Sequencing a mini-pig: The whole story

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The Wuzhishan miniature pig is one of 72 breeds native to China. New research published in BioMed Central and BGI's open access journal *GigaScience* provides the genome sequence of this rare mini-pig. An in-depth analysis of this sequence, along with comparison to human genes, has provided a wealth of knowledge for use in medical engineering and drug design.

Pigs are economically important as a food source, providing 40% of all meat consumed worldwide, and after years of evolving alongside humans (and eating human leftovers) have developed similar hearts, digestive systems and diet-related diseases, including obesity, cardiovascular disease and immunological diseases.

Their anatomical and physiological similarities to humans has led to their use in the study and treatment of human diseases. The Wuzhishan mini-pig has been inbred for generations, meaning that the animals are genetically very similar (homozygous) and any research is reproducible. This mini-pig can also been used to provide tissue for use in surgery and xenotransplantation (for example valve transplants), where its homozygosity means that the standard of clinical applications can be maintained.

In order to fully understand the special relationship between pigs and humans, researchers from the Beijing Institute of Animal Science (IAS), Chinese Academy of Agriculture Science (CAAS) and BGI-Shenzhen have sequenced and analysed the Wuzhishan mini-pig. Surprisingly for a pig with over 20 generations of inbreeding the level of polymorphic variation was high. But this variation was limited to a small percentage of the genome so that for most of the genome homozygosity was high.

The similarities between pigs and humans has a downside in that it might be possible for viruses to be transferred during transplantation. Dr Yutao Du from BGI and Prof.Shutang Feng from CAAS/IAS, explained, "Both humans and pigs carry viruses hidden within their genomes. One particular virus, porcine endogenous retrovirus (PER), once activated can infect human cells, however the genome sequence has revealed that a specific type PER virus (type C) has been lost from the mini-pig."

Dr Du and Prof Feng continued, "The physiological similarities to humans was maintained at a genetic level with 84% homology between the two species. While there was a great deal of similarity in genes known to be involved in coronary artery disease and drug target genes, detailed analysis showed that there were several important differences which need to be taken account of."

This *GiGaScience* article is part of a wider series of papers including the publication of pig genome sequences in *Nature*. The series covers varied topics including the structure and functioning of the pig genome, its annotation and the biomedical relevance of the findings, with publications in *BMC Biology*, *BMC Genomics*, *BMC Genetics*, *BMC Medical Genomics* and *BMC Cell Biology*.

More information: The sequence and analysis of an inbred pig genome Xiaodong Fang, Yulian Mu, Zhiyong Huang, Yong Li, Lijuan Han, Yanfeng Zhang, Yue Feng, Yuanxin Chen, Xuanting Jiang, Wei Zhao, Xiaoqing Sun, Zhiqiang Xiong, Lan Yang, Huan Liu, Dingding Fan, Likai Mao, Lijie Ren, Chuxin Liu, Juan Wang, Kui Li, Guangbiao Wang, Shulin Yang, Liangxue Lai, Guojie Zhang, Yingrui Li, Jun Wang, Lars Bolund, Huanming Yang, Jian Wang, Shutang Feng, Songgang Li and Yutao Du *GigaScience*, 2012 1:16 doi:10.1186/2047-217X-1-16

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Genomic data from the Wuzhishan inbred pig (Sus scrofa). Fang, X; Huang, Z; Li, Y; Feng, Y; Chen, Y; Jiang, X; Yang, L (2012): *GigaScience*. dx.doi.org/10.5524/100031

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