

SGSC Conference Call
May 19, 2008
Draft Minutes

I. **Present:** A. Archibald, M. Caccamo, R. Clark, K. Eversole, D. Hamernik, L. Matthews, D. Milan, C. Rogel-Gaillard, and L. Schook.

II. **Action Items:**

- 1) Rogel-Gaillard, Beever, Schook, and Archibald will generate a list of BAC clones for the Y chromosome that are available in their labs. They will share this information with Sanger to see if these resources would facilitate sequencing the Y chromosome.
- 2) Schook will ask Rothschild to send a reminder to the ANGEN listserv for people to register for the Hinxton Pig Annotation Workshop. Registration deadline is June 6, 2008.
- 3) Archibald will draft an abstract for ISAG on the swine sequencing project and circulate it to the group for comment. Abstract deadline is May 30, 2008.

III. **Sequence Update:** Clark reviewed the updates that he distributed to the group last week. Sequencing of chromosomes 7 and 14 are going well. Chromosome 17 has sequence coverage of about 90%. A total of ~14,000 clones have been selected for sequencing and sent to the pipeline. This covers about 86.1% of the map. There are 1,624Mb of total sequence (61.2 Mb of finished quality) from 9,797 clones. About 5,180 clones have been sequenced to the “improved/finished” stage. He estimated that about 60.5% of the genome had been sequenced. Clark reminded the group that the original proposal planned to sequence 16,500 – 17,000 clones to cover the entire genome (all of the minimal tiling path). Schook thanked Clark and the entire Sanger staff for their excellent progress.

Archibald asked about the average size of the insert. Clark said that the average insert size for the library was about 170Kb. Some clones have inserts as large as 220Kb and the overlap is estimated to be about 20Kb.

Clark and Churcher (via email) indicated that Sanger had received a grant from BBSRC (in collaboration with Nabeel Affara, Cambridge University) to “finish” sequencing the X chromosome and for mapping/sequencing and targeted finishing on the Y chromosome using a fosmid library to be made at Sanger from a Duroc male cell line provided by the U. of Illinois. Targeted finishing is planned as they anticipate that the repetitive nature of the chromosome will prevent complete closure. They do not have an official letter approving the grant and they do not have the official start date of the grant. Schook and Archibald congratulated the Sanger group for securing this additional funding.

Churcher also provided information in an email message stating that Sanger has enough money for “pre-finishing” approximately half of the clones that are needed to complete the genome. They anticipate requiring a further ~\$950,000 to complete the process. Schook, Eversole, and Archibald will take this information to the Genome Canada meeting next week being convened in Ottawa.

Rogel-Gaillard asked if BAC clones from the INRA library would be helpful in sequencing the Y chromosome. They have done some FISH on the Y chromosome and used this to pull out BAC clones for the Y chromosome. She will generate a list of available Y clones. Beaver, Schook, and Archibald will do the same. Clark said that the BAC clones could be used as a scaffold.

IV. Annotation Update: Archibald and Caccamo reported that 18-20 people have registered for the Pig Annotation Workshop at the Wellcome Trust Sanger Institute, Hinxton on July 16-18, 2008 (www.sanger.ac.uk/Projects/S_scrofa/workshop_Hinxton08/index.shtml). They would like to have 5-10 more people participate in the workshop. They have room for at least 30 participants. Caccamo said that June 6 is the deadline for registering for the workshop. After June 6, he will send an email message to all participants with detailed information for the workshop. He will also add a tutorial to the website so that participants can download software before the workshop. He will also make sure that the sequence for genes of interest to the workshop participants is ready. Schook will ask Rothschild to send this information to the ANGENMAP listserv again. Caccamo's position at Sanger has not yet been filled. Churcher is working on this process.

V. SNP Chip Update: Schook said that the calls with the Illumina group are held every other Friday at 9:00 (Eastern time, US). The next call is May 30. Anyone is welcome to join these calls. In general, sequencing for SNP discovery is going well. Martien Groenen, Tim Smith, and Schook have exchanged libraries. Smith and Schook are conducting the 454 sequencing. They appear to be on target for generating the desired number of SNPs. Groenen will send a student to Archibald's lab to work on the bioinformatics pipeline. The SNP chip will be validated on the Sequenom platform with DNA from animals in the pools. Gary Rohrer at USDA-MARC (Clay Center, NE) will conduct the validation.

Schook reminded the group that August 22, 2008 is the deadline for purchase orders for the first round of SNP chips. They would like to have some SNP from the Y chromosome on the Illumina SNP chip.

VI. Other: Hamernik asked if anyone planned to submit an abstract on the swine sequencing project to the ISAG meetings. Archibald said that he plans to attend the ISAG meetings in Amsterdam. He could use one of his slots for an abstract on the swine genome sequencing project. He will draft an abstract and circulate it to the group for comments. The deadline for submitting ISAG abstracts is May 30, 2008.

VII. Next Conference Call: The next call for the SGSC Steering Committee will be on Monday, June 16 at 8:00 am (Eastern; US).