

Going Whole Hog

Deciphering the swine genome

Genome research is going to the hogs—and humans stand to benefit.

Researchers are stepping up efforts to sequence the swine genome, and its similarity to the human genome may mean potential advantages for people as well as pigs.

“The Agricultural Research Service sees the swine genome as a tool with which we can dramatically improve the efficiency of producing pork and maybe reduce the risk of disease in swine populations,” says Gary A. Rohrer, an animal geneticist at the Roman L. Hruska U.S. Meat Animal Research Center (USMARC) at Clay Center, Nebraska.

Rohrer is leading ARS’s swine genome research efforts with help from molecular biologist Dan J. Nonneman. As a member of the Swine Genome Sequencing Consortium (SGSC), an international coalition of government and university researchers formed in 2003 to advance swine genetic research, ARS is helping to sequence the swine genome and develop publicly available DNA-based tools.

Other members of the SGSC include the University of Illinois, the Alliance for Animal Genomics, the Wellcome Trust Sanger Institute in England, Scotland’s Roslin Institute, the Korean Livestock Institute, the Beijing Genome Institute, and France’s National Institute for Agricultural Research. The tools they develop could be used to guide future breeding decisions.

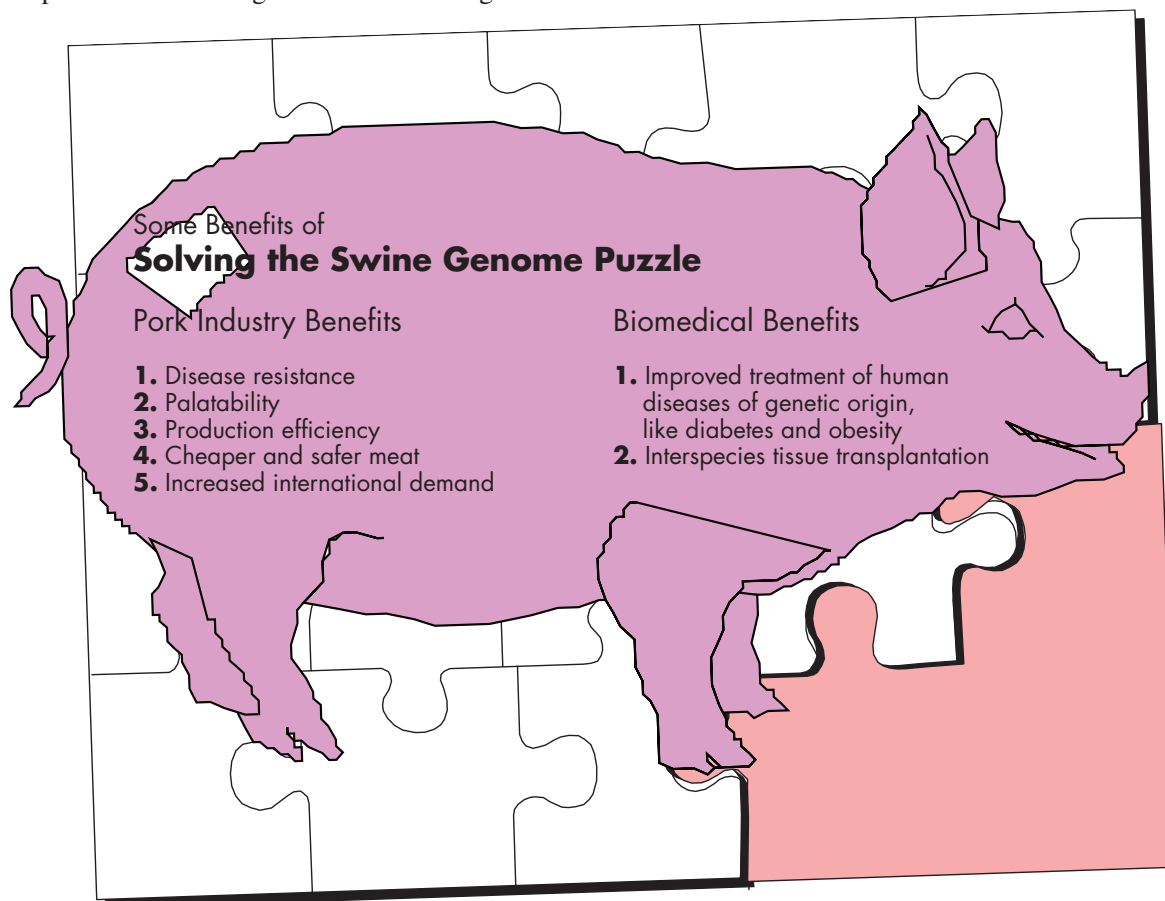
Since 2003, the SGSC has developed a bacterial artificial chromosome (BAC) map, which is useful for sequencing the pig genome and for comparing it to the human genome. The map is so named because bacterial chromosomes are used to package the animal’s DNA segments. The map can be seen at www.sanger.ac.uk/Projects/S_scrofa/.

