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Conference Review

Swine Genome Sequencing Consortium (SGSC): a strategic roadmap for sequencing the pig genome

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Abstract

The Swine Genome Sequencing Consortium (SGSC) was formed in September 2003 by academic, government and industry representatives to provide international coordination for sequencing the pig genome. The SGSC's mission is to advance biomedical research for animal production and health by the development of DNA-based tools and products resulting from the sequencing of the swine genome. During the past 2 years, the SGSC has met bi-annually to develop a strategic roadmap for creating the required scientific resources, to integrate existing physical maps, and to create a sequencing strategy that captured international participation and a broad funding base. During the past year, SGSC members have integrated their respective physical mapping data with the goal of creating a minimal tiling path (MTP) that will be used as the sequencing template. During the recent Plant and Animal Genome meeting (January 16, 2005 San Diego, CA), presentations demonstrated that a human–pig comparative map has been completed, BAC fingerprint contigs (FPC) for each of the autosomes and X chromosome have been constructed and that BAC end-sequencing has permitted, through BLAST analysis and RH-mapping, anchoring of the contigs. Thus, significant progress has been made towards the creation of a MTP. In addition, whole-genome (WG) shotgun libraries have been constructed and are currently being sequenced in various laboratories around the globe. Thus, a hybrid sequencing approach in which 3x coverage of BACs comprising the MTP and 3x of the WG-shotgun libraries will be used to develop a draft 6x coverage of the pig genome. Copyright © 2005 John Wiley & Sons, Ltd.

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Background and discussion

The pig genome is of similar size, complexity and chromosomal organization ($2n = 38$, including meta- and acrocentric chromosomes) as the human genome. Over the past decade tremendous progress

has been made in mapping and characterizing the swine genome. Currently, moderate- to high-resolution genetic linkage maps containing highly polymorphic loci (Type II) have been produced using independent mapping populations (Rohrer *et al.*, 1996; Ellegren *et al.*, 1994; Archibald *et al.*,

1995). Additionally, physical mapping methods such as somatic cell hybrid analysis (Rettenberger *et al.*, 1994; Yerle *et al.*, 1996), in situ hybridization, and ZOO-FISH (Chowdhary *et al.*, 1996; Fronicke *et al.*, 1996; Goureau *et al.*, 1996) have been employed to enrich the Type I marker map, and to perform comparative analysis with map-rich species such as the human and mouse. To date, >3000 mapped loci are catalogued for the pig genome (<http://www.thearkdb.org>). Recently, whole-genome radiation hybrid (WG-RH) panels (7500 and 12 500 rad) have been generated for swine (Hawken *et al.*, 1999; Yerle *et al.*, 2002), resulting in yet another rapid increase in the number of expressed sequences being mapped, facilitating comparative mapping with other species (Rinke *et al.*, 2002). The swine genomics community has also acquired access to resources such as bacterial artificial chromosome (BAC) libraries (Fahrenkrug *et al.*, 2001; Anderson *et al.*, 2000) that provide approximately 35× coverage of the swine genome. These BAC resources have facilitated the production of high-resolution physical maps in specific chromosomal regions (Rogel-Gaillard *et al.*, 1999; Milan *et al.*, 2000) and support the construction of sequence-ready mapping resources for the porcine genome.

Comparative maps have indicated that the porcine and human genomes are more similarly organized than when either is compared to the mouse (Thomas *et al.*, 2003). The mean length of conserved syntenic segments between human and pig is approximately twice as long as the average length of conserved syntenic segments between human and mouse (Ellergren *et al.*, 1994; Rettenberger *et al.*, 1995). Furthermore, the organizational similarities between the human and porcine genomes are reflected in similarities at the nucleotide level. In more than 600 comparisons of non-coding DNAs aligned by orthologous exonic sequences on human chromosome 7, pig (and cow, cat and dog) sequences consistently grouped closer to human and non-human primate sequences than did rodent (mouse and rat) sequences (Thomas *et al.*, 2003). Furthermore, the rodent genomes are evolving at a different (faster) rate than other representative genomes. For these reasons it is necessary to produce the genomic sequence for eutherian mammals outside the primate and rodent lineages in order to better assemble and annotate the human sequence. During the Plant and Animal

Genome meeting, it was reported that a 1.0 Mb human–pig comparative map has been completed (Meyers *et al.*, 2005). This map will provide the basis for creating a MTP that will be used as the template for genome sequencing.

