

## **Minutes of the IBSC Business Meeting at PAG XVIII**

Jan 9th, 2010, 6:00 - 9:00 pm, Town & Country, San Diego, Royal Palm Salons 1/2

Alan Schulman, Nils Stein

### Participants

MC members (representatives of MOU signing partners): Alan Schulman, Gary Muehlbauer, Roger Wise, Peter Langridge, Kazuhiro Sato, Takashi Matsumoto, Chengdao Li, Robbie Waugh, Nils Stein

Guests: M Schmitt (who was this guy?), Maria Muñoz, Bin Liu, Burkhard Steuernagel, Klaus Mayer, Thomas Wicker, David Marshall, Peter Morell, Patrick Schweizer, Takao Komatsuda, Tim Close (former MC member, representing MOU signing partner UC Riverside).

### Agenda:

item 1: annual report by IBSC chair

item 2: short reports (max 10 min each) on recent advances in barley genomics

item 3: funding, proposals submitted/under preparation

item 4: General strategic discussion:

When will barley be sequenced? Which goal to be reached when?

Review of IBSC research agenda? Revision of IBSC plan?

What can be the role of whole genome shotgun sequencing?

Do we go chromosome-wise or task-wise?

item 5: PR, consortium flyer

item 6: next meeting?

Item 1: annual report by IBSC chair

- Annual IBSC business meeting at PAG XVII
- IBSC business meeting at ITMI summer workshop
- IBSC presentation at ITMI summer workshop
- IBSC posters at PAG XVII, ITMI, IPMB
- China joined as the 9th member of IBSC
- India indicated interest, decision pending
- Visit to Roche/454, introducing IBSC

- Pending: flyer, intermediate report

The meeting was opened by the chair of IBSC (Nils) at 6:25 pm. A brief overview of the administrative activities in 2009 was provided. China (Zhejiang University) signed the Memorandum of Understanding and became 9th member of IBSC. An additional inquiry came from India but was not formalized so far. Nils is going to contact again.

A semi-annual IBSC meeting was held in conjunction with the ITMI meeting at Clermont-Ferrand, the minutes have been circulated. A presentation about the IBSC status and strategy was held.

IBSC posters were presented at PAG XVII, ITMI, and IPMB.

Still pending: IBSC flyer, intermediate status report.

## Item 2: short project reports

- TJ Close: USDA project
- N Stein: The BARLEX project
- R Waugh: Triticeae Genome project activities of anchoring
- Chengdao Li: BAC sequencing 5H China/Australia
- N.N.: further updates/progress

Tim reported about the initial progress within the newly funded USDA project:

One goal of the project is to sequence BAC pools for gene detection and assembly. The original plan to sequence ~4000 clones was changed to ~15000 clones to be sequenced on Illumina GA II. Pooling of the clones is proceeding and may be finished by end of January.

Second goal of the project is gene enrichment sequencing. Seeds were sent to Bennetzen lab. Further work planned on deep RNAseq: Roger Wise has sent RNA from *Blumeria* and BSMV infected leaves, Gary Muehlbauer provided *Fusarium* infected samples. Young inflorescences were collected by Tim Close as a complex tissue, water-stressed inflorescences, will give ½ a 454 run.

Overall plans: Methyl-filtered and high-CoT, 2 runs and 4 runs respectively. With cDNA, will see. No normalization or subtraction. Diseases: spot blotch, leaf rust also to be done, seedling stage.

Nils provided summary on the progress of high info content fingerprinting (excerpt from Daniela's and Nils' presentation in ITMI and barley workshop). Current assembly comprises 540,000 high quality fingerprints (~13x coverage). Plan is to extend until mid February to use up remaining consumables – will lead to 14x coverage eventually. Expect 10-15 k contigs after final assembly, DQing, end-merging and marker info integration. Current anchoring at IPK focused on STS markers of Okayama transcript map. Future activities will embark on ISBP markers for anchoring.

Robbie introduced the results of utilizing the Agilent 44 k for anchoring of genes to BAC addresses. Pools from barley EcoRI library, were used as probes on array. Labeled by Klenow. Label RNA and BAC library. Cy5 ref barley RNA, Cy3 barley BAC pool. 7 x 384 plates = superpool. Need to do 23 hybridizations to deconvolute any address. Each superpool has 1/15 of the genome. Should have 1 X genome coverage finished by February. 8 superpools done. So far 1,300 probe hits per superpool, about 585 BACs deconvoluted, total 794 have been genetically mapped. For superpool 1, have done Illumina sequencing validation. Have money to do 14 superpools, so should have 10-12k genes anchored to BAC clones.

