

IBSC business meeting January 12, 2013, PAG XXI San Diego

Participation: Gary Muehlbauer, Robbie Waugh, Alan Schulman, Peter Langridge, Manuel Spannagl (p.p. of Klaus Mayer), Takao Komatsuda (p.p. of Takashi Matsumoto), Chengdao Li, Tim Close, Roger Wise, Nils Stein

Guests: Burkhard Steuernagel, Thomas Wicker, Peter Morell, Jesse Poland, Martin Mascher

Meeting starts with toast and congratulations on barley paper.

1. Annual Report. Paper written and published. ☺ IBSC members were informed that Mats Hansson wanted to join. Carlsberg Research Lab joined consortium and signed the MOU. Has grant of 300 k€ for three years for joining the consortium (plan is to use for MTP sequencing).
2. Structure of the IBSC revisited. Consortium was started with the idea of producing a reference sequence. Members have come in and out. Because major milestone has been achieved, do we need to revisit individual roles? Robbie: two goals, scientific and, secondly, members are contributing financially and/or scientifically. Peter: Is there another target for barley, if the goals have been met. Goal of sequencing of chromosomes. Other issue is the naming of genes and informatic issues. Robbie, Nils, Mats, Chengdao/BGI– together enough money for seq? Expression data, brought in? Coordination – more than one consortium, parallel? Another useful function has been of having an organization for funding – NSF etc asked if one existed when funding requests were made. Peter: we are a group interested in barley genomics research. We don't need to be exclusive. We form collaborative projects as the possibilities arise. Robbie suggests we revisit our research agenda and get a new position paper together and then each puts forward what they wish to contribute or have funding to do. Such as MTP, transcriptomics, hapmap diversity profiles. IBSC strategy paper was updated two years ago. Gary, Robbie, Nils will look into this and make a suggestion as to the way forward. Names against things have to be placed against what the chances are of getting it funded.
3. Progress on MTP sequencing. Nils: **3H** project was started three years ago. MTP sequencing was completed before Christmas, using 454 with 96 clones/ picotitre plate. Switched to Illumina HiSeq, once convinced assemblies “almost” as good. Using 670 barcodes and seq 670 together per lane, so in a single illumina run get half a chromosome. Also doing 8 kb matepairs, looking to see how much this helps. Hopefully assembled by end of January. Will switch budget now into a second chrom. **1H** together with Jena. Also **4H** will start. Prepped and in place. Within 2013 **1H** and **4H** will be finished. About 20-30 contigs per BAC is coming out. Nils has started a collab with Braunschweig on a PacBio, has bought consumables for 5X in the optimal case. IPK is running individual BAC preps rather than doing it in a plate, so it is laborious but good quality DNA!

Robbie: Chrom **2H** MTP will be completed in January as paired-end Illumina, but this gives 20-30 contigs per BAC. The matepair for Illumina reduces it to 2-3, so are discussing this now. To get enough DNA to make the matepairs, will need to do all the preps again. Now discussing WGS matepair libraries. But Burkhard says this will not get all the BACs done, will only help with some. Also can do diff length libraries, as is being done for oil-palm. Robbie says has funding for two or so chroms, but depends on whether they need to go back to make more BAC DNA preps or not.

5H Chengdao Li, China: 8462 BACs., 8097 assembled. Seq work finished about 1 week ago. 500 bp paired end libraries constructed Hiseq sequencing. Three pools. Scaffold N50. Need to clarify this with BGI. Has been individually barcoded, using 384 barcodes.

Peter: is doing chrom 7A now, because has been very frustrated. Maybe Peter will take **7H**, I'll take **6H**. Peter needs to give a clear message as to what has to be done, and needs to be done in Australia. Nils will send an IBSC letter to Peter indicating needs.

Tim: MTP sequencing of gene-containing BACs. Near the end now.... Harvest-Tutorial: BAC seqs have been posted. Go by Chrom 6HS. Has zip files behind. E.g. in 6HS, 394 BACs there. Assemblies done by Velvet on combinatorial pooling. Not much done yet on annotations. Put online in October. Can blast via harvest-blast.org for gene of interest in the BACs. This data is not in the gene-ome paper. 14k BACs, but not full sequences are there for searching. But no TEs there!
➔ So have many data sets, but what we need is better connectivity! The bioinformatic/web challenge to make the data useful. – see new strategy paper!

4. Final discussion.