Conference Report:
At PAG, USDA's $10M Primes Swine Genome Consortium for Year of the Pig

The first sequence of the swine genome will be completed thanks to funding from the US Department of Agriculture, expertise from eight academic institutions, and DNA from a dead but not forgotten Duroc sow.

On the opening day of the Plant and Animal Genome conference in January, USDA Secretary Mike Johanns announced the award of a two-year, $10 million grant from the agency's Cooperative State Research, Extension, and Education Service. The announcement came one year after Joseph Jen, undersecretary for Research, Education and Economics, announced the agency's intent to issue the sequencing RFA, and little more than two years since swine researchers organized themselves in Jouy-en-Josas, France, to tackle the project.

Jen, who leaves his post this month, said at the conference that he's "heaving a sigh of relief" as he watches the swine genome consortium members get started on the draft sequence. If all goes according to plan, a low-coverage draft will be ready for 2007.

Lawrence Schook, co-chairman of the international Swine Genome Sequencing Consortium and professor of animal sciences at the University of Illinois at Urbana-Champaign, is leading the two-year project, which is expected to cost $20 million to complete. Setting a timetable to get to this point has been "the most significant thing I've ever done in my professional life," Schook said at a workshop at the conference.

Jane Rogers at the Wellcome Trust Sanger Institute will oversee the sequencing of the 2.7 Gb swine genome, itself comprised of 18 autosomes, with X and Y sex chromosomes. The initial goal of the project is to create a BAC skim of the genome at 3x coverage. At PAG, Rogers credited the international effort that has gone into putting together a sequencing strategy. "We are looking forward to getting going," she said.

Although the USDA award is earmarked for creating a low-coverage draft sequence, higher coverage is still the ultimate aim. Whole-genome shotgun libraries have already been constructed and are being sequenced. Rogers explained that a hybrid sequencing approach — in which 3x coverage of BACs are combined with 3x WG-shotgun libraries — will be used to develop a 6x coverage draft eventually.

A keystone of the consortium's strategy is to make the resulting sequence as available and useable to the public as possible, Rogers added at the conference. To that end, all sequence traces will be deposited into trace repositories, while high-throughput data will be submitted to public databases.

Jonathan Beever, professor of animal sciences at the University of Illinois, demonstrated the completion of the first high-resolution human-pig comparative map, which provides the scaffold for BAC physical map assembly.

Beever has also characterized the pig transcriptome, which required the creation of "an autologous reagent resource for genome sequencing." That is, he took the DNA from a single sow, cultured fibroblasts to create cloned piglets, and either collected tissue for cDNA libraries or generated shotgun libraries from fetal fibroblasts.

The sow on which the sequence will be based died last year, but Beever's work has ensured that its genetic legacy will live on. He also had a taxidermist preserve the pig's head, which was subsequently left on Larry Schook's desk. While the resulting sequence data will be freely available to the public without restriction, the pig's head will likely stay in Schook's office.

— *JL Crebs*

Supplemental web links:
http://www.intl-pag.org/14/14-swine-seq.html
http://www.swinegenomics.com/genome_project.php