Chengdao Li (Perth + Zhejiang University) reported on plans to partially sequence chromosome 5H. Efforts underway to dissect barley chromosome 5H regions controlling malting quality. Wants guidance as to what China can contribute to barley sequencing. IBGS will be hosted 2012 in Hangzhou – to which extent will barley be sequenced? Gave overview of QTL analysis on malting quality, focus on 5H. Plan to ask for money to do 5H. Other ideas: resequencing of Tibetan wild barley; Chinese landrace; Tibetan landrace for frost tolerance, Australian malting barley Baudin for diversity studies and SNP identification.

Peter Langridge mentioned about efforts to utilize a wheat long oligo arrays to anchor barley BACs.

Alan mentioned work in preparation for deep RNAseq.

Since several activities aim at deep RNAseq in barley and because the datasets could be very instrumental for genome annotation, Nils raised the question if IBSC should collect info on RNAseq for coordination or at least IBSC internal information flow? Dave Marshall volunteered to initiate survey on status and plans of RNAseq in IBSC community. He agreed to send a summary by mid February. Should be option for making public or not. Peter Langridge said has done a lot of Solexa small RNA seq. from stressed barleys.

Item 3: proposals (preparation/submitted/ desc.pending/accepted/rejected)

- JGI
- Leibniz
- USDA
- Japan
- Finland / Carlsberg
- China
- NSF
- Others?

Gary/Tim mentioned that JGI will not be accepting any new proposals this year. (But Dan Rokhsar would accept a sample of genomic DNA in case some unplanned opportunity for sequencing arises. Tim intends to provide a sample of Morex DNA)

Leibniz Society takes proposals from each Leibniz institute. Proposal of 2008 from Nils approved to seq 5 - 8 k BAC clones by pools for 3H MTP. Project kick-off in March 2010. Renewal of the GABI program expected but still under question.

USDA: Project funded already and started in September. Upcoming opportunities remain to be seen. Beachy new head, will reorganize priorities, but grants could be up to 25M USD. National Barley Improvement Committee, a lobby group with Mike Davis at head. Is visiting Congressmen, but may not influence USDA funding directly. Roger would like to see germplasm centers maintain mapping populations. A privately-funded barley-based biofuel plant is under construction in Virginia (!).

Japan: Proposal submitted 2009, with multiple platforms was initially accepted, however, administration changed in summer, and project was then rejected. Japan has also submitted 6B proposal for wheat Chinese Spring. Japan won't fund both in parallel. So Japan now doing 6H proposal in parallel. But this also rejected. Aim to put another proposal in, for next fiscal year. Will be BAC-by-BAC by 454.

China: Initial 2 year funding (200k USD from malting barley industry for sequencing). If good progress in the initial 2 years China will give an additional 4 years funding. Topic broad:

“understanding barley malting quality with genomic approach”. Chengdao is in discussion of the feasibility for sequencing of MTP for chromosome 5H or part of the chromosome with Nils and Peter.

Australia: No big proposal for barley.

NSF: Peter Morrell: Will lead another NSF proposal. NSF will not fund a genome sequencing proposal, at least in this round. There is a call for “comparative sequencing” – but appears to be inter-species. Gary has 6000 USD for “education” for wheat and barley.

There is a new NSF framework “BREAD” for development research. Partially funded by Gates. Foreign country if funded needs to be a developing country.

Robbie: by March 17th will put in deep RNAseq UK application to BBSRC?

Altogether, fund raising for barley sequencing was successful with 3 activities receiving funding in 2010.

#### Item 4: General strategic discussion

- When will barley be sequenced?  
1y, 5y, 10y from now? we need realistic time frame scenario?
- Which goal to be reached when?  
draft sequence, HQ reference, gold standard?
- Review of IBSC research agenda? Revision of IBSC plan?  
midterm report, adjusted whitepaper?

Discussion about the revision of the research plan agenda from a chromosome distributed organization to a task oriented organization.

