

Epigenetic signals differ across alleles

February 12 2010

Researchers from the Institute of Psychiatry (IoP), King's College London, have identified numerous novel regions of the genome where the chemical modifications involved in controlling gene expression are influenced by either genetic variation or the parental origin of that particular stretch of DNA. This contradicts previous assumptions that epigenetic signals are generally equal across both copies of a given region of the genome, except at a small number of known imprinted genes.

Sequencing the [genome](#) was only the first step in our quest to understand how genes are expressed and regulated. Epigenetics is the study of alterations to gene function, traditionally believed to occur independently of the DNA sequence. The epigenome sits above the DNA sequence and provides a second layer of information, regulating several genomic functions, including when and where genes are turned on or off. One of the best understood epigenetic mechanisms is [DNA methylation](#), a chemical modification to DNA that can interfere with [gene expression](#).

In the first quantitative genomic survey of allele-specific DNA methylation, published 11 February 2010 in The [American Journal of Human Genetics](#), scientists used sensitive high-throughput technology to detect evidence for skewed gene DNA methylation across both alleles - or copies - of the DNA sequence at almost 1 million positions in the genome.

Lead researcher Dr Jonathan Mill, Medical Research Council Social Genetic, Developmental and Psychiatry Centre at the IoP said:

"Interestingly, we found numerous examples where DNA methylation was not equal across alleles - in some instances this depended upon genotype, and in other cases it depended upon which parent that allele was inherited from.

He continues: "Our data show that allele-specific DNA methylation is a widespread phenomenon with potentially over 35,000 such sites occurring across the genome. It appears that a spectrum of skewing is likely, differing between individuals and across tissues.

Dr Mill concludes: "These findings impact upon our understanding about the origin of biological variation and have implications for genetic studies of complex disease including most psychiatric conditions. Because DNA methylation can also be influenced by various environmental factors, the variation we have uncovered provides a potential substrate for interactions between nature and nurture."

More information: Allelic Skewing of DNA Methylation Is Widespread across the Genome is published in AJHG (The American Journal of Human Genetics) and can be accessed here: [www.cell.com/AJHG/abstract/S0002-9297\(10\)00017-0](http://www.cell.com/AJHG/abstract/S0002-9297(10)00017-0)

Provided by King's College London

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