SGSC Conference Call
February 23, 2009
Draft Minutes

I. Present: A. Archibald, C. Churcher, R. Clark, K. Eversole, M. Groenen, D. Hamernik, V. Hansford, W. Liu, D. Milan, C. Rogel-Gaillard, and L. Schook.

II. Action Items:

1) Archibald, Groenen, and Schook will develop a strategy for incorporating RNASeq data into the swine sequencing/annotation projects.
2) Schook and Groenen will identify a date near the end of March for a teleconference to discuss progress on the SNP and HapMap analyses and the associated manuscript. Hamernik will set up a conference call if needed.
3) Schook and Archibald will draft an agenda for a conference to be held at Sanger in November 2009 to discuss preparation of the sequencing/assembly/annotation manuscript and companion papers.

III. Welcome Groenen and Liu: Schook welcomed Martien Groenen (Wageningen University) and Wansheng Liu (Pennsylvania State University) to the SGSC. Groenen has been working with the pig SNP chip project. Liu has been working with the BTAY and SSCY chromosomes. He is trying to place ~12,000 markers from the porcine 7,000 RAD RH panel and SNPs on the same map.

IV. Sequence Update: Clark distributed a PowerPoint file with 2 slides showing the overall progress on the swine genome sequencing project prior to the call. A total of 16,239 clones have been selected for sequencing and sent to the pipeline. This covers about 96% of the physical map. There are 2,597 Mb of total sequence (66.9 Mb of finished quality) from 14,932 clones. About 9,044 clones have been sequenced to the "improved/finished" stage. He estimated that about 88.18% of the physical map had been sequenced. Clark also said that members of the Sanger sequencing team had indentified about 620 gaps in the sequence assembly. They are working to pick some additional clones to fill in the gaps with additional sequence to increase the quality of the end product.

Churcher described the progress on sequencing SSCX and SSCY. Sanger recently received the official award letter and funding for this project. Funding was slightly decreased compared to the initial budget request. Chris Tyler-Smith is the Sanger PD for this project. The sequencing team at Sanger will begin to finish/improve SSCX and they will generate libraries for SSCY. Schook thanked Clark and the entire Sanger sequencing team for their substantial progress as well as their efforts to generate a high quality draft genome sequence for swine.

IV. Annotation Update: Archibald said that plans are being made to move SSC4, SSC7, and SSC14 sequence from pre-Ensembl to Ensembl. They will start another gene build now and plan for another gene build in the Fall. They will also start to build a gene list.

Archibald also mentioned that he was working with staff at Ensembl to try to obtain access to the BGI swine sequencing data and to develop a plan for how to use the BGI sequence in the Sanger swine genome sequencing project. The BGI data is 20-30X and some paired-end sequences using Solexa technology. The sequence is not yet available to the public but it is expected to be available after BGI performs some annotation this Summer.

Archibald also mentioned that RNASeq data with next generation sequencing technologies and a range of tissues would be extremely useful for the assembly and annotation phases of the Sanger project. Archibald has some funding to perform CAGE in macrophages and a limited number of other tissues. Groenen may have some funding for RNASeq in brain, testes, and liver. The group decided that it would be better to perform RNASeq on more tissues from one animal (rather than a few tissues from several animals) as this would provide better information for annotation.

V. SNP Chip Update: Groenen said that they now have data from all 1,150 animals in the HapMap project. About 59,000 SNPs are informative in at least one breed while about 56,000 SNPs are very useful in most of the breeds. On the last SNP chip call in December the group made assignments to individuals for various analyses and sections of the manuscript that describes design and characterization of the Illumina SNP Chip. Schook and Groenen will identify a date near the end of March for another teleconference to discuss progress on these analyses and the manuscript. Hamernik will set up a conference call if needed.

VI. Publication Strategy: Schook summarized the meeting of some SGSC members with Laura Zahn (*Science*) at PAG in January 2009. He also indicated that Pete Burfening (USDA-CSREES) encouraged Schook to submit an application to the AFRI competitive grants program for partial funding of a conference to organize a group to begin to work on the sequencing/assembly/annotation manuscript. Churcher said that the facilities at Sanger are available in early November for a small conference (50 people max). Schook said that there would likely be 30-40 people in attendance. The conference will be organized around the topical sections of the manuscript and companion papers. Schook and Archibald will draft an agenda for this conference.

VII. Next Conference Call: The next teleconference will be held on Monday, March 16 at 8:00 a.m. (Eastern Time, US).