

IBSC business meeting
Clermont-Ferrand, France, September 1, 2009, 16.00-18.00
Minutes

In attendance: Nils Stein, Kazuhiro Sato and Tsuyoshi Tanaka, Robbie Waugh, Alan Schulman (secretary for meeting), guests: Thomas Wicker

1. Nils Stein opened the meeting, presented the agenda.
2. Previous minutes: not reviewed; minutes were posted 18.09.09.
3. News: China (Zhejiang University, Hangzhou) has signed MoU. Chengdao Li has \$100 K grant for 5H contig sequencing from Morex. India (ICAR) is interested in joining, but has not yet signed the MoU or raised funds. China (and India?) will be represented at the next business meeting at PAG.
4. Funding prospects: Japan tried to get a large barley and wheat sequencing project, with the barley segment targeted at an MTP for 6H, but the proposal did not succeed. A 3H MTP proposal was scientifically approved (IPK) but funding decision is pending. Expected project start would be Jan 2010. IPK was contacted by the Patrick Boivin (Scientific Director of IFBM = French institute of brewing and malting / Qualtech, France), who expressed interest of taking advantage of the new barley genomic resources for improving malting traits in frame of a EU project. The question of bringing the brewers on board was discussed. Finland has had contacts in this regard with Carlsberg. UK has had contact with InBev (?)
5. Regarding fundraising and promotion of the project, the idea of generating an intermediate report to summarize where the genome sequencing efforts are now for barley was supported by those present. → a first draft will be prepared by Nils which then has to be circulated and advanced before PAGXVIII in January 2010.
6. Discussion on division of work. The discussion on funding strategies naturally also segued with a discussion on how to divide the work. The traditional approach, one taken by many other projects, is to place national flags on chromosomes. However, claims staked on chromosomes tend to change as funding situations change. Likewise, it may make more sense to divide work by technology inputs, especially as, or if, the BAC-by-BAC or BAC-pool strategy aimed at MTPs is complemented or supplanted by HTP shotgun approaches. (see attached discussion document)
7. Sequencing strategy discussion. Division of the work also entails the changing landscape of sequencing. The gold standard has been a MTP. The question becomes to what extent complementary and overlapping data from Solexa/SOLiD HTP short reads, paired-end/mate-pair reads, BAC-end reads, f1cDNA, HTP cDNA sequencing, gene assignment to BAC pools, using sequenced Brachypodium, rice, etc. genomes as hypothesis testers, will speed the process and complement or supplant MTP 454 sequencing. Computer simulation is needed. The question of WGS assembly was discussed. Is there but one computer in the world (Beijing?) that can do this?
8. Costs for an entire project. Nils ran through some estimates for costs, including 50-80 K BACs, 60X WGS, coming to a total of around 4 M€. (to 10 M€?)

9. A list of needs/resources/operational clusters was drawn up (if we integrate rather than go individually chromosome by chromosome, flag by flag (see attached discussion document):
 - 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

10. Nils closed the meeting.