

## **I. INTRODUCTIONS**

### **II. OPENING COMMENTS BY DETLEF WEIGEL**

Three main points made by Detlef Weigel summarized below:

First, Urgency: plant biologists are behind the vertebrate/Drosophila biologists in comparative genomics. It is an embarrassment that we had Arabidopsis and rice sequenced long ago but that other communities have medical/NIH money to do comparative genomics in Drosophila and vertebrates. Part of this is due to ease to align human genomes to mouse and even fish, while we have challenges aligning Arabidopsis to Polar or rice to maize.

Second, among plant groups, the Brassicaceae are an ideal group to sequence because of their small genomes and high quality Arabidopsis reference genome. There is also a large community of Arabidopsis systems biologists and researchers working on crop plants.

Third, to provide some context, over the last year, the USA DOE JGI expressed an interest in sequencing a dozen Brassicaceae as a "flagship project" (which would follow on past sequencing of Arabidopsis, Capsella, Thellungiella, and Boechera). So a small group of us quickly developed a preliminary plan to sequence a "Baker's dozen list" of Brassicaceae. A dozen species was chosen to mirror similar efforts among closely related species (as in Drosophila and Oryza), but our goal was to span a broader evolutionary distance across the family. However, the current status of the USA DOE JGI project is uncertain. In addition, China/BGI has just announced a 1001 genome project.

Our goal is to develop a community-driven white paper, instead of having sequencing centers lead the way, and then to find the best way to accomplish our plan.

We have a great team to develop the necessary biological materials and the brainpower/expertise in the community.

### **II. OPENING COMMENTS BY ROD WING**

Rod Wing explained the nature of his sabbatical. The plan is to have a second meeting in Germany in March, a third meeting in Asia in Spring, and a white paper by Summer 2010.

Boulos Chalhoub (France) asked "what is the originality of Brassicaceae over Solanaceae, legumes, or grasses?" The collective answer was:

First, we have largest plant community around the Arabidopsis reference genome (or second largest after rice?)

Second, the small genomes in the Brassicaceae are amenable to having complete, high quality reference genomes (to rival the 23 species of rice also being done with high quality).

Third, plants offer better insight into whole genome duplications (WGD, or polyploidy) often not seen in vertebrates, and the best-known ancient and recent polyploid events are in the Brassicaceae (Pam Soltis email further echoed this idea). Eric Lyons pointed out that these WGD events have not only allowed insight into fate of duplicate genes, but also have been critical in evolution and domestication of plants.

### **III. GOALS OF THE BMAP CONSORTIUM/WHITE PAPER**

Rod Wing and Chris Pires facilitated discussion, summary below:

- A. Identify Grand Challenge Questions relevant to not just plant biologists but also the larger scientific community to be used in justifying our efforts (grant proposals, etc).
- B. Share information on what has been done already, and coordinate future efforts, with respect to developing plant materials, genomic resources, sequencing efforts, informatics platforms (and so forth). Establish parallel public germplasm centers with identified, curated plants.
- C. Think long term beyond sequencing to future efforts in plant systems biology (including having the Brassicaceae as model for cross-species informatics with respect to metagenomics, microbial-soil ecoinformatics, plant-animal interactions, etc).
- D. Identify and prioritize a list of Brassicales to sequence (i.e., top 10, 20, 50, 100) and which groups are stakeholders to target species (i.e., German consortium interested in Cardamine).

### **IV. IDENTIFICATION OF GRAND CHALLENGE QUESTIONS**

Chris Pires facilitated discussion, summary below:

- A. Whole genome duplications (ancient, “meso”, and recent polyploidy). Distinct from animals.
- B. Genome and chromosome evolution – selection/mutation/CNS/transposons/breakpoints
- C. Morphological variation (evolutionary development studies); crop plant domestication
- D. Chemical variation (glucosinolates, etc); plant/animal interactions; crop plant domestication
- E. Hybrid vigor/heterosis; gene expression/proteome/metabolome/trait evolution
- F. Comparative systems biology of Brassicaceae; rhizosphere/metagenomics; synthetic biology

### **V. CRITERIA FOR CHOOSING GENOMES TO BE SEQUENCED**

Rod Wing and Chris Pires facilitated, summary below:

- A. Phylogenetic position
- B. Small genome size
- C. Ability to self and make crosses; easy to grow and use as a “model” (NAM/MAGIC lines)
- D. Homozygous genotypes (Selfed by single seed descent, doubled haploids, etc)
- E. Important agronomic/biological features (novel chemistry, ecology, life history, etc.)
- F. Used by a large research community (i.e., Arabidopsis, Brassica, Cardamine, Lepidium, etc.)

### **VI. CURRENT AND FUTURE WORK IN PHYLOGENY OF BRASSICACEAE**

Mark Beilstein and Chris Pires facilitated, unpublished work by Marcus Koch also shown.

The main point is that there are many areas of the phylogeny yet to be resolved and this is an active area of research. Rapid radiation (lack of sequence variation), wide hybridization (across separate genera and even tribes), ancient and recent polyploidy, and other challenges are at play. Whole chloroplast genomes, whole mitochondrial genomes, dozens to hundreds of nuclear genes (from transcriptomes and eventually genomes), and comparative chromosome painting (CCP) are just now addressing these long standing phylogenetic problems.  
(See Power Point files provided)

### **VII. CURRENT PRIORITY LIST FOR BRASSICACEAE SEQUENCING**

(See EXCEL files provided).