Pick of the Litter

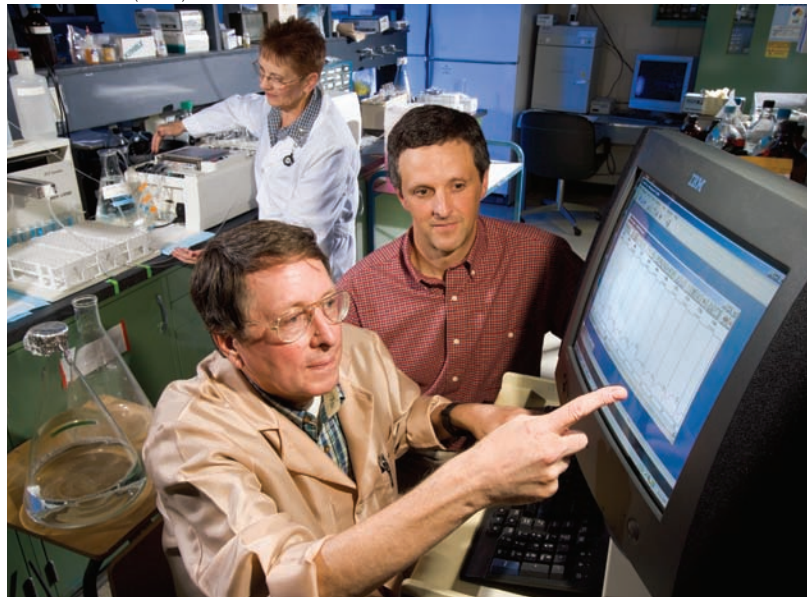
Earlier this year, USDA’s Cooperative State Research, Education, and Extension Service (CSREES) awarded the University of Illinois \$10 million to obtain a draft sequence of the swine genome.

The CSREES grant will fund a 2-year project that will enable researchers to identify genes that influence important traits and will help them develop new tools to identify and select pigs with desirable characteristics. The ability to select traits such as disease resistance, production efficiency, and palatability will enhance the competitiveness of U.S. pork in international markets, Rohrer says.

Over the past 15 years, the U.S. pork industry has steadily increased its exports. In 2005 the United States exported more than 1 million tons of pork, worth about \$2.6 billion. If the nation’s pork producers can improve their products and make them more desirable overseas, the industry will continue growing.



STEPHEN AUSMUS (D661-1)



While technician Pat Nuss prepares samples for analysis in the background, physiologist John Klindt (left) and geneticist Gary Rohrer evaluate plasma urea nitrogen data from pigs being studied to identify genetic factors affecting protein metabolism.

Which characteristics are considered the most desirable? The ideal swine population would yield cheaper, safer, tastier meat. The pigs would also be healthy, less susceptible to disease and stress, and efficient breeders, Rohrer says.

Earlier USMARC studies with Meishan pigs, which hail from southern China, demonstrate how this research could be used to improve selection decisions for future breeding programs.

With their wrinkled faces and dark pigment, these pigs look like a cross between a traditional American pig and a Shar-Pei dog. But their unusual appearance isn't the only difference between them and U.S. swine. The testes of male Meishans are 30-40 percent smaller than those of their U.S. counterparts, and they have fewer sperm-developing Sertoli cells. USMARC researchers identified the gene variation, or allele, responsible for these undesirable reproductive traits. The discovery could be used to benefit the U.S. commercial pig industry. Since many pigs are conceived through artificial insemination, prolific sperm production is a desirable trait.

"If we can identify genes that affect testes size or other important traits in our research population, we can look for similar forms of the gene in commercial pigs and use that information to guide breeding decisions," Nonneman says.

Of Pigs and Men

In addition to the many possible benefits for the pork industry, the project has biomedical potential.

"There's a lot of valuable information coming from the swine genome that may have implications for human health," Rohrer says.

Because the pig and human genomes are so similar, information gleaned from the swine genome sequencing effort could be useful to the human medical community. Pig and human genomes resemble one another in size, organization, and complexity. And pigs, like humans, are omnivores, so our diets and metabolisms are similar. This makes the pig genome a particularly apt candidate for biomedical research.

The most likely application of new genomic information is improved disease treatment for human medical problems that have a genetic component, such as obesity or diabetes. But more ambitious projects, such as interspecies tissue transplantation, could potentially develop in the future.

The Genomics Puzzle

The pig genome is the first mammalian genome to have a complete BAC map before being sequenced, Rohrer says. This is significant because it makes the sequencing much easier.

Previous genome sequencing efforts involving other organisms have used a "whole-genome shotgun" approach to assemble about 30 million sequencing reads, Rohrer says. The procedure is difficult and complicated, comparable to assembling a 30-million-piece jigsaw puzzle.

The SGSC had already identified more than 267,000 markers on the BAC map before the CSREES grant was awarded. This advantage allows the researchers to proceed in a more orderly fashion because they already know where most of the segments belong. This will be more like assembling 25,000 puzzles with 1,200 pieces each. The location in the pig genome of each puzzle is already known, so assembly should require less labor and computer processing time.

The researchers are pleased with their initial progress, Rohrer says, but the best is yet to come.

"We're still in the early stages of sequencing, but completing the entire genome will clear pathways for tremendous achievements in a number of different scientific fields," he says.—By **Laura McGinnis**, ARS.

This research is part of Food Animal Production, an ARS National Program (#101) described on the World Wide Web at www.nps.ars.usda.gov.

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