1H sequencing, assembly, annotation  
2H sequencing, assembly, annotation  
3H sequencing, assembly, annotation  
4H sequencing, assembly, annotation  
5H sequencing, assembly, annotation  
6H sequencing, assembly, annotation  
7H sequencing, assembly, annotation

or

- a. Deep transcript profiling across all tissues and conditions
- b. Genetic mapping group
- c. Data integration and processing group
- d. Sequencing group – 454, Solexa, SOLiD etc.
- e. Sequence assembly group
- f. Annotation group(s)
- g. Repository for materials being sequenced

h. Promotional group / Publication group

Nils introduced into the discussion whether IBSC needs to revisit the research plan and milestones towards sequencing the barley genome. At current there is no clear timeline visible at which we can see realistically which part of the barley genome will when be sequenced. In summer it looked promising that the chromosome-wise strategy could gain significant momentum with 3H becoming funded by Leibniz, a 6H proposal submitted in Japan, a chance for 5H funding in China, as well as by a proposal for sequencing submitted by Finland and Carlsberg. 3H and some activity on 5H were funded. However, the aim to sequence chromosomes by MTP is difficult to put in a funding frame timeline. Therefore, based on the achieved milestones and based on the technology development, is it useful to propose an intermediate goal of a draft sequence of the barley genome by different components of whole genome shotgun sequencing (WGS) without loosing the chance to reach eventually for a high quality reference sequence of barley?

Roger pointed out the difficulty to submit a major sequencing proposal to NSF. Writing a good BIOLOGY proposal and then fold in the sequencing part seems to be more aligned with NSF goals. This would become easier if the chromosome-wise strategy of IBSC would convert into a task based or object-based application. Dave Marshall supported the idea to include a WGS task into the IBSC research plan with giving up the vision of finally a high quality reference sequence.

Gary asked how the data produced in Tim's USDA project ties in into the current activities and also into the general sequencing agenda. Genes in BACs spread around the genome? How will this be integrated with other existing data?

Peter commented his impression that the direction of technology is changing, thus moving away from BAC-by-BAC towards WGS for a draft genome sequence maybe timely.

Patrick asked why not shotgun with Pacific Biosystems? It may be difficult currently to access a beta-version of the system. Tim Close and Peter Morell mentioned their contact to a person who offered them time on such an equipment for testing the kind of data quality and output format. Robbie informed about the Potato consortium which in the beginning also followed the "flag on a chromosome" approach. They shifted from chrom-by-chrom to a more task oriented structure of their consortium because of inability to carry it through. They have weekly phone-calls for all the tasks. Someone needs to take responsibility for every task.

Nils emphasized again that IBSC needs a robust time plan and strategy to convince with a timepoint barley will be sequenced, especially to convince funding bodies. So do we need to review and revise IBSC plan. How do we sell WGS? vs MTP. Then how do we organize our inputs?

A broad consent was found that a midterm IBSC report needs to be written that sums up all the achieved milestones and that will outline the strategy to continue. WGS of barley may be integrated as a task to reach for a draft barley genome sequence. We need to say: 1) we want as a goal a gold-standard sequence. 2) we might take WGS as something useful along the way. The group also agreed to propose the structure of organization of IBSC in a task oriented fashion instead in a chromosome oriented fashion. Takashi Matsumoto reminded us that sequencing should remain the major focus of IBSC because it is tough work.

A midterm report task force (Nils, Robbie, Gary, Alan) was formed. Goal is to circulate a report by mid February as well as a revised organizational structure of IBSC. This document will be circulated to all steering committee members for comments and revision.

After finishing the issue about IBSC sequencing strategy Roger Wise informed about an undertaking to build Barley iNAM (intermated nested association mapping population) to generate high-resolution populations for mapping and cloning genes and/or QTL and to optimize the recombination of important traits. Cross ~20 diverse lines to Morex, self, self, intermate (within subpopulations), self, self, intermate (within subpopulations), self, self, increase for use. Some crosses to Morex have already made in various individual labs (Schweizer, Muehlbauer) and have indicated interest in participating. Question if Morex has to be the recurrent parent? Patrick mentioned that Klaus Pillen (Halle University) is producing similar material. Others question the broad application of 4000 lines by lot of users. Nils asked Roger to survey the status of available barley populations and those underway as well as what is additionally needed.

#### Item 5: PR, outreach

No enthusiasm about the IBSC flyer option, however, consent that it would help fund raising. More important is to prepare a summary of the current status of the IBSC project as well as a clear documentation of the individual achievement that have been made until now and how they fit into eachother. Nils will start writing such summary. Robby, Gary, Alan are willing to team up for this task. Should become available as advanced draft to be circulated among IBSC members by mid February.

#### Item 6: NEXT MEETING

Next IBSC business meeting to be held at PAG XIX. In between a routine of quarterly phone calls needs to be established. For individual parts of the project more frequent phone conferences (i.e. for coordination of data integration) may be needed.

Meeting closed at 9:00 pm.