Harvesting genomic information

The porcine research community has a long history in quantitative genetics, and more recently in genomics research. The genetic contribution of many polygenic traits in pigs is well documented, and this knowledge has provided the basis for the identification and mapping of a growing number of quantitative trait loci (QTL) (Andersson *et al.*, 1994; Milan *et al.*, 2000; Rohrer *et al.*, 1999; Wilkie *et al.*, 2000; Paszek *et al.*, 2000; Malek *et al.*, 2001a,b; Nezer *et al.*, 2002). These maps have been used to identify chromosomal regions that influence quantitative traits affecting growth, body composition, reproduction and immune response (Bidanel and Rothschild, 2002). The quantitative trait loci defined in these studies often span 20–40 centiMorgans (cM) and perhaps correspond to about 20–40 Mbp of DNA. These initial scans for the gene(s) controlling the phenotype of interest generally only reduce the search space to 1–2% of the genome, perhaps to 200–400 positional candidate genes. Locating the gene(s) responsible and identifying the causal molecular genetic variation is a major challenge. Nevertheless, there have been some striking successes in achieving this goal in pigs, to which some of the co-authors have contributed.

The only limitation to performing direct genetic experiments and identifying genes underlying these traits is the lack of a complete genome sequence. Selection experiments, heterosis studies and breed comparisons have all been used in porcine genetic studies. Many populations have been used to map genes to large chromosomal regions but positional mapping of causal genes has been difficult. Sequencing the porcine genome and generating 100 000 SNPs will provide additional polymorphic markers and positional candidate genes based on the human and mouse map. Large populations with designed matings can be used to positionally map genes. The populations can be generated by natural reproduction, artificial insemination or assisted reproductive technologies. Clones can also be generated from fibroblasts or stem cells and

cryopreserved. This technology provides the opportunity for knock-out or knock-in experiments in an animal other than the mouse. Interspecies porcine hybrids are easily produced and are very valuable for knock-out/knock-in experiments and studying genomic imprinting (Andersson *et al.*, 1994).

Justification for sequence information

A CREES-USDA workshop during the summer of 2002, The Allerton III Conference ('Beyond Livestock Genomics') was designed to bring together leading investigators from broad disciplines (physiology, reproduction, animal health, nutrition and genetics) to begin to develop a plan for full utilization of genomic information to promote animal health and production (Hamernik *et al.*, 2003). In February 2002, the National Academy of Sciences organized a public workshop, 'Exploring Horizons for Domestic Animal Genomics', to identify research goals and funding needs. Subsequent discussion identified a growing need to have a broader context for discussion to ensure full utilization of the genomic information and tools in support of animal research. Thus, the Allerton III Conference provided a venue for discussion of how genome sequences could be harvested to support the broader animal agricultural community, while contributing to life science discovery. The objectives of the Allerton III Conference included: (a) identification of genomic and bioinformatic tools and reagents required to exploit information from the human genome initiative; (b) discussion of needs and opportunities for full implementation of genomic capabilities by related disciplines; and (c) identification of needs and opportunities to ensure full technology transfer and commercialization (Hamernik *et al.*, 2003).

The Swine Genome Sequencing Consortium (SGSC)

In September 2003, interested researchers convened at INRA-Jouy-en-Josas to establish the SGSC for facilitation and coordination of international efforts toward obtaining the complete porcine genome sequence. A coordinated international effort was initiated to develop a porcine BAC map with two BAC libraries (RPCI-44 and CHORI-242) made by Pieter J. de Jong, one library made at the Roslin Institute (Anderson *et al.*, 2000), and a library produced at

INRA (Rogel-Gaillard *et al.*, 1999). Through the exchange of BAC clones, data has been merged to permit a comprehensive analysis. INRA has screened more than 1000 BACs from this library for known genes and markers and has mapped them on genetic and RH maps. INRA is sharing this set of BACs to facilitate anchoring of contigs. Sequencing the ends of all fingerprinted BAC clones has also been conducted. The current status of the fingerprint contig (FPC) was discussed at the PAG 2005 meeting (Humphray *et al.*, 2005; see Table 1). The final product, which is scheduled for completion in July 2005, will represent 20× coverage of the porcine genome.

During the past year, significant allocation of resources has occurred with respect to positioning the porcine genome sequencing initiative. This has included the development of a whole genome porcine BAC fingerprint with complete BAC end-sequencing. Thus, to date, the SGSC has completed sequencing of over 500 000 BAC ends (see Table 2), which represents over 13% sequence coverage of the pig genome (Humphray *et al.*, 2005).

Table 1. FPC Database (Wellcome Trust Sanger Institute)

Library	Fingerprints	Complexity ^c
CHORI-242	103 762 ^a	6.3×
PigE BAC (Roslin)	73 971 ^a	4.0×
RPCI-44	61 104 ^b	4.0×
INRA	28 478 ^{a,b}	1.0×
TOTAL	267 826	15.3×

^a Wellcome Trust Sanger Institute: <http://www.sanger.ac.uk/Projects/S.scrofa/>

^b University of Illinois at Urbana-Champaign.

