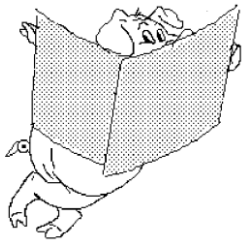

Pig Genome Update
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Special Issue

Happy Holidays and New Year to you, your families and colleagues!!

Pig Genome Update **reaches the century mark!** It seems hard to believe that this publication has now been published for over 13 years. A lot has happened in the "pig genome business" and I feel especially proud to have worked with those of you in the community who have not only contributed to the effort but have helped to move forward the science of genomics of livestock species. It seems premature to predict what the next 5 or even 10 years will produce in opportunities, challenges or discoveries but one thing is clear is that we have, as a community, accomplished a great deal and we owe thanks to many people. In this special issue I have asked for a few contributions from people from science, government and industry who have different viewpoints of the progress made. These items are listed below.

First draft sequence of the pig genome was announced at the recent Pig Genome III meeting at the Sanger institute. We owe a big thanks to all the many contributors, and all those within the field that have helped at Sanger and around the world to get us to that point. A total of 160 attendees came to this historic meeting where speakers presented updates on several subjects related to the sequencing effort and plans for the future. The deadline has passed for new clones to enter the sequencing pipeline. However, some new clones are being identified as a possible resource for future sequence gap closure. These identified BACs currently stand at ~150 and have been identified using physical map and sequence information. All chromosomes are over 90% sequenced taking the genome to 95.72% from 16,974 sequenced clones. About 94% of the genome is at the "Improved" status (15720 clones). There is 123Mb of finished quality data within the 2.994Gb currently available. Sanger will continue with chromosome X/Y sequencing – chromosome X clones sequenced in the genome project will be finished and the map will continue to be refined using a fosmid library too. Sanger has produced a chromosome Y fosmid library which is currently being fingerprinted. This will be used to select up to 1100 fosmid clones for sequencing and finishing. This work is funded by BBSRC. In collaboration with TGAC (Norwich, UK) the remaining BAC clones which have been selected from the fingerprint map will be pooled and sequenced on the Illumina platform. A further x10 coverage of Duroc sow DNA will be produced on the Illumina platform to be combined with the BGI data and assembled (also in collaboration with TGAC). Automatic annotation will continue to be provided by Ensembl. Another annotation jamboree is to be organized in 2010 (kindly provided by Carol Churcher and Richard Clark).

Communication, Collaboration, and Leveraging…the goal of federal funds. It's hard to believe that 100 issues of the bimonthly Pig Genome Update have been published! Way back in 1993, the USDA National Animal Genome Research Program was established and supported by off-the-top Hatch formula funds. Much has changed with regard to funding research in animal genomics…and the future of funding for animal genomics will undoubtedly continue to change as the world recovers from the current economic recession, as new zoonotic diseases such as H1N1 emerge, and

as pork producers deal with competing demands on corn and soybeans for feeds and fuels. What hasn't changed is the importance of ***communication, coordination***, and ***leveraging of resources***…and these are the major impacts of the bimonthly Pig Genome Update from an administrative point of view. ***Communication***…including timely dissemination of funding opportunities, changes in policies and procedures at the USDA-NIFA (CSREES), and upcoming conferences are a regular feature of the bimonthly Pig Genome Updates. In addition, all of this information (and more) is archived on a user-friendly website (www.animalgenome.org/pigs). ***Coordination***...of scientists to participate in multi-state research projects, replication of experiments at different research stations, and the opportunity to provide stakeholder input on how best to spend limited funding to generate resources for the pig genomics research community have resulted in extremely valuable genomics tools for pigs (e.g., genetic maps, QTL maps and databases, primers and probes, a 13,000 element oligo microarray, and a 60,000 SNP chip). ***Leveraging of resources***…a relatively small amount of off-the-top Hatch formula funds invested in the Pig Genome Coordination Program have resulted in several NRI, AFRI, and National Pork Board grants to independent investigators as well as larger grants to teams of investigators to sequence the swine genome, develop a SNP-based genotyping platform, and address issues related to the genetics of swine health and disease. As we look to the future…the new NIFA administrators are emphasizing *focus, scale, and impact* as well as increased funding for competitive grants. Thus, another 100 issues of the bimonthly Pig Genome Update will likely be needed for effective communication between scientists and federal funding agencies as well as coordination of the pig genome research community as we move toward implementing whole genome selection and marker-assisted management strategies in pork production systems. We owe a tremendous thanks to our Coordinator for volunteering to serve as the Pig Genome Coordinator nonstop since 1993 (kindly provided by Dr. Deb Hamernik).

