Epigenetic research uncovers new targets for modification enzymes

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Enzymes regulating genetic expression can be just as important as the genome itself, increasing evidence shows. The expanding field of epigenetics focuses on the multiple influences on DNA and surrounding molecules that determine whether genes are turned on or off during development and disease processes.

A consortium of scientists, led by Albert Jeltsch at Jacobs University, Breman, Germany, Yoichi Shinkai at Kyoto University, Japan, and Xiaodong Cheng at Emory University, has now discovered new non-histone targets for one enzyme previously believed to modify only histones--the group of proteins that creates tightly bundled packages of DNA strands. The research is reported online in the journal *Nature Chemical Biology*.

These modification enzymes, called protein methyltransferases, add methyl groups to lysine amino acids within the histones and change their influence on gene expression. The newly identified non-histone targets add yet another influence on gene expression in addition to the already-known DNA methylation and histone modifications in the epigenome.

The international research team has found that a histone methyltransferase called G9a adds methyl groups to other proteins in addition to histones and changes the behavior of those proteins. The researchers used a peptide array technology called SPOT to identify the new enzyme targets.

"This discovery broadens our view of methyltransferases and tells us that epigenetic regulation in cells is even more complicated than we thought," says principal investigator Xiaodong Cheng, PhD, professor of biochemistry at Emory University School of Medicine and a Georgia Research Alliance Eminent Scholar.

"We have known for some time that we had a great deal more to discover about methyltransferases. This is an important piece of the puzzle, and additional research will continue to help us unwind the multiple mechanisms involved in epigenetic gene regulation."

Source: Emory University