Swine Genome Sequencing Consortium
Conference Call

18th June 2007

On call: Alan Archibald, Jon Beever, Mario Caccamo, Patrick Chardon, Ronnie Green, Deb Hamernik, Denis Milan, Sean Humphray, Jane Rogers, Larry Schook.

Minutes: Sancha Martin (Sanger)

1) Update on Sequencing Pipeline

Sean circulated a Power Point presentation immediately prior to the call which demonstrated the progress of sequencing across the chromosomes (see below). Chromosomes 4, 7, 14 and 17 have had essentially all clones possible across the map picked due to the push to expend the additional funding secured on these particular chromosomes. Next Sanger will concentrate on chromosomes 11 and 1 which are over 40% sequenced and aim to include these in the next ensemble release.

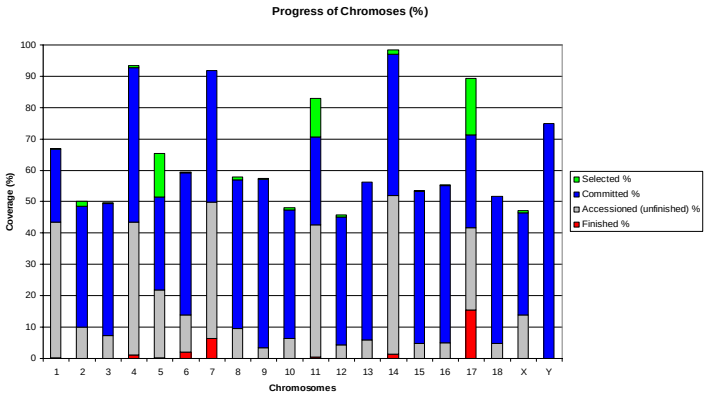

Figure 1. Sequence Clone Progress 18/06/07

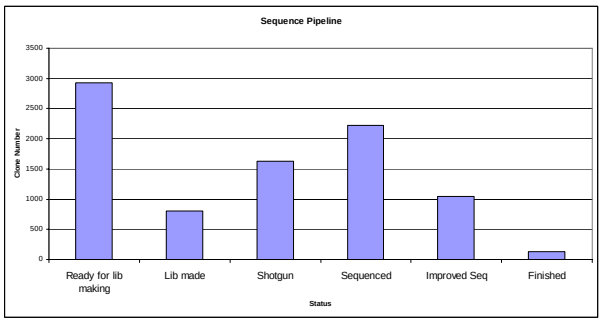

Figure 2: Internal Sanger Clone Pipeline Status

Figure 2 details the internal Sanger figures, where the first 3 columns represent clones that are either confirmed and waiting to be library made, library made but queued to go on the sequencing machines or sequencing is actually in progress. The last three columns show statistics that are externally available.

Recently Sanger has experienced some difficulties securing commercial sequencing vector of appropriate quality and have resorted to making their own. They have carried out tests with modified protocols and hope to resolve the problems very quickly.

Mario is working on the release of chromosomes 1 and 11 with approximately 40% sequence coverage, and is hoping to assemble and run analysis touching on gene like structures identified using conservative criteria which can be viewed in pre-Ensembl. All other chromosomes will be updated to include data from clones generated in the last few months.

Alan informed the group that the Roslin Institute has filled their annotation post and has appointed Dr. Tang, who will communicate with Sanger to coordinate tasks.

Jane confirmed that Sanger have trialled sequencing of pig BAC clones with 2 sequencing runs on the Illumina sequencer using one lane of 5 overlapping combined BACs and another lane of 5 non-overlapping combined BACs. These were single ended runs that Ewan Birney has assessed and provided stats that indicate that contiguation of the data to larger portions is not yet possible. More information is required to build scaffolds and Sanger will look at whether this should come from a paired end run or by fosmid sequencing. The high polyA content of the genome means that it does not lend itself to 454 technology at this time. Jane will update the group as information becomes available.

2) Update on ARS Funding

Ronnie Green reported that he anticipated $840,000 will be provided from ARS and there may be a possibility of increasing this figures to $1M. Ronnie would discuss arrangements with Larry for transfer of the funds to Sanger.

3) Update on Genome Canada Meeting

To clarify: additional funding is required to deliver a draft equivalent to 6x – that is actually 4x coverage with prefinishing across the genome which should provide more information on the order and orientation of the genome. It will provide 99% sequence coverage with approximately 65,000 contigs, an average contig length of 42Kb and 5% of genes are expected to be misordered. This method ensures that the species will be at a competitive level for the future.

Feedback from Genome Canada after the meeting indicated that the lack of strong industry support for the genome project reduced the chance of an initiative being developed.

4) National Pork Board Funding Request

Larry had forwarded a set of Power Point slides to Mark Boggess, National Pork Board, to illustrate the need for further funding and will contact Mark to discuss next steps. Larry expressed his grateful thanks for Sean's input to the slides.

5) EU funding requests and opportunities

Alan reported on a recent meeting held in Paris to discuss a Framework7 application, which might include funding for pig sequencing – between €600,000 and €1M could be available. The application is coordinated by André Eggen and was likely to include new sequencing technologies – Jane will contact André.

6) Next SGSC Workshop

It was agreed that it would be most sensible to host the meeting at INRA on the 26th October as a satellite meeting to the Animal Genomics for Health meeting already scheduled for 23-25th October.

7) Other business

Jon has constructed cDNA libraries and has sequenced ~200 clones to look for a G cap the results so far have been results. Illinois are processing the MTA for Hirohide at the moment and Jon will follow up to discuss whether specific tissues or cDNA's would be transferred.