

Modern pigs found to have more wild boar genes than thought

September 1 2015, by Bob Yirka



Domestic pig. Credit: Scott Bauer, USDA

(Phys.org)—An international team of researchers has found that domesticated pigs in Europe have a lot more wild boar in them than has been thought. In their paper published in *Nature Genetics*, the team describes their genetic survey of a large number of domesticated pigs



and wild boars in both Europe and Asia.

The modern pig has become an icon of sorts, providing food and entertainment and sometimes fodder for jokes—but its origins appear to differ from what scientists have assumed for most of modern history—namely that pigs were domesticated approximately 9000 years ago and have been kept separate from their wild cousins, leading to the different-looking creature so familiar to us today.

In this new study, the researchers started out by collecting samples from 600 pigs and boars from a variety of locations in Europe and Asia, they then focused on a subset of those, eventually testing 103 whole genomes. Next, they combined their results with those from a prior study that had done a less through analysis on an additional 600 wild and domesticated pigs. To trace the lineage of the animals, the team conducted a Bayesian computation analyses, focusing on gene flow—which led to the development of models to describe the history of both pigs and boars.

In studying their data and models, the researchers concluded that modern pigs are not the result of isolated breeding, but instead are the result of cross breeding between domesticated pigs and wild boars over the span of many years—and some of those boar genes were not in the dataset at all, which suggest they might have been from a now extinct species. The data also supports the theory that pigs were actually first domesticated in two places, Asia and the Middle East. Pigs in Europe, the analysis indicates, first came from the Middle East, then were mixed with wild boars, and then were mixed again with pigs from Asia, resulting in what the researchers call the mutts of today.

As for why modern domesticated pigs do not look much like wild hogs, the researchers suggest it is due to selective breeding by early farmers—they tended to mate pigs with others that had traits they desired, which might have led to what they deem "islands of



domestication" which favored many traits in spite of the occasional crossbreeding with wild hogs.

More information: Evidence of long-term gene flow and selection during domestication from analyses of Eurasian wild and domestic pig genomes, *Nature Genetics* (2015) DOI: 10.1038/ng.3394

Abstract

Traditionally, the process of domestication is assumed to be initiated by humans, involve few individuals and rely on reproductive isolation between wild and domestic forms. We analyzed pig domestication using over 100 genome sequences and tested whether pig domestication followed a traditional linear model or a more complex, reticulate model. We found that the assumptions of traditional models, such as reproductive isolation and strong domestication bottlenecks, are incompatible with the genetic data. In addition, our results show that, despite gene flow, the genomes of domestic pigs have strong signatures of selection at loci that affect behavior and morphology. We argue that recurrent selection for domestic traits likely counteracted the homogenizing effect of gene flow from wild boars and created 'islands of domestication' in the genome. Our results have major ramifications for the understanding of animal domestication and suggest that future studies should employ models that do not assume reproductive isolation.

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