^c Based on 2.7 Gb genome size.

Table 2. BAC end sequencing results

Library	Passed reads	Paired ends (%)	Average GC (%)	Average length (bp)
CHORI-242 ^{a,b}	276 758	92	41	698
PigE BAC ^a	145 110	93	42	700
RPCI-44 ^b	71 847	87	40	521
INRA ^c	64 102	94	42	613
Total	557 898	BACs representing 13% of pig genome		

^a Wellcome Trust Sanger.

^b University of Illinois at Urbana-Champaign.

^c INRA.

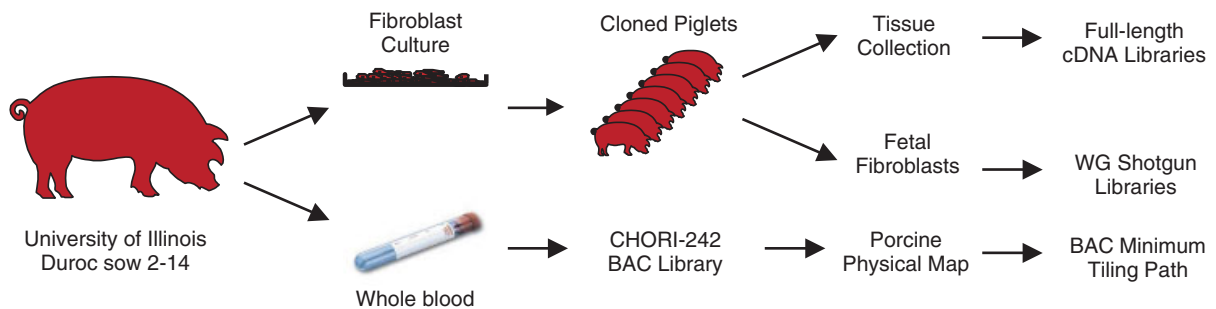


Figure 1. Schema for the production of autologous reagents for sequencing the porcine genome. Duroc sow 2–14 was selected as the donor of the DNA used to create the CHORI-242 BAC library. She has been ‘immortalized’ by the establishment of fibroblast cell cultures that have been successfully used for nuclear transfer. Fetal fibroblast cultures from cloned piglets have been transferred to the Sanger Institute and genomic DNA from these cell lines has been used to create whole-genome shotgun libraries. Tissues from embryos at various stages of gestation have also been collected for use in the construction of full-length cDNA libraries

The sequencing template

The majority of clones that have been fingerprinted and end-sequenced have come from the CHORI-242 BAC library. This library was constructed from a single female pig that was raised at the University of Illinois (Figure 1). To facilitate sequence assembly, efforts will be made to select as many CHORI-242 clones as possible for the BAC minimum tiling path. Additionally, the WGS libraries will be made from autologous DNA to further enhance sequence assembly between WGS reads and those from the BAC skim. Full-length cDNA libraries will also be constructed from tissues belonging to the original sow or her clones, providing autologous sequence for gene annotation.

Strategy for genomic sequencing

The strategy that we espouse for sequencing the pig genome combines the whole-genome shotgun (WGS) approach with skim sequencing of BAC clones selected to represent a minimum tiling path through the pig genome (Engler *et al.*, 2003; She *et al.*, 2004). We propose that a draft sequence of the pig genome with 6–7× genome coverage be produced by this hybrid approach. A draft sequence does not provide complete coverage of the entire genome; indeed, there are still gaps in the current ‘finished’ human genome sequence. One of the key strengths of the hybrid approach is that the resources (BAC clones) will be in place for targeted sequence closure in regions of interest. An important difference between the application

of this approach to the pig genome and its use for other species to date is that the porcine fingerprint map and BAC end sequence information will be completed before the sequencing project starts. Thus, it should be possible to determine a BAC tiling path from these two datasets, identifying a set of BACs with minimal overlap at the outset of the sequencing project. Current calculations predict that at most 25 000 BACs will need to be sequence-skimmed, since the human genome is approximately 2.9 GB and the pig genome is approximately 2.6 GB. This calculation is also supported by the increased size of the BAC inserts from 150 kb to a range of 160–180 kb, thus reducing the number of BACs to be sequence-skimmed. The project will then sequence 3× coverage and the remaining 3–4× coverage will come from whole-genome sequencing of 3 kb, 10 kb and 50 kb libraries. The sequence will be released into public databases as it is generated, and sequence traces will be deposited in the trace repositories hosted at NCBI and EBI. Sequence assemblies >2 kb will be deposited in the HTGS databases at NCBI and EMBL. It is anticipated that after the first year of sequencing, a draft 3× assembly of the genome will be released into public databases.

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