This pig gene went to market – an industry perspective. The meeting at Hinxton to celebrate the "completion" of the pig genome sequence was a great opportunity to reflect on how far we have come since our lab cloned a repeat sequence from the pig Y chromosome to enable us to evaluate semen sexing in the late 80's. Commercial semen sexing still remains to be cracked for the pig, but the Y chromosome is going to yield more information in the coming months as my old Cambridge collaborators take it through targeted sequencing. The results will provide new insight into sex chromosome evolution and may even help understand the potential to change the sex ratio and take me back to the beginning again. It would have been difficult to believe then that we would, within 20 years, be able to search for any sequence of interest from our desks and put it to work. We were about to start hunting for the "halothane" gene and begin to think about candidate gene approaches utilizing the first results being generated from our model species, man and mouse. It was a relatively slow process with lots of false starts or dead ends and industry geneticists had a relatively short list of targets. Molecular biology was only expected to have a role in helping identify "major genes" such as the mutation causing porcine stress syndrome (and pale soft exudative meat) or the dominant white color – the list was short. However, at that time results from tomatoes pointed some of us towards "quantitative trait loci" and the potential for a new approach to pig improvement. The PiGMaP project began in 1991 and included the development of the statistical tools as well as beginning the mapping of QTLs in the pig. Fittingly, many of those pioneering this international collaboration were at Hinxton. Then in 1994 researchers presented results showing an association between a polymorphism in the estrogen receptor locus and litter size in pigs kicking off renewed industry interest in the search for DNA markers that could help make faster progress for "difficult to

measure" traits. Progress has definitely been slower than we had hoped, one of my current colleagues often reflects on how optimistic, or was it deluded, we were to think we could do it with such limited tools. However, all of the major pig breeding companies are already using DNA markers within their programs and they continue to embrace the opportunity presented by the new high throughput tools such as the Porcine 60K Beadchip: one of the by-products generated by the Pig Genome Sequencing Consortium. Remarkably this provides a SNP genotype at something like one ten thousandth of the cost of the first commercial marker test introduced in 1991. Much still needs to be done but the genomic tools are not the hurdle nowadays, it is the development of the phenotypes required to exploit them which is the next issue to consider. It was pleasing to see how the community is rising to the challenge and investigating traits such as disease susceptibility, sow longevity, and even maternal infanticide (sow aggression). Congratulations everyone on setting the standard for collaboration and delivery (kindly submitted by Graham Plastow).

Pigs as humans? Much of the emphasis to sequence the pig genome came from agriculture, as the pig is a very important source of protein as food for the world's population. But the pig has another great, but often underappreciated value, i.e. that of a scientific model for humans. The National Institutes of Health spends millions of dollars each year extramurally on research based on the pig. Why? Because the pig not only has a size and physiology similar to humans, but as we continue to learn it also has a genome that is similar to humans. The pig is an excellent model for things like cardiovascular disease, cutaneous pharmacology, ophthalmology, obesity, etc., and pigs are considered as a possible source of organs for xenotransplantation. Even without a completed genome genetic modification of pigs has moved forward as transgenes have been added to create pigs that produce pharmaceuticals such as human coagulation factors VIII and FIX, other transgenes have been added to create disease models like retinitis pigmentosa and Alzheimer's Disease. Genes have been knocked out to develop pigs for xenotransplantation or create pigs with cystic fibrosis. Previously, if a genetic modification was to be made in the pig the basic genetic information had to first be assembled. Now with a draft of the genome a researcher that wants to knockout or knockin a gene can immediately access the genomic information for the pig and begin building the necessary constructs. The sequence of the pig's genome is so important that if the pig genome sequencing project did not move forward the pig would have become a second-class species to the biomedical community. Now the pig will remain an important component of understanding human health (kindly submitted by Randall S. Prather).

Regular news items

Dreaming of San Diego and PAG? Warmer weather and great meetings are just around the corner. See http://www.intl-pag.org/ for more information. Scheduled PAG XVIII plenary speakers include Eric Schadt, Peter Raven, Howard Jacob, Evan Eichler, Joanne Chory, Robb Fraley and Vicki Chandler. It promises to be a great meeting. Cathy Ernst (ernstc@msu.edu) is organizing the Swine workshop for January 9.

National Swine Improvement federation meeting was recently held in Nashville, TN. Attended by nearly 75 people, the meeting included a special session devoted to genetic markers, genomic selection and opportunities for the future. Featured speakers were Mark Boggess, USDA ARS, Sally NorthCutt, American Angus Association and Alan Mileham, PIC. Other speakers also presented early SNP chip data. The proceedings should be available in the near future.

