*

*Homozygous KO lines that were produced in labs using publicly available stocks should not be under any kind of MTA, but instead when they are published should be sent to the stock center to make it again publicly available.  
MASC statement and recommendation to journals and community.*

According to me the most urgent community needs are:

- the development of an Arabidopsis phenotype ontology, built in sync with the gene and anatomical ontology;
- the capture of all the information already published in the primary literature about phenotypes, according to this formal phenotype ontology and to rational choices framing the compromise between the level of detail versus the comprehensiveness we want to reach;
  - finally and gradually, the implementation of methods and tools that will allow authors to format their results according to the various ontology sections or, at the very least, the establishment of a system that will capture this information as it is published. This cannot be simply an automatic task and needs active curation.