

Introgression in the pig genome leads to their altitude adaptation

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Scientists from Jiangxi Agricultural University, BGI and University of California published their latest research on genetic mechanism of pig altitude-adaptations in *Nature Genetics* online. Their research underlined the importance of introgression for the first time as a potential reason for pig adaptations to cold and hot environments, which provided novel insights into the evolutionary history of pigs and the role of introgression in adaptation more generally.

Pigs, as one of the earliest domesticated animals, were domesticated largely in Near East and China approximately 10,000 years ago. Since then, under the combined effects of natural selection and human-driven artificial selection, pigs evolved phenotypic diversity in appearance, fertility, growth, palatability, and local fitness. As the [genetic basis](#) of those adaptive evolution remained largely unexplored, scientists of this article conducted whole-genome sequencing and selective sweep analysis trying to figure out the genetic basis contributed to the adaptation of domesticated Chinese pig breeds, especially related to thermostatic regulation for varying-latitude environments.

In the current study, the scientists selected 69 pig individuals represented 11 geographically diverse breeds and 3 populations of wild boar from cold and hot environments in China. This is one of the first population genomics analyses to use high-coverage whole-genome sequencing in pigs, each individual has been sequenced more than 20-fold depth with the genome coverage of 95%. Totally, 41 million variants have been identified, with 21 million variants were absent from the dbSNP

database. Substantially, a nearly complete catalogue of the genetic variants has been compiled, which allowed the scientist to identify a genome-wide set of loci for local adaptation in Chinese [pigs](#).

From the genome wide scan, a set of gene loci correspond to thermostatic regulation has been identified. Notably, an exceptionally large (14 Mb) and low-recombination region on the X chromosome appeared to have two distinct haplotypes in the high- and low-latitude populations, which may be possibly responsible for [adaptations](#) to cold and hot environments respectively. Another surprising finding of this study was that the adaptive haplotype in the high-latitude populations was likely introduced from another divergent *Sus* species. This is the first example of [adaptive evolution](#) triggered by interspecies introgression in [domesticated animals](#), which gave us a clue that introgression event between divergent species may be an important resource for evolutionary adaptation and could largely facilitate this process.

Likai Mao, the project manager of BGI, said, "We found lots of loci could be related with environmental adaptation. When we noticed a big region with special pattern on the haplotype figure of chromosome X, we knew something must be there. "

Provided by BGI Shenzhen

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