New tool probes gene regulation

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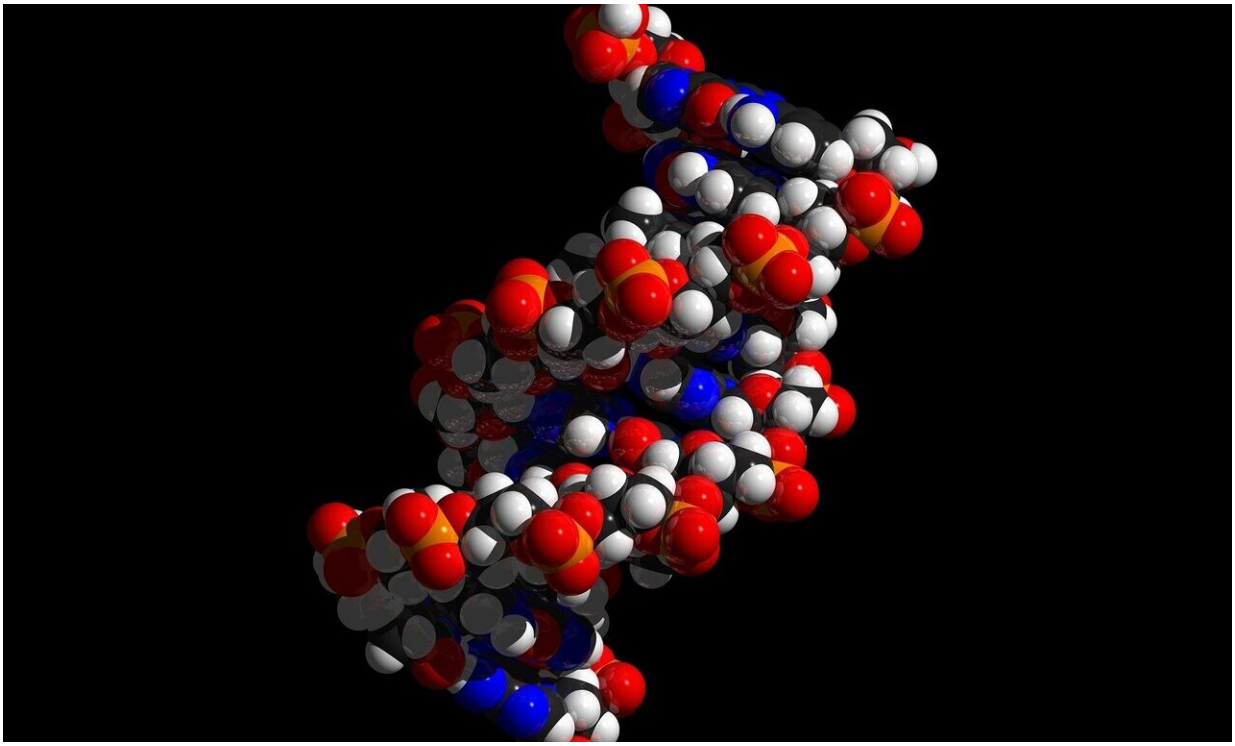

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DNA methylation (DNAme) is a modification of the genome—an epigenetic "mark"—that is required for proper cellular differentiation. It has been implicated in the regulation of gene expression, but its role in this stepwise process is poorly understood.

Emily Hodges, Ph.D., graduate student Kelly Barnett and colleagues

have developed a new tool, ATAC-Me, to simultaneously measure DNAme and chromatin accessibility in the same population of DNA molecules. The researchers used ATAC-Me to probe the differentiation of white blood cells from monocytes to macrophages.

They identified waves of chromatin accessibility occurring rapidly across thousands of enhancers (regions of DNA involved in regulating gene expression). They also found unexpected prolonged methylation states at a majority of the sites, challenging the long-held belief that DNA methylation is a barrier to gene activation.

The studies, reported in *Molecular Cell*, highlight the value of ATAC-Me for exploring the role of DNA methylation in gene regulation.

More information: Kelly R. Barnett et al. ATAC-Me Captures Prolonged DNA Methylation of Dynamic Chromatin Accessibility Loci during Cell Fate Transitions, *Molecular Cell* (2020). DOI: 10.1016/j.molcel.2020.01.004

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