The 2009 International Porcine reproductive and respiratory syndrome (PRRS) Symposium was held December 4-5, 2009 in Chicago. PRRS is the most economically significant disease of swine in the U.S. and worldwide. The PRRS Symposium brings together scientists involved in all aspects of PRRS research; researchers, students, swine health specialists, and pork producers. This year over 280 scientists from 25 countries attended the meetings that included 2 keynote talks, the first by Juergen Richt, Kansas State Univ., on "Swine Influenza and the Need for Rationally Designed Vaccines" and the second by Tomasz Stadejek, National Veterinary Research Institute, Poland, on "Genetic diversity of PRRSV - global emergence and evolution." There were an additional 16 talks selected from the 97 submitted abstracts that were all presented as posters [a 23% increase over 2008]. The abstracts covered viral structure, design of infectious clones, host-virus interaction, vaccines, immunity, genetic resistance, ecology and viral elimination strategies. The Proceedings of the 2009 PRRS Symposium will be posted on the website www.prrssymposium.org. Next year's meeting will be held December 3-4, 2010 in Chicago. An association trial aimed at resistance to initial PRRSV infection, supported in part by the Pig Genome Coordinator is well underway. (kindly submitted by Joan Lunney).

Help exists for Genetic Line Preservation and Use. The USDA ARS National Animal Germplasm Program (NAGP) can serve as a way to preserve your research lines. NAGP has the ability to freeze semen, and other tissues, and securely store it long term. These resources are available to preserve research lines either to capture genetic variation at phases during the project, freeze the foundation population as an example, or to preserve material from lines that are being terminated. So, if you are interested in preserving any of your genetic lines, contact either Terry Stewart (tstewart@purdue.edu, 765-494-0138), chairman of the swine species committee or Harvey Blackburn (Harvey.Blackburn@ars.usda.gov, 970/495-3268). For parties interested in maintaining ownership of the material there is the option of establishing a material transfer agreement with USDA/ARS. NAGP can also be a source of genetic material for genomic studies in all the economic species. To learn more NAGP and the extensive material already in the collection, visit the NAGP web site at http://www.ars.usda.gov/Main/docs.htm?docid=16979 (kindly submitted by Terry Stewart).

Upcoming meetings (see: http://www.animalgenome.org/pigs/community/meetings.html**)**

Tenth International Long-oligonucleotide Microarray Workshop, Jan. 3-8, 2010, U. of Arizona, Tucson, AZ. For further details and to register, please contact David Galbraith (galbraith@arizona.edu) or Georgina Lambert (georgina@cals.arizona.edu).

Plant & Animal Genome Conference, PAG XVIII, Jan. 9-13, 2010, Town & Country Hotel, San Diego, CA. Information available at http://www.intl- pag.org/ and see above.

Advances in Genome Biology & Technology meeting, Feb. 24-27, 2010, Marco Island, FL. See www.agbt.org for more info.

Animal Genomics for Animal Health International Symposium, 31 May - 2 June 2010, at the Maison de la Chimie, Paris France, See https://colloque.inra.fr/agah2010/ for more info.

International Society of Animal Genetics conference will take place in Edinburgh (UK), July 26-30, 2010. For details see http://www.isag.org.uk/society/conferences.asp

The 9th World Congress on Genetics Applied to Livestock Production (WCGALP), Aug. 1-6, 2010, Leipzig, Germany. For more details visit http://www.wcgalp2010.org/.

The 9th International Veterinary Immunology Symposium, August 16-20, 2010, Tokyo, Japan For more details visit http://9th-ivis.jtbcom.co.jp.

Pig Genome Update Newsletters are distributed electronically through AnGenMap, the Animal Genome Discussion Group (http://www.animalgenome.org/community/discuss.html). Previous newsletters are at http://www.animalgenome.org/pigs/newsletter/index.html. Coordinator updates can also be found http://www.animalgenome.org/pigs/community/NRSP8/. Please provide your input as the Swine Genome Coordinator is always glad to hear from NRSP-8 members and other readers about ways that we can improve the coordination effort or provide resources that are needed and with which we may be able to help. Also, let us know if you have items of general interest to include in this Newsletter.

Refunding of the NRSP8 requires some help from each of you. We are continually asked what the coordinators money does. Many of you have received reagents, arrays, SNP chip and some of this has been augmented by funds from coordinator activities. Please send by December 1, 2009 to mfrothsc@iastate.edu any grant titles and dollar amounts for the past 3 years for any project helped by reagents, tools and bioinformatics in part supplied by the Pig genome Coordination program.

Items for *Pig Genome Update 101* can be sent to me by no later than February 15 please.

Max F. Rothschild
U.S. Pig Genome Coordinator
2255 Kildee Hall
Department of Animal Science
Iowa State University
Ames, Iowa 50011
Phone: 515-294-6202
Fax: 515-294-2401
mfrothsc@iastate.edu

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