

Researchers unravel the relation between DNA methylomes and obesity

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In a highlighted paper published online in *Nature Communications*, researchers from Sichuan Agricultural University and BGI reported the atlas of DNA methylomes in porcine adipose and muscle tissues, providing a valuable epigenomic source for obesity prediction and prevention as well as boosting the further development of pig as a model animal for human obesity research.

Obesity could be considered as an epidemic that presents a risk to human health in modern society. It has become an important risk factor for a number of [chronic diseases](#), including diabetes, cardiovascular diseases and cancer. It is predicted that by 2030, about 58% of the world's [adult population](#) might be either overweight or obesity, revealing the severe situation of [obesity epidemic](#).

To meet this challenge, researchers worldwide are contributing tremendous efforts on hunting for obesity genes. "Although DNA sequence contains all the information to make who we are, many of the details of our behavior and appearance are actually determined by gene regulation." said Professor Mingzhou Li from Sichuan Agricultural University, "In order to advance obesity research, it is necessary to understand the epigenetic factors, especially DNA methylation, which plays a important role in obesity development."

In this study, researchers took pig as a model. Three breeds of pig were selected, including the Landrace, the Tibetan and the Rongchang pig, to investigate the systematic association between DNA methylation and

obesity. The pig is an exceptional restenosis model, and is emerging rapidly as a biomedical model for [energy metabolism](#) and obesity in human because of their similarities on metabolic features, cardiovascular systems, and proportional organ sizes.

Adipose tissues (ATs) and skeletal muscle tissues (SMTs) are known to play important roles in the pathogenesis of obesity. Researchers in this study sampled eight ATs and two SMTs from each of the three pig breeds living in comparable environments. 180 methylated DNA immunoprecipitation libraries were developed from the samples, after sequencing with MeDIP-Seq method and data processing, 1,381 Gb data were generated. Based on the epigenomic data, researchers constructed a genome-wide DNA methylation map as well as a [gene expression](#) map for adipose and muscle studies.

Through further analysis, researchers found the different methylated regions in promoters, which play a more important role in regulating gene expression and were highly associated with obesity development. Honglong Wu, Project Manager of this project at BGI, said, "We also found that the methylation pattern of IAD (intermuscular adipose) is more similar with that of the VATs (visceral ATs). This finding provides the first epigenomic evidence for IAD as a candidate risk factor for obesity."

Ruiqiang Li, Principal Investigator of this project from Peking University, said, "The work reports the largest dataset of directly sequenced animal DNA methylomes to date, and will serve as a valuable resource for future functional validation, promoting further development of pig as a model organism for [human obesity](#) research, as well as maximizing the economic benefits in producing high quality pork."

Professor Xuewei Li from Sichuan Agricultural University, said, "Based on the genomic data associated with [DNA methylation](#), we conducted a

comprehensive genome-wide epigenetic survey on ATs and SMTs. I believe our results will lay a solid foundation for exploring epigenetic mechanisms of adipose deposition and muscle growth in the future."

Professor Jun Wang, Executive Director of BGI, said, "Environmental factors can have influences on the way our genes are expressed, making even identical twins different. Rapid advances in the field of epigenetics provide a robust tool for studying gene expression and regulation. Understanding the genetic mechanism of [obesity](#) will have a great implication in future development of treatment and therapy."

Provided by BGI Shenzhen

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