

Pig genome sequenced: Research could help combat animal and human disease

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A new analysis of pigs (left) and their ancestor-like cousins, the wild boars, reveals much about their evolutionary history, sensory perceptions and similarity to humans. Credit: Duroc (left): L. Brian Stauffer; Wild boar: Martien Groenen

The pig and its cousin the wild boar have much in common with humans. They are world travelers. They're adaptable, invasive and often damage their own habitat. They are easy to seduce (with food) and susceptible to domestication, but when conditions allow, they revert to a feral lifestyle.

A new [genomic analysis](#) reveals some new, unexpected and potentially beneficial similarities between pigs and humans, along with a few distinct differences. The International Swine Genome Sequencing Consortium – led by researchers at the University of Illinois, Wageningen University in the Netherlands and the University of

Edinburgh – conducted the analysis. Theirs is the most thorough genomic study yet conducted of the domestic pig and its wild boar counterparts.

A report of the study appears as the cover article in the November 15, 2012, issue of the journal *Nature*.

"It is exciting that the [genomic sequence](#) of the domestic pig now is in the public domain and available to enable more powerful approaches to [domestic swine](#) and pork improvement," said Ronnie Green, University of Nebraska Vice Chancellor for the Institute of Agriculture and Natural Resources and an early supporter of the pig genome sequencing project at the U.S. [Department of Agriculture](#). "It will also aid efforts to use the pig as a model for biomedical research and the improvement of human health."

"This new analysis helps us understand the [genetic mechanisms](#) that enable high-quality pork production, feed efficiency and resistance to disease," said Sonny Ramaswamy, the director of the U.S. Department of Agriculture's National Institute of Food and Agriculture. "This knowledge can ultimately help producers breed high-quality swine, lower production costs and improve sustainability."

The researchers compared the genome of a common farm pig, *Sus scrofa domestica*, with those of 10 wild boars – all from different parts of Europe and Asia. They also compared the pig genome with the human, mouse, dog, horse and cow genomes.

The team discovered new details of *Sus scrofa* evolution after the ancestors of the domestic pig, which most resembled today's wild boars, first emerged in Southeast Asia and gradually migrated across Eurasia.

Comparisons of Asian and European wild boars revealed significant

genetic differences, the result of their separating from one another roughly 1 million years ago, said University of Illinois Vice President for Research Lawrence Schook, a principal investigator on the study.

"They have been separated so long that the Asian and European lineages are almost sub-species now," Schook said. The European and Asian wild boars lost a lot of genetic diversity about 20,000 years ago, likely as a result of a global glaciation event.

Comparisons of domestic and wild pigs also "revealed a clear distinction between European and Asian breeds," the researchers wrote. This adds to the evidence that "pigs were independently domesticated in western Eurasia and East Asia."

"We had evidence from previous studies, but those studies focused on the mitochondrial DNA, a small DNA molecule only inherited from the mother," said Wageningen University professor Martien Groenen, also a principal investigator on the study. "With the complete genome sequence of multiple [wild boars](#) we now have a much clearer picture about these events."

"This understanding of the genetic origins of modern pigs is important as we breed pigs to meet growing demand more efficiently and to resist old and emerging diseases," said Alan Archibald, a professor at The Roslin Institute at the University of Edinburgh and a principal investigator on the study.

Some gene families are undergoing relatively fast evolution in the domestic pig, with immune genes and (perhaps not surprisingly) olfactory genes quickly expanding. The pig has more unique olfactory genes than humans, mice or dogs, the researchers report.

And while pigs can smell a world of things humans and many other

animals can't – think truffles – their sense of taste is somewhat impaired.

"Pigs have a high tolerance for eating things that have a lot of salt or that we would find repulsive by taste," Schook said.

Pigs have significantly fewer bitter taste receptor genes than humans, for example, and genes involved in perception of sweet and umami (which humans perceive as meaty) flavors are also different in pigs and humans, the researchers found.

"Understanding the genes that shape the characteristics of pigs can point to how and why they were domesticated by humans," Archibald said.

"Perhaps it was their ability to eat stuff that is unpalatable to us humans."

The new analysis also supports the use of the pig in studies of human diseases.

"In total, we found 112 positions where the porcine protein has the same amino acid that is implicated in a disease in humans," the researchers wrote.

By also sequencing the genomes of another 48 pigs, "we identified many more gene variants implicated in human disease, further supporting the pig as a valuable biomedical model," Groenen said.

Some of the protein aberrations [pigs](#) share with humans are associated with obesity, diabetes, dyslexia, Parkinson's disease and Alzheimer's disease, the researchers report.

The new analysis also has important implications for agriculture, particularly since the [domestic pig](#) still has an ancestor-like wild cousin on the loose, the researchers said. Unlike the domestic cow, whose

ancestors, the aurochs, are now extinct, the porcine lineage has a lot of genetic diversity remaining.

"We can easily go find genes that might be still in the wild that we could use for breeding purposes today," said Schook, who is the Gutgsell Professor of Animal Sciences, Bioengineering, Pathobiology, Nutritional Sciences, Pathology and Surgery at Illinois.

"This study demonstrates the benefits of basic genomic research on agricultural animals and their closest living relatives," said U. of I. President Bob Easter, who helped secure funding for the [pig genome](#) sequencing effort when he was the dean of the College of Agricultural, Consumer and Environmental Sciences at Illinois. "This work has important implications for agriculture, contributes to our understanding of evolution and will aid in human medicine," said Easter, who also is an emeritus professor of animal sciences and of nutritional sciences.

More information: Groenen et al. (2012) Pig genomes provide insight into porcine demography and evolution, *Nature*, [DOI: 10.1038/nature11622](https://doi.org/10.1038/nature11622)

Rubin et al. (2012) Strong signatures of selection in the domestic pig genome. *Proceedings of the National Academy of Sciences*, [DOI: 10.1073/pnas.1217149109](https://doi.org/10.1073/pnas.1217149109)

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