

Lessons from epigenome evolution: Exploring the epigenome's regulatory function

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Sheng Zhong, of the Institute for Genomic Biology and Department of Bioengineering at the University of Illinois. Zhong and his lab study causal relationships between gene regulation and cellular behaviors, by developing computational and experimental methods on network modeling, stem cell engineering, epigenomic and single-cell analyses. Recently he has contributed to introducing "comparative epigenomics" -- using cross-species epigenomic comparison to annotate the genomes. Credit: Photo by Kathryn Coulter, courtesy of Institute for Genomic Biology

The sequencing of the human genome has provided a wealth of genetic information, yet the goal of understanding the function of every gene remains outstanding. New research from the University of Illinois published in *Cell* suggests determining the purpose of genes through a new method they call "comparative epigenomics."

"Comparative epigenomics is to use [interspecies](#) comparison of [DNA](#) and histone modifications—as an approach for annotation of the regulatory genome," says Sheng Zhong, of the Institute for Genomic Biology and Department of Bioengineering at the University of Illinois.

While the genome of an organism contains all its [genes](#), it is the epigenome that decides which are expressed, or "turned on." Though genomic science has long focused on comparative genomics—comparing the genomes of similar species and finding the commonalities to determine how common traits are regulated—comparative epigenetics provides a more in-depth look at regulatory functions.

The researchers, led by Zhong, in collaboration with Ting Wang at Washington University, Harris Lewin, and Franklin West at University of Georgia, focused their work on three species: humans, mice, and pigs. By analyzing 9 epigenomic marks in pluripotent stem cells, they were able to create an epigenomic map for each which they could then compare.

The team concluded that, with proper analysis procedures, traces of interspecies epigenomic conservation could be identified. They then demonstrated that the conserved epigenetic markers can be effectively used to annotate the genome, clarifying the genome's regulatory function.

Understanding the genome is one of the most pressing problems for science, and this study sheds light on a promising alternative method.

"Comparative epigenomics enables us to find more clues from evolution about the functions of our genomes," adds Zhong.

More information: "Comparative Epigenomic Annotation of Regulatory DNA," Shu Xiao, Dan Xie, Xiaoyi Cao, Pengfei Yu, Xiaoyun Xing, Chieh-Chun Chen, Meagan Musselman, Mingchao Xie, Franklin D. West, Harris A. Lewin, Ting Wang, Sheng Zhong. [doi:10.1016/j.cell.2012.04.029](https://doi.org/10.1016/j.cell.2012.04.029) (volume 149 issue 6 pp.1381 - 1392)

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