SGSC Conference Call
August 18, 2008
Draft Minutes

I. Present: A. Archibald, M. Caccamo, J. Cassady, C. Churcher, R. Clark, K. Eversole, D. Hamernik, V. Hansford, L. Matthews, E-W. Park, C. Rogel-Gaillard, G. Rohrer, and L. Schook.

II. Action Items:

1) Archibald will work with Tim Hubbard to determine how to move the annotations to Ensembl to make the information available to the public.
2) Caccamo said that the annotations could be made available to the public through Vega and he will check with Hubbard about doing this.
3) Schook and Churcher will submit a request for second, one-year, no-cost extension for the USDA-NRI grant to Hamernik soon after October 1, 2008.
4) At PAG in January 2009, Schook will begin to discuss a strategy for publishing the swine genome sequencing project and associated companion papers. He will also contact potential journal editors to gauge their interest in this project.

III. Sequence Update: Clark discussed the two graphs of sequence data that he distributed prior to the call. A total of ~15,262 clones have been selected for sequencing and sent to the pipeline. This covers about 92.4% of the physical map. There are 1,941Mb of total sequence (62.5 Mb of finished quality) from 11,721 clones. About 6,528 clones have been sequenced to the "improved/finished" stage. About 71% of the physical map has been sequenced. Fourteen of the chromosomes have more than 90% sequence coverage. They are now selecting the final 10% of clones from the physical map. The X chromosome is now about 60% sequenced. Clark estimates that about 16,500 clones will be needed to cover the entire genome (all of the minimal tiling path). They are also selecting some fosmid clones to close the gaps. Schook thanked Clark and the entire Sanger staff for their excellent progress.

Archibald noted that sequencing of SSC 4, 7, and 14 is almost completed. He asked when the sequencing of these three chromosomes would be finished. Clark indicated that they would keep sequencing these chromosomes until the end of the project. They will continue to select clones to fill in the gaps by a chromosome walking method. They are currently selecting one clone at a time to fill the gaps. This is the most efficient process but it is also time consuming. There are no BAC end alignments to the human sequence that are useful anymore.

IV. Annotation Update: Archibald and Caccamo reported that about 30 people participated in the Annotation workshop at Hinxton. The workshop was designed to facilitate training and about 100-200 genes were annotated. The annotations are not available in pre-Ensembl. Archibald will work with Tim Hubbard to determine how to move the annotations to Ensembl to make the information available to the public. Rogel-Gaillard attended the workshop and said that it was very well done. She asked how the annotations would be verified. Caccamo said that Tim Hubbard would conduct standard checks of the annotations before they were released to the public. He also said that the annotations could be made available to the public through Vega and he will check with Hubbard about doing this.

V. SNP Chip Update: Schook said that the consortium has finished sequencing for SNP discovery. More than 300,000 SNP have been generated with the reduced representation sequencing approach in a very short amount of time. They are now selecting 60,000 SNP for the chip. They will likely use 50-100 SNP from wild boars. Some SNP from the Y chromosome may also be used to distinguish wild boars from domestic boars. Schook thanked the Illumina staff, Jerry Taylor, Bob Schnabel, and Curt Van Tassell for their assistance.

The consortium is also selecting 288 animals to validate the chip through Illumina. They plan to use about 30 animals/breed for the validation assay. Breeds will include those that were used in SNP discovery (e.g., Yorkshire, Duroc, Pietrain, Landrace, and Large White).

Schook reminded the group that August 22, 2008 (5:00 p.m. Pacific Time) is the deadline for purchase orders for the first round of SNP chips. They are very close to having $4 million in orders which would make the cost $100/sample (Tier C = the cheapest rate).

IV. Reminder--No-cost Extension for USDA-NRI Grant: Hamernik reminded Schook to submit a request for a second, one-year no-cost extension. The request can be submitted to Hamernik anytime after October 1, 2008. Schook and Churcher have the deadline on their calendars.

V. Eversole asked if anyone had begun to discuss plans for publishing the swine genome sequencing project. She was recently asked about the status of the swine genome sequencing project by an editor from *Science*. Schook said that these conversations had not yet been initiated. He plans to discuss this topic at PAG in January 2009. He will also begin to compile a list of potential companion papers to discuss at PAG in 2009. He will also contact appropriate journals to gauge interest in publishing these papers.

Churcher reported that they are still waiting on the official letter to begin sequencing the Y chromosome. She expects the letter in October 2008. The grant is for three years.

Archibald plans to travel to Genome Canada around September 1, 2008. He will visit with Marco Marra about full-length cDNA sequencing or the use of next generation DNA sequencing technologies. In the past, Marra has been interested in the swine genome sequencing project but has indicated a lack of funding at Genome Canada for the project.

VI. Next Conference Call: The next call for the SGSC Steering Committee will be on Monday, September 15 at 8:00 am (Eastern; US).