Mini-pig tale provides trove of genomic data for human health

The international open-access journal *GigaScience* (a BGI and BioMed Central journal) has recently announced the publication of the whole-genome sequencing and analysis of the Wuzhishan Pig, an extensively inbred, miniature pig, which can serve as an excellent model for human medical research. The availability of the mini-pig genome provides a wealth of genetic tools that will enable detailed and well thought-out analyses on an animal that shares a substantial number of complex diseases with humans. The work here, led by researchers from the BGI, Beijing Institute of Animal Science (IAS), and Chinese Academy of Agriculture Science (CAAS), also revealed potentially actionable resources including the identification of the porcine counterparts of human drug target genes.

Pigs are one of the oldest domesticated livestock species, and as well as providing one of the largest sources of meat worldwide, also provide important medical industrial resources, such as pharmaceutical-grade heparin and heart valves for xenotransplantation. The pig shares many of the same complex genetic diseases as humans, making them excellent models for studying the underlying biology of human disease. Furthermore, the similarity of the pig diet and digestive system with humans makes them ideal for investigation of metabolic diseases and nutritional analyses. The Wuzhishan pig used in this study provides additional advantages for medical analysis: its small size makes it easy to handle; and its long history of inbreeding have resulted in a breed of pigs made up of individuals that are genetically very similar, allowing greater reproducibility in scientific analyses.

To provide the best understanding of the genetics of the Wuzhishan pig and tools for laboratory studies, the researchers at the BGI in collaboration with scientists from several institutions in China and Denmark, carried out whole genome sequencing. They obtained a genome sequence of exceptionally high quality and used this to assess genomic structure and functional elements and investigate characteristics that would be of great interest for medical studies.

In particular, they looked at genes and protein domains that were the pig counterpart of human genes that are important for therapeutic drug activity. These analyses showed that the Wuzhishan pig genome contained a very large number of similar drug target genes for several types of human disorders, indicating that this pig would serve as an excellent model for drug testing in these cases. However, the researchers also found that there were several situations where target genes showed important differences from the human versions. This information is of great use as well, as it provides a clear indication of the types of drug testing for which this organism is not as useful, saving unnecessary experimentation, time, and money.

Lead researchers Dr Yutao Du and Prof Shutang Feng note that, "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."

The scientists also assessed the presence of viruses integrated into the genome, which is a concern given that pigs have been considered as a possible source of xenotransplantation and thus viruses could be transferred to the human patients through transplantation.

Drs Du and Feng noted that the viral analyses provide tools and information for investigating such concerns by allowing more direct assessment of the risk of transmission. They explained that, "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."

Overall, the extensive amount of work in this study serves as a springboard for more economical and directed means of carrying out biomedical analyses and also provides a new resource for investigation of economically important traits, domestication events, and the evolution of this group of animals.

The sequence and analysis of an inbred pig genome [1]
[1]
Genomic data from the Wuzhishan inbred pig [2]

Source: GigaScience [3]

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